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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:38:06 ; Search time 67.441 Seconds
(without alignments)
703.621 Million cell updates/sec

Title: US-10-665-658-2
Perfect score: 560
Sequence: 1 DIQMTPSPSLASVGVDRVT.....QQHNEYPLTFGGQTKVEIKR 108

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	560	100.0	108	2	AAW62017	AAW62017 Light cha
2	560	100.0	108	2	AAW63529	AAW63529 Humanised
3	560	100.0	108	3	AAW82343	AAW82343 Humanised
4	560	100.0	108	8	ADG38990	ADG38990 Humanised
5	560	100.0	108	8	ADRO3365	ADRO3365 Humanised
6	560	100.0	108	8	ADM38457	ADM38457 CD11a lig
7	560	100.0	108	8	ADX80645	ADX80645 Humanized
8	560	100.0	214	8	ADP11669	ADP11669 anti-CD11
9	546.5	97.6	109	2	AAW29449	AAW29449 Human lig
10	546.5	97.6	109	3	AAW77752	AAW77752 Human lig
11	546.5	97.6	109	3	AAW30309	AAW30309 Human lig
12	546.5	97.6	109	6	ABU13786	ABU13786 Human lig
13	546.5	97.6	109	6	ABU59499	ABU59499 Human lig
14	546.5	97.6	109	7	AAE39082	AAE39082 Human lig
15	512	91.4	240	4	AAW46020	AAW46020 Human MUC
16	506	90.4	108	2	AAW70622	AAW70622 Human con
17	506	90.4	108	3	AAW82345	AAW82345 Human con
18	506	90.4	108	5	ABP61191	ABP61191 Human ant
19	506	90.4	108	8	ADG38991	ADG38991 Human con
20	506	90.4	108	8	ADRO3366	ADRO3366 Human sub
21	506	90.4	108	8	ADP79572	ADP79572 Human kap
22	506	90.4	109	8	AAU74544	AAU74544 Human sub
23	506	90.4	109	9	AEA38745	AEA38745 Human VL
24	506	90.4	110	5	AAE28149	AAE28149 Human con

25	505	90.2	127	4	AAU09917	AAU09917 Light cha
26	505	90.2	127	5	ABG75526	ABG75526 Humanised
27	505	90.2	233	7	ADL23195	ADL23195 Human ant
28	504	90.0	109	2	AAW40956	AAW40956 Human ger
29	503	89.8	240	4	AAW45991	AAW45991 Human MUC
30	502	89.6	108	9	ADM04801	ADM04801 PAP-A-1m
31	501	89.5	107	4	AAW62087	AAW62087 Human VL
32	501	89.5	107	4	AAW60400	AAW60400 Consensus
33	501	89.5	107	4	AAW61585	AAW61585 Human var
34	501	89.5	107	8	ADE71454	ADE71454 Human ant
35	501	89.5	107	8	ADJ88008	ADJ88008 Human var
36	501	89.5	107	8	ADN12054	ADN12054 Variable
37	501	89.5	107	8	ADP43328	ADP43328 Human mon
38	501	89.5	108	6	ABJ18679	ABJ18679 Antibody
39	501	89.5	109	2	AAW27543	AAW27543 Human Ab
40	501	89.5	240	4	AAW46004	AAW46004 Human MUC
41	489	89.1	130	3	AAW56737	AAW56737 Human act
42	489	89.1	234	7	ADM47073	ADM47073 Mouse ant
43	499	89.1	240	4	AAW45993	AAW45993 Human MUC
44	497	88.8	108	8	ADG36411	ADG36411 Intracell
45	497	88.8	108	9	AEA41087	AEA41087 Germiline

ALIGNMENTS

RESULT 1
AAW62017
ID AAW62017 standard; peptide; 108 AA.
AC AAW62017;
DT 01-OCT-1998 (first entry)
DE Light chain variable region of humanised anti-CD11a antibody.
XX Complementarity determining region; light chain variable region;
XX humanised antibody; MHM24P(ab)-8; anti-CD11a antibody;
XX human CD11a I domain; MHM24 epitope; alpha subunit;
XX lymphocyte function-associated antigen 1; LFA-1; immunoassay;
XX in vivo imaging; diagnosis; CD11a-associated disease.
XX Muc sp.
XX Homo sapiens.
OS
OS
PN W09823761-A1.
PD 04-JUN-1998.
XX
PF 20-OCT-1997; 97WO-US019041.
XX
PR 27-NOV-1996; 96US-00757205.
XX
XX (GETH) GENENTECH INC.
PI Jardieu PM, Presta LG;
PI WPI; 1998-322737/28.
DR New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
XX also to treat conditions such as immunological or inflammatory disease.
XX
XX Claim 9; Page 48; 66pp; English.
XX The present sequence represents the light chain variable region of a
XX humanised anti-CD11a antibody that binds specifically to the human CD11a
XX I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte
XX function-associated antigen 1 (LFA-1) from any mammal. The humanised anti
XX -CD11a antibodies are used to determine presence of CD11a in usual
XX immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-
XX associated diseases (typically immune responses and inflammation such as
XX psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
XX leukaemia, etc

XX SQ Sequence 108 AA; 100.0%; Score 560; DB 2; Length 108;
 Query Match Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPS 60
 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPS 60

DB 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPS 60
 61 RFSGSGSTDPFTLTISLQPEDFATYYCQQHNEYPPLTFGGTKVEIKR 108
 61 RFSGSGSTDPFTLTISLQPEDFATYYCQQHNEYPPLTFGGTKVEIKR 108

Db 61 RFSGSGSTDPFTLTISLQPEDFATYYCQQHNEYPPLTFGGTKVEIKR 108

RESULT 2
 AAM63529 standard; protein; 108 AA.
 ID AAM63529
 AC AAM63529;
 DT 06-OCT-1998 (first entry)
 DE Humanised MEM24 light chain.
 XX Antibody mutant production; species-dependent antibody; malignancy;
 XX infection; haematopoiesis; lymphocyte function-associated antigen-1;
 XX intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 XX autoimmune disease; transplant rejection; tumour cell invasion;
 XX human immune deficiency virus infection; light chain.
 OS Synthetic.
 XX WO9823746-A1.
 XX 04-JUN-1998.
 XX 29-OCT-1997; 97WO-US020169.
 XX 27-NOV-1996; 96US-00756150.
 XX (GETH) GENENTECH INC.
 XX Jardiou PM, Presta LG;
 XX WPI; 1998-322726/28.
 XX Mutants of species-dependent antibodies with affinity for non-human
 XX mammalian antigen - greater than for parent antibody, particularly used
 XX for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 XX directed against CD11a.
 PS Disclosure; Page 53; 71pp; English.
 XX This sequence represents the light chain of the humanised antibody MEM24,
 XX and was used to produce a mutant of the invention. The mutants are of a
 XX species-dependent antibody (Ab), and have an amino acid substitution in a
 XX variable region of the Ab, and binding affinity for an antigen (Ag) from
 XX a non-human mammal at least 10 times stronger than for the wild type Ab
 XX against the Ag. The mutant antibodies are particularly intended for
 XX administration to a non-human mammal in preclinical studies (e.g. of
 XX infection, immunity, haematopoiesis or transplantation). They can also be
 XX used diagnostically (to identify specific proteins) or therapeutically,
 XX e.g. where directed against CD11a (lymphocyte function-associated antigen
 XX -1) or intercellular adhesion molecule-1 against a wide variety of
 XX inflammatory or autoimmune diseases, malignancies, transplant rejection,
 XX human immune deficiency virus infection and tumour cell invasion.
 XX Conversion to the mutant form allows useful antibodies to be produced
 XX from antibodies which normally have affinity for non-human analogues of
 XX the Ag too low to be of any use
 XX Sequence 108 AA;

XX SQ Sequence 108 AA; 100.0%; Score 560; DB 2; Length 108;
 Query Match Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPS 60
 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPS 60

DB 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPS 60
 61 RFSGSGSTDPFTLTISLQPEDFATYYCQQHNEYPPLTFGGTKVEIKR 108
 61 RFSGSGSTDPFTLTISLQPEDFATYYCQQHNEYPPLTFGGTKVEIKR 108

Db 61 RFSGSGSTDPFTLTISLQPEDFATYYCQQHNEYPPLTFGGTKVEIKR 108

RESULT 3
 AAY82343 standard; protein; 108 AA.
 ID AAY82343
 AC AAY82343;
 DT 22-JUN-2000 (first entry)
 DE Humanised anti-CD11a antibody light chain variable region SEQ ID NO:2.
 XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 XX antitumour; antiviral; inflammation; immunological response; LFA-1;
 XX lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 XX inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 XX viral infection; transplant rejection; graft rejection.
 OS Homo sapiens.
 XX Mus sp.
 XX US6037454-A.
 XX 14-MAR-2000.
 XX 20-NOV-1997; 97US-00974899.
 XX 27-NOV-1996; 96US-0031971P.
 XX (GETH) GENENTECH INC.
 XX Jardiou PM, Presta LG;
 XX WPI; 2000-282241/24.
 XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 XX inflammation and transplant rejection, contains human heavy variable
 XX region complementarily determining regions.
 PS Claim 5; Fig 1; 38pp; English.
 XX The present invention describes a humanised anti-CD11a antibody (Ab) that
 XX binds specifically to the human CD11a I-domain. The Ab has anti-
 XX inflammatory, immunosuppressant, antitumour and antiviral activities. The
 XX Ab blocks lymphocyte adhesion associated antigen (LFA-1) which is
 XX involved in leucocyte adhesion associated with inflammatory and
 XX immunological responses. The Ab are used: (i) optionally when coupled to
 XX a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 XX function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 XX inflammatory bowel disease, eczema, systemic lupus erythematosus,
 XX rhinitis, leukaemia, viral infections and many others, also for
 XX inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 XX tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 XX to active anticancer agent; and (v) for affinity chromatography. The Ab
 XX retain about the same activity in adhesion and mixed lymphocyte response
 XX assays as the murine antibodies from which they are derived. The murine
 XX anti-CD11a antibody MEM24 has IC50 0.09 nM for preventing adhesion
 XX between Jurkat cells (expressing LFA-1) and normal epidermal
 XX keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 XX The fully humanized version of MEM24 had IC50 0.13 nM. The present
 XX sequence represents the light chain variable region of the humanised anti

CC -CD11a Ab
 XX Sequence 108 AA;
 SQ Query Match 100.0%; Score 560; DB 3; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTITCRASKTISKYLAAYQKPKAPKLLIYSGSTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVDRTITCRASKTISKYLAAYQKPKAPKLLIYSGSTLQSGVPS 60

QY 61 RFGSGSGGTDFTLTITSLQPEDPATYYCOQHNEYPLTFQGTKEIKR 108
 DB 61 RFGSGSGGTDFTLTITSLQPEDPATYYCOQHNEYPLTFQGTKEIKR 108

RESULT 4
 ADG38990
 ID ADG38990 standard; protein; 108 AA.
 AC ADG38990;
 DT 26-FEB-2004 (first entry)
 XX
 DE Humanised Mouse anti-CD11a antibody light chain variable region.

XX Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
 KM VL; cluster of differentiation 11a; mixed lymphocyte response assay;
 KM Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 KM ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 KM psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 KM rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KM diabetes mellitus; prodrug activating enzyme; humanised.
 XX Synthetic.
 OS Mus sp.
 XX
 PN US2003207336-A1.
 PD 06-NOV-2003.
 XX
 PF 28-FEB-2001; 2001US-00795798.
 XX
 PR 27-NOV-1996; 96US-0031971P.
 PR 20-NOV-1997; 97US-00974899.
 PR 20-OCT-1999; 99US-00420745.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-051511/05.
 XX
 PT Humanized anti-CD11a antibody useful for treating lymphocyte function-
 PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 PS
 PS Claim 9; SEQ ID NO 2; 43bp; English.

The invention relates to a Humanised anti-cluster of differentiation
 (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 inhibition (IC50) (nm) value of not more than 1 nM in mixed lymphocyte
 response assay or for preventing adhesion of Jurkat cells to normal human
 epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 -1. Also included are a kit comprising the antibody and instructions for
 use to detect the CD11a protein, an isolated nucleic acid encoding the
 antibody, a vector comprising the nucleic acid, a host cell comprising
 the vector and producing the antibody by culturing the cell so that the
 antibody is expressed. The antibody binds to epitope MM24 on CD11a. The
 antibody is useful for determining the presence of CD11a protein and for
 treating lymphocyte function-associated antigen 1 mediated disorder such

CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is the light chain variable region (VL) of the humanised
 CC mouse anti-CD11a I domain monoclonal antibody MM24.
 XX
 SQ Sequence 108 AA;
 Query Match 100.0%; Score 560; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.9e-33;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDRTITCRASKTISKYLAAYQKPKAPKLLIYSGSTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVDRTITCRASKTISKYLAAYQKPKAPKLLIYSGSTLQSGVPS 60

QY 61 RFGSGSGGTDFTLTITSLQPEDPATYYCOQHNEYPLTFQGTKEIKR 108
 DB 61 RFGSGSGGTDFTLTITSLQPEDPATYYCOQHNEYPLTFQGTKEIKR 108

RESULT 5
 ADR03365
 ID ADR03365 standard; protein; 108 AA.
 AC ADR03365;
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MM24 F(ab)-8 antibody variable light chain protein.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KM rhinovirus infection; inflammatory skin disease; psoriasis;
 KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculosis; sarcoidosis; polymyositis;
 KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KM skin hypersensitivity disorder; poison ivy; poison oak;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD11a monoclonal antibody; MM24; variable light chain;
 KM VL; murine; human; fusion protein.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 PD 29-JUL-2004.
 XX
 PF 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 PS Example; SEQ ID NO 2; 54bp; English.

The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful

for treating and preventing infectious diseases such as human immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin disease such as psoriasis, inflammatory bowel diseases such as Crohn's disease and ulcerative colitis, adult respiratory distress syndrome, allergic diseases such as eczema and asthma, autoimmune diseases such as rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes mellitus, Reynaud's syndrome, immunological diseases such as tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary disease (COPD), CNS inflammatory disorder, skin hypersensitivity disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is humanised murine anti-human CD11a monoclonal antibody (MH24) Flab)-8 variable light chain protein. This sequence is used in the exemplification of the invention.

Sequence 108 AA;

Query Match 100.0%; Score 560; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHQKPKAPKLLIYSGSTLQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHQKPKAPKLLIYSGSTLQGVPS 60
QY 61 RPSGSGSGTDFLTITSSLOPEDPATYTCQHNHEVPLTFGQTKVEIKR 108
DB 61 RPSGSGSGTDFLTITSSLOPEDPATYTCQHNHEVPLTFGQTKVEIKR 108

RESULT 6

ADM38457
ID ADM38457 standard; protein; 108 AA.

ADM38457;

DT 24-MAR-2005 (first entry)

DE CD11a light chain variable region #2.

KW monoclonal antibody; CD11a; light-chain variable region;
XX heavy-chain variable region.

OS Homo sapiens.

PN CN1439651-A.

PD 03-SEP-2003.

PF 20-FEB-2002; 2002CN-00110866.

PR 20-FEB-2002; 2002CN-00110866.

PA (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.

PI Wang H, Wang J;

DR WPI; 2004-169719/17.

PT Recombinant human CD11a monoclonal antibody and its preparation and
XX medicinal composition.

PS Claim 1, Page 14; 16pp; Chinese.

XX The present invention relates to a recombinant monoclonal antibody for
CC human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
CC No.5 in light-chain variable region and the amino acid sequence shown by
CC SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
CC bioactivity and the expression in host cell are greatly increased. The
CC DNA molecule for coding the antibody, its preparation process and the
CC medicinal composition containing it are also disclosed. The present
CC sequence represents a light chain variable region of human CD11a.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 560; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHQKPKAPKLLIYSGSTLQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHQKPKAPKLLIYSGSTLQGVPS 60
QY 61 RPSGSGSGTDFLTITSSLOPEDPATYTCQHNHEVPLTFGQTKVEIKR 108
DB 61 RPSGSGSGTDFLTITSSLOPEDPATYTCQHNHEVPLTFGQTKVEIKR 108

RESULT 7

ADX80645
ID ADX80645 standard; protein; 108 AA.

ADX80645;

DT 05-MAY-2005 (first entry)

DE Humanized CD11a variable light chain amino acid sequence, seq id 5.

KW Protein purification; leaching; protein A affinity chromatography; CD11a;
XX antibody.

OS Synthetic.

PN US2005038231-A1.

PD 17-FEB-2005.

PF 24-JUN-2004; 2004US-00877532.

PR 28-JUL-2003; 2003US-0490500P.

PA (GETH) GENENTECH INC.

PI Fahrner RL, Laverdiere A, McDonald PJ, O'leary RM;

DR WPI; 2005-172327/18.

PT Purifying a protein, e.g. antibody or immunoadhesin, comprises reducing
XX the temperature of a composition subjected to protein A affinity
XX chromatography to 3-20 degrees C, where protein A leaching is reduced.

PS Disclosure; SEQ ID NO 5; 27pp; English.

XX The invention relates to a method of purifying a protein which comprises
CC a CH2/CH3 region by protein A affinity chromatography. The method
CC involves reducing the temperature of a composition comprising the protein
CC and one or more impurities subjected to protein A affinity chromatography
CC to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably
CC the protein is antibody. The antibody is selected from Trastuzumab,
CC humanized 2C4, humanized CD11a antibody, and humanized VEGF antibody.
CC Preferably, the antibody binds HER2 antigen, where the antibody is
CC Trastuzumab or humanized 2C4. The protein is an immunoadhesin,
CC specifically a TWE receptor immunoadhesin. The methods are useful for
CC purifying a protein, which comprises a CH2/CH3 region by protein A
CC affinity chromatography and for reducing leaching of protein A during
CC protein A affinity chromatography. The current sequence represents the
CC variable light chain amino acid sequence of CD11a.

Sequence 108 AA;

Query Match 100.0%; Score 560; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHQKPKAPKLLIYSGSTLQGVPS 60

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Db      1 DIQMTQSPSSLSASVDRTVITCRASKTISKYLAAYQQRGKAPKLLIYSGSTLQSGVPS 60
QY      61 RFSGSGSGTDFTLTISLQPEDPATYTCQQHNEVPLTFGGTKVEIKR 108
Db      61 RFSGSGSGTDFTLTISLQPEDPATYTCQQHNEVPLTFGGTKVEIKR 108

RESULT 8
ADP11669
ID      ADP11669 standard; protein; 214 AA.
XX
XX      ADP11669;
AC
XX      26-FEB-2004 (first entry)
DT
XX      anti-CD11a rhmAb light chain amino acid sequence #SEQ ID 3.
DE
XX      Purifying; target protein; non-affinity purification;
XX      high-performance tangential flow filtration; HPTFF; pharmaceutical;
XX      diagnostic; therapeutic; antibody.
XX      Synthetic.
OS
XX      WO2003102132-A2.
PN
XX      11-DEC-2003.
PD
XX      25-APR-2003; 2003WO-US013054.
PF
XX      26-APR-2002; 2002US-0375953P.
PR
XX      (GETH ) GENENTECH INC.
PA
XX      Fahner RL, Pollman D, Lebreton B, Van Reis R;
PI
XX      WPI; 2004-043096/04.
PT
XX      Purifying target protein from mixture containing host cell protein
PT      involves subjecting mixture to non-affinity purification, high-
PT      performance tangential flow filtration and isolating purified protein.
PT
XX      Disclosure; SEQ ID NO 3; 77pp; English.
XX
XX      The invention relates to a method for purifying a target protein from a
XX      mixture containing a host cell protein. This method comprises subjecting
XX      the mixture to a non-affinity purification followed by high-performance
XX      tangential flow filtration (HPTFF) and isolating the protein in a purity
XX      containing less than 100 parts/million (ppm) of the host cell protein,
XX      where the method of the invention includes no affinity purification
XX      process. The method of the invention is useful for purifying a target
XX      protein from a mixture containing a host cell protein, and is useful for
XX      incorporating the isolated protein into a pharmaceutical formulation.
XX      Proteins purified using the method of the invention are useful in a
XX      pharmaceutical respect, and are also useful in various diagnostic and
XX      therapeutic purposes. The method of the invention is efficient in
XX      purifying a target protein from a mixture containing a host cell protein,
XX      and may also be effectively performed at low cost. The current sequence
XX      represents the anti-CD11a rhmAb light chain amino acid sequence. This
XX      particular protein was used to demonstrate the method of the invention.
XX
SQ      Sequence 214 AA;

Query Match      100.0%; Score 560; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 8.9e-33;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DIQMTQSPSSLSASVDRTVITCRASKTISKYLAAYQQRGKAPKLLIYSGSTLQSGVPS 60
Db      1 DIQMTQSPSSLSASVDRTVITCRASKTISKYLAAYQQRGKAPKLLIYSGSTLQSGVPS 60
QY      61 RFSGSGSGTDFTLTISLQPEDPATYTCQQHNEVPLTFGGTKVEIKR 108
Db      61 RFSGSGSGTDFTLTISLQPEDPATYTCQQHNEVPLTFGGTKVEIKR 108
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Db      61 RFSGSGSGTDFTLTISLQPEDPATYTCQQHNEVPLTFGGTKVEIKR 108

RESULT 9
AAV29449
ID      AAV29449 standard; protein; 109 AA.
XX
XX      AAV29449;
AC
XX      05-OCT-1999 (first entry)
DT
XX      Human light chain kappa-I consensus framework.
DE
XX      Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
XX      diagnosis; inflammatory disorder; conjugate; immunoglobulin;
XX      fusion protein.
XX      Homo sapiens.
OS
XX      WO9937779-A1.
PN
XX      29-JUL-1999.
PD
XX      19-JAN-1999; 99WO-US001081.
PF
XX      22-JAN-1998; 98US-00012116.
PR      20-FEB-1998; 98WO-US003337.
PR      24-JUL-1998; 98US-00121952.
PR      24-JUL-1998; 98US-00122513.
XX
XX      (GETH ) GENENTECH INC.
PA
XX      Hseel V, Koumentis I, Leong SJ, Presta LG, Shahrokh Z, Zapata GA;
PI
XX      WPI; 1999-469134/39.
PT
XX      New conjugates of nonproteaceous polymers with antibody fragments, used
PT      for treating inflammatory disorders.
PT
XX      Disclosure; Fig 29; 360pp; English.
XX
XX      The present invention describes a novel conjugate having one or more
XX      antibody fragments covalently attached to one or more nonproteaceous
XX      polymer molecules, where the apparent size of the conjugate is at least
XX      about 500 kDa. Conjugates of antibody fragments which bind the human
XX      interleukin (IL) 8 with a nonproteaceous polymer can be used for
XX      treating inflammatory disorders e.g. acute lung injury, ischemic
XX      reperfusion disorder, and autoimmune diseases. They can also be used for
XX      treating e.g. inflammatory skin diseases including psoriasis and atopic
XX      dermatitis, systemic scleroderma and sclerosis, and aetmatic diseases.
XX      The conjugates can also be used as reagents in an animal model system for
XX      in vivo study of the biological functions of the antigen recognised by
XX      the conjugate. The present sequence represents the human light chain
XX      kappa-I consensus framework from the present invention
XX
SQ      Sequence 109 AA;

Query Match      97.6%; Score 546.5; DB 2; Length 109;
Best Local Similarity 98.2%; Pred. No. 4.6e-32;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY      1 DIQMTQSPSSLSASVDRTVITCRASKTISKYLAAYQQRGKAPKLLI-YSGSTLQSGVP 59
Db      1 DIQMTQSPSSLSASVDRTVITCRASKTISKYLAAYQQRGKAPKLLIYSGSTLESQVP 60
QY      60 SRFSGSGSGTDFTLTISLQPEDPATYTCQQHNEVPLTFGGTKVEIKR 108
Db      61 SRFSGSGSGTDFTLTISLQPEDPATYTCQQHNEVPLTFGGTKVEIKR 109

RESULT 10
AAV77752
ID      AAV77752 standard; protein; 109 AA.
```

```

XX AC AAY77752;
XX DT 06-JUN-2000 (first entry)
XX DE Human light chain K1 consensus framework.
XX KM Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4.2.SV1LN35A;
XX KM inflammatory disorder; adult respiratory distress syndrome; chimeric;
XX KM affinity purification; 6G4.2.5.
XX OS Homo sapiens.
XX PN US6025158-A.
XX PD 15-FEB-2000.
XX PF 20-FEB-1998; 98US-00027449.
XX PR 21-FEB-1997; 97US-0038664P.
XX PR 22-JAN-1998; 98US-0074330P.
XX PA (GETH ) GENENTECH INC.
XX PI Presta LG, Leong SR, Gonzalez TN;
XX DR WPI, 2000-181809/16.
XX PT New nucleic acid molecule encodes a polypeptide which is an anti-
XX PT interleukin-8 monoclonal antibody or antibody fragment useful for the
XX PT production of anti-interleukin-8 monoclonal antibodies or fragments.
XX PS Example; Fig 29; 188pp; English.
XX CC The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
XX CC (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs
XX CC (complementarity determining regions) of the humanized anti-IL-8
XX CC 6G4.2.SV1LN35A light chain; and amino acids 24-253 of the humanized anti-
XX CC IL-8 6G4.2.SV1LN35A heavy chain. The anti-IL-8 MAb and fragments can be
XX CC used in diagnosis, for affinity purification of IL-8 from recombinant
XX CC cell culture or natural sources and for the treatment of inflammatory
XX CC disorders e.g. adult respiratory distress syndrome. Nucleic acids
XX CC encoding the anti-IL-8 MAb can be associated in a vector with another
XX CC gene encoding another protein or protein fragment to produce a fusion
XX CC protein which can make isolation and/or purification of the protein an
XX CC easier process
XX SQ Sequence 109 AA;

Query Match          97.6%; Score 546.5; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 4.6e-32;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVDGVITTCRAKSTISKYLAWYQQRKAPKLLI-YSGSTLQSGVP 59
DB 1 DIQMTQSPSSLSASVDGVITTCRAKSTISKYLAWYQQRKAPKLLIYSGSTLQSGVP 60
QY 60 SRFSGSGSGTDFTLTSSIQPEDFATYYCOQHNEYPFLTGGQTKVEIKR 108
DB 61 SRFSGSGSGTDFTLTSSIQPEDFATYYCOQHNEYPFLTGGQTKVEIKR 109

RESULT 11
AAB30309
ID AAB30309 standard; protein; 109 AA.
XX AC AAB30309;
XX DT 12-FEB-2001 (first entry)
XX DE Human light chain kappa consensus framework SEQ ID NO: 47.
XX KM Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;

```

```

KM adult respiratory distress syndrome; multiple organ failure;
KM bacterial pneumonia; inflammatory bowel disease.
XX OS Homo sapiens.
XX PN US6133426-A.
XX PD 17-OCT-2000.
XX PF 20-FEB-1998; 98US-00026985.
XX PR 21-FEB-1997; 97US-0038664P.
XX PR 22-JAN-1998; 98US-0074330P.
XX PA (GETH ) GENENTECH INC.
XX PI Presta LG, Leong SR, Gonzalez TN;
XX DR WPI, 2000-686027/67.
XX PT Humanized anti-interleukin 8 monoclonal antibody variant useful for
XX PT treating inflammatory disorders, such as adult respiratory distress
XX PT syndrome, hypovolemic shock and ulcerative colitis.
XX PS Disclosure; Col 161-162; 240pp; English.
XX CC The present invention provides a number of humanised monoclonal anti-IL-8
XX CC antibodies which can be used in the diagnosis and treatment of
XX CC inflammatory disorders, including adult respiratory distress syndrome,
XX CC septic shock, multiple organ failure, bacterial pneumonia and
XX CC inflammatory bowel disease. The present sequence comprises one of the
XX CC antibodies of the invention
XX SQ Sequence 109 AA;

Query Match          97.6%; Score 546.5; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 4.6e-32;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVDGVITTCRAKSTISKYLAWYQQRKAPKLLI-YSGSTLQSGVP 59
DB 1 DIQMTQSPSSLSASVDGVITTCRAKSTISKYLAWYQQRKAPKLLIYSGSTLQSGVP 60
QY 60 SRFSGSGSGTDFTLTSSIQPEDFATYYCOQHNEYPFLTGGQTKVEIKR 108
DB 61 SRFSGSGSGTDFTLTSSIQPEDFATYYCOQHNEYPFLTGGQTKVEIKR 109

RESULT 12
ABU13786
ID ABU13786 standard; protein; 109 AA.
XX AC ABU13786;
XX DT 25-FEB-2003 (first entry)
XX DE Human light chain kappa consensus framework sequence.
XX KM Antibody; monoclonal antibody; 5.12.14; 6G4.2.5; interleukin-8; mAb;
XX KM antiinflammatory; respiratory; acute lung injury; polyethylene glycol;
XX KM PEG; lung injury; adult respiratory distress syndrome; ARDS; asthma;
XX KM inflammatory disease; inflammatory bowel disease; psoriasis; sclerosis;
XX KM ischaemic reperfusion disorder; stroke; multiple sclerosis; meningitis;
XX KM osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis;
XX KM alcoholic hepatitis; cystic fibrosis; human.
XX OS Homo sapiens.
XX PN US6468532-B1.
XX PD 22-OCT-2002.
XX PF 20-JAN-1999; 99US-00234340.

```

XX 22-JAN-1998; 98US-0074330P.
 XX 20-FEB-1998; 98US-0075467P.
 XX 24-JUL-1998; 98US-0094003P.
 XX 24-JUL-1998; 98US-0094013P.
 XX (GETH) GENENTECH INC.
 XX Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 XX WPI, 2003-138230/13.
 XX
 XX Treating acute lung injury in mammal by administering to mammal a 500 kD
 PT conjugate comprising F(ab')₂ antibody fragment that binds to human
 PT interleukin-8, covalently attached to one or two polyethylene glycol
 PT molecules.
 XX
 XX Example G; Fig 29; 259pp; English.
 XX
 CC The invention relates to treating acute lung injury in a mammal,
 CC comprising administering to the mammal an effective amount of a conjugate
 CC of a single antibody fragment covalently attached to 1 or 2 polyethylene
 CC glycol (PEG) molecules, where the antibody fragment is a F(ab')₂
 CC comprising: (a) first chain that is either a light chain or a heavy chain
 CC ; (b) a first opposite chain that is either a light chain opposite the
 CC first light chain or a light chain opposite the first heavy chain; (c) a
 CC second chain that is either a light chain or a heavy chain; and (d) a
 CC second opposite chain that is either a heavy chain opposite the second
 CC light chain or a light chain opposite the second heavy chain; where every
 CC PEG molecule is covalently attached to a first cysteine residue in the
 CC first or second chain that would ordinarily form a disulphide bridge with
 CC a second cysteine residue in the first or second opposite chain, where
 CC the disulphide bridge is avoided by substitution of another amino acid
 CC residue for the second cysteine residue in the first or second opposite
 CC chain, where the F(ab')₂ comprises an antigen binding site that binds to
 CC human interleukin-8 (IL-8), and where the apparent size of the conjugate
 CC is at least about 500 kD. The antigen binding sites may be derived from
 CC murine monoclonal antibodies 5.12.14 or 6G4.2.5. The method is useful for
 CC treating lung injury, including adult respiratory distress syndrome
 CC (ARDS) in a mammal and inflammatory diseases (such as asthma,
 CC inflammatory bowel disease, psoriasis and sclerosis), ischaemic
 CC reperfusion disorders, stroke, multiple sclerosis, meningitis,
 CC osteoarthritis, septic shock, autoimmune disease (e.g. Rheumatoid
 CC arthritis), alcoholic hepatitis, cystic fibrosis and many other diseases
 CC and disorders listed in the specification. The present sequence
 CC represents a human antibody sequence included for comparison with the
 CC mouse humanised monoclonal antibody sequences
 XX
 XX Sequence 109 AA;
 SO
 CC Query Match 97.6%; Score 546.5; DB 6; Length 109;
 CC Best Local Similarity 98.2%; Pred. No. 4.6e-32;
 CC Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 1 DIGNOTSSSLASVGRVITTCASAKTISKYLAAMYQKQKAPKLI-YSGSTLQSGVP 59
 DB 1 DIGNOTSSSLASVGRVITTCASAKTISKYLAAMYQKQKAPKLIYSGSTLQSGVP 60
 QY 60 SRFSGSGSGTDFTLTISLTQPEDPATYCCOQHNEYPLTFQGTVEIKR 108
 DB 61 SRFSGSGSGTDFTLTISLTQPEDPATYCCOQHNEYPLTFQGTVEIKR 109
 RESULT 13
 ABUS9499
 ID ABUS9499 standard; protein; 109 AA.
 XX
 AC ABUS9499;
 XX
 DT 22-APR-2003 (first entry)
 XX
 DE Human light chain kappa consensus framework.

KW Interleukin-8; IL-8; humanised antibody; antibody; 5.12.14; 6G4.2.5;
 KW inflammatory disorder; psoriasis; atopic dermatitis; sclerosis;
 KW systemic scleroderma; inflammatory bowel disease; Crohn's disease;
 KW ulcerative colitis; ischaemia; reperfusion; myocardial infarction;
 KW stroke; adult respiratory distress syndrome; rheumatoid arthritis;
 KW alcoholic hepatitis; acute lung injury; asthma; cerebral oedema;
 KW myocardial ischaemia; cranial trauma; asphyxia; Behcet's disease;
 KW dermatomyositis; polymyositis; multiple sclerosis; meningitis;
 KW encephalitis; uveitis; osteoarthritis; lupus nephritis; trauma;
 KW autoimmune disease; Sjogren's syndrome; vasculitis; septicaemia;
 KW central nervous system inflammatory disorder; sepsis; sarcoidosis;
 KW multiple organ injury syndrome; bacterial pneumonia; glomerulonephritis;
 KW inflammation of the lung; human.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US6458355-B1.
 PN
 XX
 XX 01-OCT-2002.
 PD
 XX
 XX 24-JUL-1998; 98US-00121952.
 PF
 XX
 XX 22-JAN-1998; 98US-0074330P.
 PR 20-FEB-1998; 98US-0075467P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 XX WPI, 2003-208759/20.
 XX
 XX Treating inflammatory disorder in a mammal, involves administering a
 PT conjugate of polyethylene glycol and a single antibody fragment
 PT comprising antigen binding site that binds to human interleukin-8, to
 PT mammal.
 XX
 XX Example 3G; Fig 29; 259pp; English.
 XX
 CC The invention relates to treating an inflammatory disorder in a mammal,
 CC comprising administering to the mammal, an effective amount of a
 CC conjugate of a single antibody fragment (e.g. the heavy or light chains
 CC of the humanised mouse monoclonal antibodies 5.12.14 and 6G4.2.5, which
 CC also have their intramolecular disulphide bridges ablated by substitution
 CC mutations) covalently attached to one or two polyethylene glycol (PEG)
 CC molecules. The antibodies comprise an antigen binding site that binds to
 CC human interleukin-8 (IL-8), and the apparent size of the conjugate is at
 CC least 500 kDa. The method is useful for treating an inflammatory disorder
 CC e.g. ischaemic reperfusion disorder such as surgical tissue reperfusion
 CC injury, myocardial ischaemia or myocardial infarction, or hypovolemic
 CC shock, in a mammal e.g. human. The method is useful for treating
 CC inflammatory disorders including psoriasis, atopic dermatitis, systemic
 CC scleroderma and sclerosis, responses associated with inflammatory bowel
 CC disease, ischaemic reperfusion disorders, myocardial ischaemic
 CC conditions, cerebral oedema secondary to stroke, cranial trauma,
 CC asphyxia, adult respiratory distress syndrome, acute lung injury,
 CC Behcet's disease, dermatomyositis, polymyositis, multiple sclerosis,
 CC meningitis, meningitis, encephalitis, uveitis, osteoarthritis, lupus
 CC nephritis, autoimmune diseases such as rheumatoid arthritis, Sjogren's
 CC syndrome, vasculitis, central nervous system inflammatory disorder,
 CC multiple organ injury syndrome secondary to septicaemia or trauma,
 CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
 CC mediated diseases including glomerulonephritis, sepsis, sarcoidosis,
 CC immunopathologic responses to tissue/organ transplantation, inflammations
 CC of the lung, inflammatory bowel disease such as ulcerative colitis and
 CC asthma. The present sequence represents the light or heavy chain of human
 CC IgG, used to design the humanising mutations in the two mouse antibodies
 XX
 XX Sequence 109 AA;
 SO
 CC Query Match 97.6%; Score 546.5; DB 6; Length 109;
 CC Best Local Similarity 98.2%; Pred. No. 4.6e-32;
 CC Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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OY 1 DIOMTOSPSLSASVGDRTVITTCRASKTISKYLAWYQGRKAPKLLI-YSGSTLQSGVP 59
DB 1 DIOMTOSPSLSASVGDRTVITTCRASKTISKYLAWYQGRKAPKLLIYSGSTLQSGVP 60
OY 60 SRFSSGSGSTDFTLTISLQPEDFATYCCQOHNEYPILTFGGGTVEIKR 108
DB 61 SRFSSGSGSTDFTLTISLQPEDFATYCCQOHNEYPILTFGGGTVEIKR 109

RESULT 14
AAE39082
ID AAE39082 standard; protein; 109 AA.
XX
AC AAE39082;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human light chain kappa1 consensus framework protein.
XX
KM Interleukin-8 mediated disease; adult respiratory distress syndrome; IL;
KM bacterial pneumonia; inflammatory bowel disease; hypovolemic shock; ARDS;
KM ulcerative colitis; ischaemic reperfusion injury; myocardial infarction;
KM acute lung injury; inflammatory disease; asthma; antibody; human.
XX
OS Homo sapiens.
XX
PN US2003021790-A1.
XX
PD 30-JAN-2003.
XX
PF 29-NOV-2000; 2000US-00726258.
XX
PR 22-JAN-1998; 98US-0074330P.
PR 20-FEB-1998; 98US-0075467P.
PR 24-JUL-1998; 98US-0094003P.
PR 24-JUL-1998; 98US-0094013P.
PR 20-JAN-1999; 99US-00234182.
XX
PA (GETH ) GENENTECH INC.
XX
PI Hsael V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
XX
DR WPI; 2003-605694/57.
XX
PT Novel conjugates comprising antibody fragments covalently attached to
PT nonproteinnaceous polymer molecules, useful for treating inflammatory
PT diseases, acute lung injury, ischemic reperfusion injury, pneumonia and
PT asthma.
XX
PS Example; Fig 29; 266pp; English.
XX
CC The invention relates to novel conjugates comprising antibody fragments
CC covalently attached to nonproteinnaceous polymer molecules. The invention
CC is useful for treating interleukin (IL)-8 mediated diseases or disorders
CC such as inflammatory diseases, acute lung injury e.g. adult respiratory
CC distress syndrome (ARDS), ischaemic reperfusion injury e.g. myocardial
CC infarction, hypovolemic shock, inflammatory bowel disease e.g. ulcerative
CC colitis, bacterial pneumonia and asthma. The invention is also useful as
CC a reagent in an animal model system for in vivo study of the biological
CC functions of the antigen recognised by the conjugate. The present
CC sequence is human light chain kappa1 consensus framework protein. This
CC sequence is used in the exemplification of the invention
XX
SQ Sequence 109 AA;
XX
Query Match 97.6%; Score 546.5; DB 7; Length 109;
Best Local Similarity 98.2%; Pred. No. 4.6e-12;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
OY 1 DIOMTOSPSLSASVGDRTVITTCRASKTISKYLAWYQGRKAPKLLI-YSGSTLQSGVP 59
DB 1 DIOMTOSPSLSASVGDRTVITTCRASKTISKYLAWYQGRKAPKLLIYSGSTLQSGVP 60

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```

OY 60 SRFSSGSGSTDFTLTISLQPEDFATYCCQOHNEYPILTFGGGTVEIKR 108
DB 61 SRFSSGSGSTDFTLTISLQPEDFATYCCQOHNEYPILTFGGGTVEIKR 109

RESULT 15
AAB46020
ID AAB46020 standard; peptide; 240 AA.
XX
AC AAB46020;
XX
DT 23-MAR-2001 (first entry)
XX
DE Human MUC-1 scFv clone N1.
XX
KM MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;
KM antidiabetic antibody; cytostatic; virucidal; antibacterial; IF antigen;
KM antiparasitic; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200073430-A2.
XX
PD 07-DEC-2000.
XX
PF 29-MAY-2000; 2000WO-DE001809.
XX
PR 27-MAY-1999; 99DE-01024405.
PR 09-SEP-1999; 99DE-01043016.
XX
PA (DELB-) DELBARECK CENT MOLEKULARE MEDIZIN MAX.
XX
PI Goletz S, Karsten U;
XX
DR WPI; 2001-049937/06.
XX
PT Vaccines against conformation-dependent or non-peptide antigens, based on
PT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor
PT vaccines.
XX
PS Disclosure; Page 5-9; 36pp; German.
XX
CC This invention describes a novel vaccine (V1) against conformation-
CC dependent antigens (CDA) comprising DNA (I) and/or an antibody, or
CC peptide which immunologically imitates CDA, is new. (I) encodes a region
CC of an antidiabetic antibody (Ab2) or another peptide which: (a)
CC specifically binds to the binding site of an antibody (Ab1) or an antigen
CC binding molecule; and (b) immunologically mimics the initial antigen. The
CC immunogenic structure defined by a specific spatial conformation of amino
CC acids. (I) is used in the form of linear or circular naked DNA and/or
CC with a viral vector and/or adjuvants. The products of the invention have
CC cytostatic, virucidal, antibacterial and antiparasitic. The invention
CC also describes (1) a corresponding vaccine (V2) against antigens which
CC are not proteins or peptides, as defined above but which have epitopes
CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)
CC human antidiabetic antibody fragments against the MUC1-conformation
CC epitope having one of 31 approximately 60 residue amino acids sequences,
CC all fully defined in the specification; (4) MUC1-conformation epitope
CC mimics having one of 16 9-17 residue amino acid sequences, all fully in
CC the specification; (5) antidiabetic antibody fragments against the TF
CC antigen having one of 24 approximately 200 residue amino acid sequences,
CC fully defined in the specification; (6) TF carbohydrate epitope mimics
CC having one of 25 7-13 residue amino acid sequences, all fully defined in
CC the specification; and (7) DNA sequences encoding the fragments and
CC derivatives defined in (3), (4), (5), or (6). (V1) and (V2) are used to treat
CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
CC and parasites. The vaccines are effective in cases where vaccination has
CC previously not been possible
XX
SQ Sequence 240 AA;
XX
Query Match 91.4%; Score 512; DB 4; Length 240;

```

Best Local Similarity 91.7%; Pred. No. 2.8e-29;
Matches 99; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
Qy 1 DIOMTOSPSLSASVGDRTVITCRASKTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
Db 133 DIOMTOSPSLSASVGDRTVITCRASQSISSYLNMYQKPKAPKLLIYGASVLOSQVPS 192
Qy 61 RPSGSGSGTDFLTITSSLOPEDPFIATYYCQAHNEYPLTFGQGTKEIKR 108
Db 193 RPSGSGSGTDFLTITSSLOPEDPFIATYYCQAHNEYPLTFGQGTKEIKR 240

Search completed: January 17, 2006, 11:44:26
Job time : 70.441 secs

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:40:01 ; Search time 11.3188 Seconds
(without alignments)
918.068 Million cell updates/sec

Title: US-10-665-658-2

Perfect score: 560

Sequence: 1 DIQMTQSPPSLSASVGDVLT.....QQHNEYPLTFGGTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	493	88.0	125	2 S40333	Ig kappa chain V-J
2	490	87.5	108	2 B49047	Ig kappa chain V r
3	490	87.5	129	2 S40369	Ig kappa chain - h
4	489	87.3	117	2 S46371	Ig kappa chain V-J
5	487	87.0	125	2 S40349	Ig kappa chain V-J
6	487	87.0	127	2 S40367	Ig kappa chain V-J
7	486	86.8	108	2 S19674	Ig kappa chain V r
8	486	86.8	123	2 S40331	Ig kappa chain - h
9	486	86.8	131	2 S40352	Ig kappa chain V-J
10	484.5	86.5	124	2 S40336	Ig kappa chain V-J
11	483	86.2	107	2 S36284	Ig kappa chain V
12	483	86.2	132	2 S40334	Ig kappa chain - h
13	481	85.9	108	1 K1HUBN	Ig kappa chain V-I
14	479	85.5	128	2 S46372	Ig kappa chain V-I
15	478	85.4	107	2 I69017	Ig light chain var
16	476.5	85.1	107	2 S36275	Ig kappa chain V
17	476	85.0	117	2 S46376	Ig kappa chain V-J
18	474	84.6	108	1 K1HUBU	Ig kappa chain V-I
19	474	84.6	108	2 S36277	Ig kappa chain V
20	474	84.6	132	2 S38646	Ig kappa chain V r
21	473	84.5	106	2 S26345	Ig light chain V r
22	473	84.5	109	2 S31998	Ig kappa chain - h
23	473	84.5	125	2 S40353	Ig kappa chain V-J
24	473	84.5	127	2 S04574	Ig kappa chain pre
25	472	84.3	108	2 S44132	Ig kappa chain V r
26	471	84.1	124	2 S40318	Ig kappa chain V r
27	469	83.8	125	2 S40316	Ig kappa chain - h
28	467.5	83.5	108	2 S30521	Ig kappa chain V r
29	466	83.2	108	2 S36279	Ig lambda chain V

30	466	83.2	108	2 S47182	Ig kappa chain - h
31	465	83.0	109	2 S31981	Ig kappa chain - h
32	465	83.0	129	2 S52793	Ig kappa chain V r
33	464	82.9	107	2 S36269	Ig lambda chain V
34	464	82.9	108	1 K1HUBU	Ig kappa chain V-I
35	463.5	82.8	108	2 S34007	Ig kappa chain V r
36	462.5	82.6	107	2 S47183	Ig kappa chain - h
37	462	82.5	122	2 S40370	Ig kappa chain - h
38	462	82.5	125	2 S40350	Ig kappa chain - h
39	462	82.5	127	2 S11240	Ig kappa chain V r
40	461	82.3	108	1 K1HUGL	Ig kappa chain V-I
41	461	82.3	108	1 K1HUKU	Ig kappa chain V-I
42	461	82.3	129	2 S52789	Ig kappa chain V r
43	460	82.1	108	1 K1HUBS	Ig kappa chain V-I
44	460	82.1	108	2 I39154	Ig kappa chain (BR
45	460	82.1	120	2 S46370	Ig kappa chain V-J

ALIGNMENTS

RESULT 1

S40333

Ig kappa chain V-J region - human

C/Species: Homo sapiens (man)

C/Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S40333

R/Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A/Title: Expressed human immunoglobulin chi genes and their hypermutation.

A/Reference number: S40312; PMID:94080891; PMID:8258341

A/Accession: S40333

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-125 <RTS>

A/References: UNIPARC:UP10000116153; EMBL:X72443; NID:g441354; PIDN:CA51111.1; P

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-108/Domain: immunoglobulin homology <IMM>

Query Match 88.0%; Score 493; DB 2; Length 125;

Best Local Similarity 86.9%; Pred. No. 3,2e-34;

Matches 93; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPPSLSASVGDVLTITCRASKTISKYLAWYQQRGKAPKLLIYSGSTLQSGVPS 60

DB 19 DIQMTQSPPSLSASVGDVLTITCRASQSSISMLAWYQQRGKAPKLLIYKASLSGVS 78

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEYPLTFGGTKVEIK 107

DB 79 RFGSGSGTDFLTITSSLOPEDFATYYCOQVNSYPTTFGGTKVEIK 125

RESULT 2

Ig kappa chain V region (monoclonal strictional autoantibody StrAB SA-1A) - human (Erag

C/Species: Homo sapiens (man)

C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: B49047

R/Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.

Eur. J. Immunol. 22, 2231-2236, 1992

A/Title: Human monoclonal strictional autoantibodies isolated from thymic B lymphocytes

A/Reference number: A49047; PMID:92387224; PMID:1516616

A/Accession: B49047

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-108 <VIC>

A/Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UP10000176B44

A/Experimental source: thymic B lymphocytes

A/Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIIP:113209)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/16-90/Domain: immunoglobulin homology <IMM>

```
Query Match      87.5%; Score 490; DB 2; Length 108;
Best Local Similarity 88.9%; Pred. No. 5e-34;
Matches 96; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLASVGDRTVITCRASKTISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 DIQMTSPSSLASVGDRTVITCRASQSSISYLAWYQQRKAPKLLIYAASLSQSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQHNHEYPLTFGGGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 RFGSGSGTDFLTITSSLOPEDPATYCCQSYSTPLTFGGGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
S40369
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40369
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; PMID:94080891; PMID:8258341
A:Accession: S40369
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLB>
A:Cross-references: UNIPARC:UPI0000116177; EMBL:X72479; NID:g441426; PIDN:CAA51147.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match      87.5%; Score 490; DB 2; Length 129;
Best Local Similarity 86.1%; Pred. No. 5.9e-34;
Matches 93; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLASVGDRTVITCRASKTISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 22 DIQMTSPSSLASVGDRTVITCRASHVSNHLVWYQQRKAPKLLIYAASLSQSGVPS 81
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQHNHEYPLTFGGGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 82 RFGSGSGTDFLTITSSLOPEDPATYCCQYNSYPTFGGTKEIKR 129
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46371; S38645
R:Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A:Reference number: S46369; PMID:94313975; PMID:8039491
A:Accession: S46371
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: UNIPARC:UPI0000116544; EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:23-97/Domain: immunoglobulin homology <IMM>

Query Match      87.3%; Score 489; DB 2; Length 117;
Best Local Similarity 85.5%; Pred. No. 6.5e-34;
Matches 94; Conservative 9; Mismatches 5; Indels 2; Gaps 1;

QY 1 DIQMTSPSSLASVGDRTVITCRASKTISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 8 DIQMTSPSSLASVGDRTVITCRASRISITWLAWYQQRKAPKLLIYAASLSQSGVPS 67
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQHNHEYPLTFGGGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
DB 68 RFGSGSGTDFLTITSSLOPEDPATYCCQYNSYFPPTFGGTKEIKR 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
S40349
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S40349
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; PMID:94080891; PMID:8258341
A:Accession: S40349
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: UNIPARC:UPI0000116163; EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match      87.0%; Score 487; DB 2; Length 125;
Best Local Similarity 88.8%; Pred. No. 1e-33;
Matches 95; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 DIQMTSPSSLASVGDRTVITCRASKTISKYLAWYQQRKAPKLLIYSGSTLQSGVPSR 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 19 IULTPSSLASVGDRTVITCRASQSSISALAWYQQRKAPKLLIYDASLSQSGVSR 78
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 RFGSGSGTDFLTITSSLOPEDPATYCCQHNHEYPLTFGGGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 79 RFGSGSGTDFLTITSSLOPEDPATYCCQFNTPPLTFGGGTKEIKR 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
S40367
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40367
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; PMID:94080891; PMID:8258341
A:Accession: S40367
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLB>
A:Cross-references: UNIPARC:UPI0000176CB4; EMBL:X72477
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match      87.0%; Score 487; DB 2; Length 127;
Best Local Similarity 88.0%; Pred. No. 1e-33;
Matches 95; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLASVGDRTVITCRASKTISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 18 DIQMTSPSSLASVGDRTVITCRASQSSISYLAWYQQRKAPKLLIYAASLSQSGVPS 77
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RFGSGSGTDFLTITSSLOPEDPATYCCQHNHEYPLTFGGGTKEIKR 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 78 RFGSGSGTDFLTITSSLOPEDPATYCCQSYNTPTFGGTKEIKR 125
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
S19674
Ig kappa chain V region (clone alpha-TEL9) - human
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19674
```


Db 1 EIVLTQSPSSLSASVGDRTVITCRASQGISSTLAWYQOKPGKAPKLLIYAASSTLQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEYPPLTFGGTKVEIK 107

Db 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNSYPTFGGTKVQIKR 107

RESULT 12

S40334

Ig kappa chain - human

C.Species: Homo sapiens (man)

C.Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C.Accession: S40334

R.Klein, R.; Jaenichen, R.; Zachau, H.G.

Bar, J. Immunol. 23, 3248-3271, 1993

A.Title: Expressed human immunoglobulin chi genes and their hypermutation.

A.Reference number: S40312; MUID:94080891; PMID:8258341

A.Accession: S40334

A.Status: preliminary; translation not shown

A.Molecule type: mRNA

A.Residues: 1-132 <KLE>

A.Cross-references: UNIPARC:UPI0000176CA9; EMBL:X72444

C.Superfamily: immunoglobulin V region; immunoglobulin homology

C.Keywords: heterotrimer; immunoglobulin

F.37-111/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 483; DB 2; Length 132;

Best Local Similarity 85.2%; Pred. No. 2.3e-33;

Matches 92; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGDRTVITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPS 60

Db 22 DIQVTPSSLSASVGDRTVITCRASQGISSTLAWYQOKPGKAPKLLIYAASSTLQSGVPS 81

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEYPPLTFGGTKVEIKR 108

Db 82 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNSYPTFGGTKVEIKR 129

RESULT 13

KIHUNB

Ig kappa chain V-I region (Ban) - human

C.Species: Homo sapiens (man)

C.Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C.Accession: A01878

R.Dwulet, F.E.; O'Connor, T.P.; Benson, M.D.

Mol. Immunol. 23, 73-78, 1986

A.Title: Polymorphism in a kappa I primary (AL) amyloid protein (BAN).

A.Reference number: A01878; MUID:86174817; PMID:3083240

A.Accession: A01878

A.Molecule type: protein

A.Residues: 1-108 <DMU>

A.Cross-references: UNIPROT:P04430; UNIPARC:UPI000012E150

C.Genetics:

A.Gene: GDB:IGKV1

A.Cross-references: GDB:136264

A.Map position: 2p12-2p12

C.Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C.Superfamily: immunoglobulin V region; immunoglobulin homology

C.Keywords: amyloid; heterotrimer; immunoglobulin

F.1-23/Region: framework 1

F.16-90/Domain: immunoglobulin homology <IMM>

F.24-34/Region: complementarity-determining 1

F.35-49/Region: framework 2

F.50-56/Region: complementarity-determining 2

F.57-88/Region: framework 3

F.89-97/Region: complementarity-determining 3

F.98-107/Region: framework 4

F.23-88/Disulfide bonds: #status predicted

Query Match 85.9%; Score 481; DB 1; Length 108;

Best Local Similarity 83.3%; Pred. No. 2.8e-33;

Matches 90; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGDRTVITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPS 60

Db 1 DIQVTPSSLSASVGDRTVITCRASQGISSTLAWYQOKPGKAPKLLIYAASSTLQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEYPPLTFGGTKVEIKR 108

Db 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNSYPTFGGTKVQIKR 108

RESULT 14

S46372

Ig light chain variable region (VJ) - human

C.Species: Homo sapiens (man)

C.Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C.Accession: S46372

R.Bensimon, C.; Chastagner, P.; Zouali, M.

EMBO J. 13, 2951-2962, 1994

A.Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(ch1) gene recombination.

A.Reference number: S46369; MUID:94313975; PMID:8039491

A.Accession: S46372

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-128 <BEN>

A.Cross-references: UNIPARC:UPI0000176CA4; EMBL:Z27173

C.Superfamily: immunoglobulin V region; immunoglobulin homology

C.Keywords: immunoglobulin

F.36-110/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 479; DB 2; Length 128;

Best Local Similarity 86.9%; Pred. No. 4.8e-33;

Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 2 IQMTSPSSLSASVGDRTVITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPSR 61

Db 22 IRITQSPSSLSASVGDRTVITCRASQGISSTLAWYQOKPGKAPKLLIYAASSTLQSGVPSR 81

Qy 62 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEYPPLTFGGTKVEIKR 108

Db 82 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNSYPTFGGTKVEIKR 128

RESULT 15

I69017

anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (F)

C.Species: Homo sapiens (man)

C.Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000

C.Accession: I69017

R.Chin, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Mahren, B.; Borrebaeck, C.A.

Immunol. Lett. 44, 25-30, 1995

A.Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a

A.Reference number: I64563; MUID:95237884; PMID:7721339

A.Accession: I69017

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-107 <RES>

A.Cross-references: UNIPARC:UPI0000113P9C; GB:S77140; NID:9913352; PIDN:AAB34102.1; PID:

C.Genetics:

A.Gene: Ig VKappa

C.Superfamily: immunoglobulin V region; immunoglobulin homology

F.16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.4%; Score 478; DB 2; Length 107;

Best Local Similarity 86.0%; Pred. No. 4.9e-33;

Matches 92; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 DIQMTSPSSLSASVGDRTVITCRASKTISKYLAAYQOKPGKAPKLLIYSGSTLQSGVPS 60

Db 1 DIQVTPSSLSASVGDRTVITCRASHDIGSTLAWYQOKPGKAPKLLIYAASSTLQSGVPS 60

Qy 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEYPPLTFGGTKVEIK 107

Db 61 RPSGSGGTDFLTITLISLOPEDPATYCCQYNSYPITFGQTKVLK 107

Search completed: January 17, 2006, 11:47:22
Job time : 12.3188 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 11:39:01 ; Search time 62.2533 Seconds
(without alignments)
1223.985 Million cell updates/sec

Title: US-10-665-658-2

Perfect score: 560

Sequence: 1 DIQMTQSPESLSASVGDRTV.....OOHNEYLTFGQSTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	86.8	236	2	Q6GMX8 HUMAN
2	481	85.9	108	1	KV1V_HUMAN
3	481	85.9	236	2	Q7Z3Y4 HUMAN
4	479	85.5	108	2	Q9UL70_HUMAN
5	479	85.5	236	2	Q6GMX9_HUMAN
6	478	85.0	236	2	Q6PIH7_HUMAN
7	476	85.0	236	2	Q6GMW1_HUMAN
8	475	84.8	108	2	Q9UL77_HUMAN
9	474	84.6	108	1	KV1H_HUMAN
10	473.5	84.6	107	2	Q96S89_HUMAN
11	471	84.1	236	2	Q502M4_HUMAN
12	471	84.1	244	2	Q652C8_HUMAN
13	470	83.9	240	2	Q652C9_HUMAN
14	464	82.9	108	1	KV1M_HUMAN
15	463	82.7	234	2	Q7Z473_HUMAN
16	463	82.7	236	2	Q6GMX0_HUMAN
17	462	82.5	108	2	Q9UL79_HUMAN
18	461	82.3	108	1	KV1G_HUMAN
19	461	82.3	108	1	KV1J_HUMAN
20	460	82.1	107	1	KV1S_HUMAN
21	458.5	81.9	108	1	KV1D_HUMAN
22	458	81.8	108	1	KV1B_HUMAN
23	458	81.8	129	1	KV1W_HUMAN
24	456	81.4	236	2	Q6PI75_HUMAN
25	455	81.2	108	1	KV1F_HUMAN
26	455	81.2	108	1	KV1O_HUMAN
27	455	81.2	108	1	KV1R_HUMAN
28	452	80.7	108	1	KV1P_HUMAN
29	452	80.7	108	1	KV1P_HUMAN
30	452	80.7	108	1	KV1Y_HUMAN
31	451.5	80.6	107	2	Q9UL81_HUMAN

32	450	80.4	108	1	KV1K_HUMAN	P01603 homo sapien
33	449	80.2	236	2	Q6PIH4_HUMAN	Q6PIH4 homo sapien
34	447	79.8	108	1	KV1E_HUMAN	P01597 homo sapien
35	447	79.8	108	1	KV1Q_HUMAN	P01609 homo sapien
36	443	79.1	234	2	Q5EPE6_HUMAN	Q5EPE6 homo sapien
37	442	78.9	189	2	Q56917_HUMAN	Q56917 homo sapien
38	439	78.4	108	1	KV1A_HUMAN	P01593 homo sapien
39	434	77.5	129	1	KV1X_HUMAN	P04432 homo sapien
40	432	77.1	117	1	KV1J_HUMAN	P01602 homo sapien
41	431	77.0	117	1	KV1I_HUMAN	P01601 homo sapien
42	430	76.8	108	1	KV1C_HUMAN	P01595 homo sapien
43	428	76.6	106	2	Q6P6F6_HUMAN	Q6P6F6 homo sapien
44	423.5	75.6	109	1	KV1T_HUMAN	P01612 homo sapien
45	412	73.6	108	1	KVSD_MOUSE	P01636 mus musculu

ALIGNMENTS

RESULT 1
Q6GMX8 HUMAN
ID Q6GMX8 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE IGKC protein.
OS Name=IGKC;
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Musny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttrick A.Y.S.N., Krzywicki M.T., Skalska U., Smalins D.E.,
RA Schnerch A., Schein U.E., Jones S.J.M., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -; mRNA.
DR SMR; Q6GMX8; 24-235.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-sec; 1.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 1.

Db 83 KESGSGSGTDFLTLLISLQPEDPATYCCQYKSYPTFGGTKEIKR 130

RESULT 4
ID Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.

AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]

NUCLEOTIDE SEQUENCE.
RP PubMed=1660528;
RA Maniatis L., Katz J.B., Pillinger M., Ghosein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype."
RL J. Exp. Med. 174:1639-1652 (1991).
EMBL AF035044; AAD56280.1; -, mRNA.
DR PIR; P01607; 1BWW.
DR HSSP; P01607; 1BWW.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCA37 CRC64;

Query Match 85.5%; Score 479; DB 2; Length 108;
Best Local Similarity 86.1%; Pred. No. 4e-41;
Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRVTITCRASKTIISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVDGRVTITCRASKTIISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60

QY 61 RFSGSGSGTDFLTLLISLQPEDPATYCCQYKSYPTFGGTKEIKR 108
DB 61 RFSGSGSGTDFLTLLISLQPEDPATYCCQYKSYPTFGGTKEIKR 108

RESULT 5
ID Q6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6GMX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

NUCLEOTIDE SEQUENCE.
RP TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -, mRNA.
DR SMR; Q6GMX9; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-secl; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR SEQUENCE 236 AA; 25924 MW; FDE203DC560CF7 CRC64;

Query Match 85.5%; Score 479; DB 2; Length 236;
Best Local Similarity 85.2%; Pred. No. 9.9e-41;
Matches 92; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRVTITCRASKTIISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60
DB 23 DIQMTQSPSSLSASVDGRVTITCRASQNVSWLAWYQQRKAPKSLIYATSSLSHGVS 82

QY 61 RFSGSGSGTDFLTLLISLQPEDPATYCCQYKSYPTFGGTKEIKR 108
DB 83 RFSGSGSGTDFLTLLISLQPEDPATYCCQYKSYPTFGGTKEIKR 130

RESULT 6
ID Q6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]

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RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -; mRNA.
DR HSR; P01607; IAR2.
DR SRR; O6P1H7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003557; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 85.4%; Score 478; DB 2; Length 236;
Best Local Similarity 87.0%; Pred. No. 1.3e-40;
Matches 94; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVITTCRAAKTISKYLAHWQQRKAPKLLIYSGSTLQSGVPS 60
DB 23 DIQLTQSPFSLASVDGVITTCRAAGISSTYLAHWQQRKAPKLLIYAASSTLQSGVPS 82
QY 61 FSGSGSGTDFTLTISLQPEDPATYCCQOHNEYPPLTFGQGTVEIKR 108
DB 83 FSGSGSGTDFTLTISLQPEDPATYCCQOHNEYPPLTFGQGTVEIKR 130

RESULT 7
Q6GMW1 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
DE Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -; mRNA.
DR SRR; O6GMW1; 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFA437 CRC64;

Query Match 85.0%; Score 476; DB 2; Length 236;
Best Local Similarity 87.9%; Pred. No. 2e-40;
Matches 94; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVDGVITTCRAAKTISKYLAHWQQRKAPKLLIYSGSTLQSGVPSR 61
DB 24 IQMTQSPSSLSASVDGVITTCRAAGISSTYLAHWQQRKAPKLLIYAASSTLQSGVPSR 83
QY 62 FSGSGSGTDFTLTISLQPEDPATYCCQOHNEYPPLTFGQGTVEIKR 108
DB 84 FSGSGSGTDFTLTISLQPEDPATYCCQOHNEYPPLTFGQGTVEIKR 130

RESULT 8
Q9UL77 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
```

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=151616;
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
 RT "Human monoclonal stratiational autoantibodies isolated from thymic B
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene
 RT segments associated with the autoimmune repertoire";
 RL Eur. J. Immunol. 22:2231-2236 (1992).
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=8436174;
 RX Wagner S.D., Luzzatto L.;
 RA "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation";
 RL Eur. J. Immunol. 23:391-397 (1993).
 DR EMBL; AF035037; AAD56273.1; -; mRNA.
 DR PIR; B49047; B49047.
 DR PIR; S34083; S34083.
 DR HSSP; P01607; 1BMW.
 DR SMR; Q9UL77; 1-108.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1 108
 FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;
 SQ
 Query Match 84.8%; Score 475; DB 2; Length 108;
 Best Local Similarity 86.1%; Pred. No. 1e-40;
 Matches 93; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVDRTITTCRASTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVDRTITTCRASTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
 QY 61 RPSGSGSGTDFLTITSLQPEDPATYTCQOHNEYPLTFGGQTVKEIKR 108
 DB 61 RPSGSGSGTDFLTITSLQPEDPATYTCQOHNEYPLTFGGQTVKEIKR 108
 RESULT 9
 KVIH_HUMAN STANDARD; PRT; 108 AA.
 ID P01600;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE IG kappa chain V-I region Hau.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX PROTEIN SEQUENCE.
 RX MEDLINE=1032830; PubMed=4097974;
 RA Watanabe S., Hirschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
 RT subgroups";
 RL Hoppe-Seiler's Z. Physiol. Chem. 351:1291-1295 (1970).
 CC - MISCLEANEODS: The C region of this chain has the INV (3) marker.
 CC - MISCLEANEODS: This is a Bence-Jones protein.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

 DR PIR; A01868; K1RHU.
 DR PDB; 1F6L; X-ray; L=1-108.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR 3D-structure; Bence-Jones protein; direct protein sequencing;
 KW Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23
 FT REGION 24 34
 FT REGION 35 49
 FT REGION 50 56
 FT REGION 57 88
 FT REGION 89 97
 FT REGION 98 107
 FT DISULFID 23 88
 FT NON TER 108
 FT SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
 SQ
 Query Match 84.6%; Score 474; DB 1; Length 108;
 Best Local Similarity 84.3%; Pred. No. 1.3e-40;
 Matches 91; Conservative 10; Mismatches 7; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVDRTITTCRASTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVDRTITTCRASTISKYLAWYQKPKAPKLLIYSGSTLQSGVPS 60
 QY 61 RPSGSGSGTDFLTITSLQPEDPATYTCQOHNEYPLTFGGQTVKEIKR 108
 DB 61 RPSGSGSGTDFLTITSLQPEDPATYTCQOHNEYPLTFGGQTVKEIKR 108
 RESULT 10
 Q96SA9_HUMAN PRELIMINARY; PRT; 107 AA.
 ID Q96SA9;
 AC 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
 DE variable region (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98375893; PubMed=9712075;
 RA Adderson E.E., Shikhan A.R., Ward K.B., Cunningham M.W.;
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
 RT antibody V region genes";
 RL J. Immunol. 161:2020-2031 (1998).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=151616;
 RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
 RT "Human monoclonal stratiational autoantibodies isolated from thymic B
 RT lymphocytes of patients with myasthenia gravis use VH and VL gene
 RT segments associated with the autoimmune repertoire";
 RL Eur. J. Immunol. 22:2231-2236 (1992).
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RX PubMed=8436174;

RA Wagner S.D., Luzzatto L.;
 RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
 RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation.";
 RL Eur. J. Immunol. 23:391-397(1993).
 [4]
 RN NUCLEOTIDE SEQUENCE.
 RP Published=1660528;
 RX Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
 RA Diamond B.;
 RT "Molecular characteristics of antibodies bearing an anti-DNA-
 RT associated idiotype.";
 RL J. Exp. Med. 174:1639-1652(1991).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=1903706;
 RX Blaison G., Kuntz J.L., Pasquali J.L.;
 RT "Molecular analysis of V kappa III variable regions of polyclonal
 RT rheumatoid factors during rheumatoid arthritis.";
 RL Eur. J. Immunol. 21:1221-1227(1991).
 DR EMBL: U96396; AAB68785.1; -, mRNA.
 DR PIR: B49047; B49047.
 DR PIR: PH0867; PH0867.
 DR PIR: S16840; S16840.
 DR PIR: S31977; S31977.
 DR PIR: S34083; S34083.
 DR PIR: S34086; S34086.
 DR HSSP: P01607; 1BMW.
 DR SMR: Q96SA9; 1-107.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 107 1
 FT NON_TER 107 1
 SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
 Query Match 84.6%; Score 473.5; DB 2; Length 107;
 Best Local Similarity 88.0%; Pred. No. 1.5e-40;
 Matches 95; Conservative 5; Mismatches 7; Indels 1; Gaps 1;
 QY 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAHWYQKPKAPKLLIYSGSTLQSGVPS 60
 DB 1 DIQMTQSPSSLSASVGDRTVITCRASQSISSYLAHWYQKPKAPKLLIYAASLQSGVPS 60
 QY 61 RFSSGSGSTDFLTITISLQPEDFATYYCOQHNEVPLTFGGGKVEIKR 108
 DB 61 RFSSGSGSTDFLTITISLQPEDFATYYCOO-SYSTLTFFGGGKVEIKR 107
 RESULT 11
 Q502W4_HUMAN PRELIMINARY; PRT; 236 AA.
 ID Q502W4;
 AC Q502W4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, last annotation update)
 DE 1GKC protein.
 GN Name=1GKC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NCB1_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RX TISSUE=Glandular pool - thyroid; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Heide F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Small D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Maitra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Glandular pool - thyroid;
 RC NIH MGC Project;
 RG Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC095489; AAH95489.1; -, mRNA.
 DR SMR: Q502W4; 23-236.
 DR EneembL: ENSG00000163245; Homo sapiens.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; IG_c1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF07654; CI-sect; 1.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGV; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;
 Query Match 84.1%; Score 471; DB 2; Length 236;
 Best Local Similarity 84.3%; Pred. No. 6.6e-40;
 Matches 91; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
 QY 1 DIQMTQSPSSLSASVGDRTVITCRASKTISKYLAHWYQKPKAPKLLIYSGSTLQSGVPS 60
 DB 23 DIQMTQSPSSLSASVGDRTVITCRASQGIKNDLQWYQKPKAPKLLIFAASLQSGVPS 82
 QY 61 RFSSGSGSTDFLTITISLQPEDFATYYCOQHNEVPLTFGGGKVEIKR 108
 DB 63 RFSSGSGSTDFLTITISLQPEDFATYYCLOQNSVPRTFGGGKVEIKR 130
 RESULT 12
 Q65ZC8_HUMAN PRELIMINARY; PRT; 244 AA.
 ID Q65ZC8;
 AC Q65ZC8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
 DE Single-chain Fv (Fragment).
 GN Name=scFv;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NCB1_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/hbct0797-629;
 RA Kontermann R.E., Wing M.G., Winter G.;
 RT "Complement recruitment using bispecific diabodies.";
 RL Nat. Biotechnol. 15:629-631(1997).
 DR EMBL: Y13057; CAA73500.1; -, mRNA.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; IG_v.

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DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS00835; IG_LIKE; 2.
FT NON_TER 1 1
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17668338F2BF CRC64;

Query Match
Best Local Similarity 84.1%; Score 471; DB 2; Length 244;
Matches 89; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTVITCRASKTISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60
DB 137 DIQMTQSPSTLSASISDRVTITCRASEGIYHWLAWYQQRKAPKFLIYKASISLGSAPS 196
61 RFSGSGSGTDFLTITISLQPEDPATYTCQOHNEYPITFGGKTVEIKR 108
197 RFSGSGSGTDFLTITISLQPDPAFYTCQOYSNYPITFGGKTVEIKR 244

RESULT 13
Q65ZC9_HUMAN PRELIMINARY; PRT; 240 AA.
ID Q65ZC9_HUMAN PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RX NUCLEOTIDE SEQUENCE.
RC STRAIN=C1q/7;
RA MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RT Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAAT3499.1; -; mRNA.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER 1 1
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match
Best Local Similarity 83.9%; Score 470; DB 2; Length 240;
Matches 89; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTVITCRASKTISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60
DB 133 DIQMTQSPSTLSASISGRVTITCRASEGIYHWLAWYQQRKAPKFLIYKASISLGSAPS 192
61 RFSGSGSGTDFLTITISLQPEDPATYTCQOHNEYPITFGGKTVEIKR 108
193 RFSGSGSGTDFLTITISLQPDPAFYTCQOYSNYPITFGGKTVEIKR 240

RESULT 14
KV1M_HUMAN STANDARD; PRT; 108 AA.
ID KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig kappa chain V-I region lay.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RX NUCLEOTIDE SEQUENCE.
RP PROTEIN SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IgM
anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
RN 12
RP PROTEIN SEQUENCE OF 1-104.
RX MEDLINE=89215279; PubMed=2496160;
RA Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
RA Carson D., Solomon A., Mendez E., Frangione B.;
RT "Structural and idiotypic characterization of the L chains of human
IgM autoantibodies with different specificities.";
RL J. Immunol. 142:3158-3163(1989).
RN 3
RP ERRATUM.
RA Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
RA Carson D., Solomon A., Mendez E., Frangione B.;
RL J. Immunol. 143:3864-3864(1989).
CC -1- MISCELLANEOUS: The second and third hypervariable regions of this
chain are identical with those of the human PWM V-II kappa chain,
with which it shares certain idiotypic determinants.
CC -1- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
globulin activity.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR PIR; A01871; K1HULY.
DR HSSP; P01607; 1BMW.
DR SMR; P01605; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Framework-2.
FT REGION 35 49 Framework-3.
FT REGION 50 56 Framework-4.
FT REGION 57 88 Complementarity-determining-1.
FT REGION 89 97 Complementarity-determining-2.
FT REGION 98 107 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT NON_TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match
Best Local Similarity 82.9%; Score 464; DB 1; Length 108;
Matches 87; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGRTVITCRASKTISKYLAWYQQRKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSTLSASISGRVTITCRASEGIYHWLAWYQQRKAPKFLIYKASISLGSAPS 196
61 RFSGSGSGTDFLTITISLQPEDPATYTCQOHNEYPITFGGKTVEIKR 108
193 RFSGSGSGTDFLTITISLQPDPAFYTCQOYSNYPITFGGKTVEIKR 108

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RESULT 15
Q72473_HUMAN
ID Q72473_HUMAN PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBT_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra W.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC056256.1; AAH56256.1; -; mRNA.
DR HSPF: P01834.1; HEZ.
DR SMR: Q72473.2; 22-234.
DR Ensembl: ENSG00000163245; Homo sapiens.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig C1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF07654; C1-sec; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ
SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 82.7%; Score 463; DB 2; Length 234;
Best Local Similarity 83.2%; Pred. No. 4.3e-39;
Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 IQMTQSPSSLSASVGRVITTCASKTIKYLAWYQOKPKAKKLIIYSGSTLQSGVPSR 61
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 22 IRMTQSPSSSFASSTGRVITTCRASQISGYLAWYQOKPKAPOLLIIYAASLTQSGVPSR 81
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 62 FSGSGSGTDTFTLTISLQPEDFATYYCOQHNEYPLTFGQSTKVEIKR 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 82 FSGSASGTDPTLTISLQSEDPATYYCQOYITTPWTFGQSTKVEIKR 128
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:40:17 ; Search time 19.3362 Seconds
(without alignments)
461.774 Million cell updates/sec

Title: US-10-665-658-2

Perfect score: 560

Sequence: 1 DIQMTQSPSSLSASVGRVT.....QQHNEYPLTGGTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5 COMB .pep:*
2: /cgn2_6/prodata/1/1aa/6 COMB .pep:*
3: /cgn2_6/prodata/1/1aa/H COMB .pep:*
4: /cgn2_6/prodata/1/1aa/PCTUS COMB .pep:*
5: /cgn2_6/prodata/1/1aa/RB COMB .pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	560	100.0	108	2	US-08-974-899-2
2	560	100.0	108	2	US-09-795-798-2
3	546.5	97.6	109	2	US-09-027-449-47
4	546.5	97.6	109	2	US-08-804-444A-47
5	546.5	97.6	109	2	US-09-026-985-47
6	546.5	97.6	109	2	US-09-121-952A-47
7	546.5	97.6	109	2	US-09-234-340A-47
8	546.5	97.6	109	2	US-09-355-014-47
9	506	90.4	108	2	US-08-974-899-3
10	506	90.4	108	2	US-09-795-798-3
11	506	90.4	108	2	US-08-908-469-12
12	505	90.2	127	2	US-09-809-739-10
13	504	90.0	109	1	US-07-934-373C-3
14	504	90.0	109	2	US-08-437-642B-3
15	504	90.0	109	2	US-08-146-206C-3
16	504	90.0	109	2	US-09-705-686-3
17	504	90.0	109	2	US-09-705-392A-3
18	504	90.0	109	2	US-09-705-398-3
19	504	90.0	109	4	PCT-US93-07832-3
20	501	89.5	107	2	US-07-934-373C-18
21	501	89.5	107	2	US-08-437-642B-18
22	501	89.5	107	2	US-08-146-206C-18
23	501	89.5	107	2	US-09-648-067A-14
24	501	89.5	107	2	US-09-705-686-18
25	501	89.5	107	2	US-09-705-392A-18
26	501	89.5	107	2	US-09-705-398-18
27	501	89.5	107	2	US-09-602-812A-5

28	501	89.5	107	4	PCT-US93-07832-18	Sequence 18, Appl
29	501	89.5	109	2	US-09-025-769B-28	Sequence 28, Appl
30	501	89.5	109	2	US-09-025-769B-43	Sequence 43, Appl
31	501	89.5	109	2	US-09-490-070A-28	Sequence 28, Appl
32	501	89.5	109	2	US-09-490-070A-43	Sequence 43, Appl
33	501	89.5	109	2	US-09-490-153-28	Sequence 28, Appl
34	501	89.5	109	2	US-09-490-153-43	Sequence 43, Appl
35	501	89.5	109	2	US-09-490-324-28	Sequence 28, Appl
36	501	89.5	109	2	US-09-490-324-43	Sequence 43, Appl
37	497	88.8	109	2	US-09-157-370-3	Sequence 30, Appl
38	494	88.2	236	2	US-09-859-053-30	Sequence 14, Appl
39	493	88.0	108	2	US-09-025-769B-14	Sequence 14, Appl
40	493	88.0	108	2	US-09-490-070A-14	Sequence 14, Appl
41	493	88.0	108	2	US-09-490-153-14	Sequence 14, Appl
42	490	87.5	108	2	US-09-490-324-14	Sequence 14, Appl
43	490	87.5	108	1	US-08-379-057-29	Sequence 29, Appl
44	490	87.5	108	2	US-09-920-262A-8	Sequence 8, Appl
45	490	87.5	240	2	US-09-192-854-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-974-899-2
; Sequence 2, Application US/08974899
; Patent No. 6037454

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,899

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971

FILING DATE: 11/27/96

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-974-899-2

Query Match 100.0%; Score 560; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 7e-42;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKLYAQQKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASKTISKLYAQQKAPKLLIYSGSTLQSGVPS 60

Qy 61 RFGSGSGTDFTLTISLQPEDFATYYCQHNEYPLTFGGTKVEIKR 108
Db 61 RFGSGSGTDFTLTISLQPEDFATYYCQHNEYPLTFGGTKVEIKR 108

RESULT 2

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US-09-795-798-2
Sequence 2, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpacin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-795-798-2

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[illegible]

RESULT 3
 US-09-027-449-47
 ; Sequence 47, Application US/09027449
 ; Patent No. 6025158
 ; GENERAL INFORMATION:
 ; APPLICANT: Gonzalez, Tania R.
 ; APPLICANT: Leon, Steven R.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
 ; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ;

```

;
; ADDRESS: Genentech, Inc
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COMPANY: TCS

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatln (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: Pl1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

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Query Match	97.6%	Score 546.5;	DB 2;	Length 109;
Best Local Similarity	98.2%	Pred. No. 1.1e-40;		
Matches 107; Conservative	1;	Mismatches 0;	Indels 1;	Gaps 1;

Qy	Db	Qy	Db
DIOMTOSPSLSASVGRVITITCRASATISIKYLAWQOKRGKAPKLI -YSGTLOSQV 59	1 DIQMTQSPSLSASVGRVITITCRASATISIKYLAWQOKRGKAPKLIITLYSGSTLESQV 60	60 SRFEGSSSGTDFTLITSLSPEDPFAITYYCOQHNEVPLTGGQCKVAKIR 108	61 SRFEGSSSGTDFTLITSLSPEDPFAITYYCOQHNEVPLTGGQCKVAKIR 109

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1      RESULT 4
2      US-08-804-444A-47
3      ; Sequence 47, Application US/0880444A
4      ; Patent No. 6117960
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Gonzalez, Tania N
7      ; APPLICANT: Leon, Steven R.
8      ; APPLICANT: Presta, Leonard G.
9      ; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
10     ; NUMBER OF SEQUENCES: 61
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSEE: Genentech, Inc.
13     ; STREET: 1 DNA Way
14     ; CITY: South San Francisco
15     ; STATE: California
16     ; COUNTRY: USA
17     ; ZIP: 94080
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
20     ; COMPUTER: IBM PC compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: WinPatIn (Genentech)
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/804,444A
25     ; FILING DATE: 21-Feb-1997

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RESULT 7

US-09-234-340A-47
; Sequence 47, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hseil, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952
; FILING DATE: 24-Jul-1998
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-234-340A-47
; Query Match 97.6%; Score 546.5; DB 2; Length 109;
; Best Local Similarity 98.2%; Pred. No. 1.1e-40;
; Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
; QY 1 DIQMTQSPSSLSASVDGVYITTCRAKSTISKYLAHYQOKRGPAPKLLI-YSGSTLQSGVP 59
; DB 1 DIQMTQSPSSLSASVDGVYITTCRAKSTISKYLAHYQOKRGPAPKLLIYSGSTLQSGVP 60
; QY 60 SRFSSGSGSTDPFTLTITSSIQPEDFATYYCOQHNEYPLTFGQGTKEIKR 108
; DB 61 SRFSSGSGSTDPFTLTITSSIQPEDFATYYCOQHNEYPLTFGQGTKEIKR 109
; RESULT 8
; US-09-355-014-47
; Sequence 47, Application US/09355014
; Patent No. 6870033
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hseil, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.

Shahrokh, Zahra
; Zapata, Gerardo A.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/355,014
; FILING DATE: 21-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
; US-09-355-014-47
; Query Match 97.6%; Score 546.5; DB 2; Length 109;
; Best Local Similarity 98.2%; Pred. No. 1.1e-40;
; Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
; QY 1 DIQMTQSPSSLSASVDGVYITTCRAKSTISKYLAHYQOKRGPAPKLLI-YSGSTLQSGVP 59
; DB 1 DIQMTQSPSSLSASVDGVYITTCRAKSTISKYLAHYQOKRGPAPKLLIYSGSTLQSGVP 60
; QY 60 SRFSSGSGSTDPFTLTITSSIQPEDFATYYCOQHNEYPLTFGQGTKEIKR 108
; DB 61 SRFSSGSGSTDPFTLTITSSIQPEDFATYYCOQHNEYPLTFGQGTKEIKR 109
; RESULT 9
; US-08-974-899-3
; Sequence 3, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-3

Query Match 90.4%; Score 506; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 3,6e-37;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKITSLKTLAYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQISINYLAWYQOKPGKAPKLLIYAASLSGVS 60

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEYPLTFGQGTKEIKR 108
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNSLPWTGQGTKEIKR 108

RESULT 10
US-09-795-798-3
Sequence 3, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-795-798-3

Query Match 90.4%; Score 506; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 3,6e-37;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKITSLKTLAYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQISINYLAWYQOKPGKAPKLLIYAASLSGVS 60

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEYPLTFGQGTKEIKR 108
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNSLPWTGQGTKEIKR 108

RESULT 11
US-08-908-469-12
Sequence 12, Application US/08908469
Patent No. 6884879
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Chai, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-08-908-469-12

Query Match 90.4%; Score 506; DB 2; Length 108;
Best Local Similarity 89.8%; Pred. No. 3,6e-37;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKITSLKTLAYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQISINYLAWYQOKPGKAPKLLIYAASLSGVS 60

QY 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQHNEYPLTFGQGTKEIKR 108
DB 61 RFGSGSGTDFLTITSSLOPEDFATYYCOQYNSLPWTGQGTKEIKR 108

RESULT 12
US-09-809-739-10
Sequence 10, Application US/09809739
Patent No. 6663863
GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia B.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
TITLE OF INVENTION: Restenosis
FILE REFERENCE: 1855,1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 127
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized light chain variable region with signal
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-09-809-739-10

Query Match 90.2%; Score 505; DB 2; Length 127;
Best Local Similarity 90.7%; Pred. No. 5,2e-37;
Matches 98; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAAYQKPKAPKLLIYSGSTLQGVPS 60
DB 20 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAAYQKPKAPKLLIYSGSTLQGVPS 79
QY 61 RFSGSGSGTDFTLTITSLQPEDPATYTCQYHNEYPLTFGGSTKVEIKR 108
DB 80 RFSGSGSGTDFTLTITSLQPEDPATYTCQYHNEYPLTFGGSTKVEIKR 127

RESULT 13
US-07-934-373C-3
Sequence 3, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Prestea
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-3

Query Match 90.0%; Score 504; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 5.4e-37;
Matches 96; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAAYQKPKAPKLLIYSGSTLQGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDVSSYLAAYQKPKAPKLLIYASLSQGVPS 60
QY 61 RFSGSGSGTDFTLTITSLQPEDPATYTCQYHNEYPLTFGGSTKVEIKR 108
DB 61 RFSGSGSGTDFTLTITSLQPEDPATYTCQYHNEYPLTFGGSTKVEIKR 108

RESULT 14
US-08-437-642B-3
Sequence 3, Application US/08437642B
Patent No. 6054297

GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Prestea
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:42:07 ; Search time 52.821 Seconds
(without alignments)
854.312 Million cell updates/sec

Title: US-10-665-658-2
Perfect score: 560
Sequence: 1 DIQMTQSPSSLSASVGRVT.....QQHNEYPLTGGQTKVEIKR 108

Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560	100.0	108	3	US-09-795-798-2
2	560	100.0	108	4	US-10-727-737-2
3	560	100.0	108	5	US-10-877-532-5
4	560	100.0	214	4	US-10-423-299-3
5	546.5	97.6	109	3	US-09-726-258-47
6	506	90.4	108	3	US-09-056-1608-12
7	506	90.4	108	3	US-09-795-798-3
8	506	90.4	108	4	US-10-234-671-12
9	506	90.4	108	4	US-10-727-737-3
10	506	90.4	108	5	US-10-861-049-38
11	506	90.4	108	5	US-10-974-591-12
12	506	90.4	108	6	US-11-021-874-38
13	506	90.4	109	3	US-09-811-123-6
14	505	90.4	110	4	US-10-044-896-4
15	505	90.2	127	3	US-09-809-739-10
16	505	90.2	127	5	US-10-662-061-10
17	505	90.2	233	4	US-10-404-724-68
18	504	90.0	109	5	US-10-835-641-3
19	502	89.6	108	5	US-10-783-511-126
20	501	89.5	107	4	US-10-268-501-5
21	501	89.5	107	4	US-10-608-626-5
22	501	89.5	107	4	US-10-600-152-14
23	501	89.5	107	5	US-10-619-754-5
24	501	89.5	107	5	US-10-835-641-18
25	501	89.5	107	5	US-10-719-510-5
26	501	89.5	107	6	US-11-044-749-5
27	501	89.5	107	6	US-11-154-465-5

28	501	89.5	108	4	US-10-125-687-8	Sequence 8, Appli
29	501	89.5	108	5	US-10-996-191-8	Sequence 8, Appli
30	497	88.8	108	5	US-10-938-353-117	Sequence 117, App
31	494	88.2	108	5	US-10-725-962-36	Sequence 36, Appl
32	494	88.2	108	5	US-10-725-962-38	Sequence 38, Appl
33	494	88.2	236	3	US-09-859-053-30	Sequence 30, Appl
34	494	88.2	236	4	US-10-800-250-30	Sequence 30, Appl
35	494	88.2	236	4	US-10-625-105-30	Sequence 30, Appl
36	493	88.0	107	5	US-10-727-155-312	Sequence 312, App
37	493	88.0	108	4	US-10-408-901-20	Sequence 20, Appl
38	493	88.0	126	5	US-10-469-125-8	Sequence 8, Appli
39	493	88.0	129	4	US-10-910-901-20	Sequence 20, Appl
40	493	88.0	214	4	US-10-408-901-44	Sequence 44, Appl
41	493	88.0	233	5	US-10-769-144-6	Sequence 6, Appli
42	493	88.0	233	5	US-10-903-191-6	Sequence 6, Appli
43	493	88.0	234	4	US-10-292-088-24	Sequence 24, Appl
44	492	87.9	107	4	US-10-292-088-105	Sequence 105, App
45	492	87.9	108	5	US-10-726-332-18	Sequence 18, Appl

ALIGNMENTS

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RESULT 1
US-09-795-798-2
; Sequence 2, Application US/09795798
; Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-795-798-2
Query Match 100.0%; Score 560; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 4e-39;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKLYAQKPKGLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASKTISKLYAQKPKGLIYSGSTLQSGVPS 60
```

Qy 61 RFGSGSGSTDFTLTISLQPEDFATYYCCQHNHYPLTFGGSTKVEIKR 108
Db 61 RFGSGSGSTDFTLTISLQPEDFATYYCCQHNHYPLTFGGSTKVEIKR 108

RESULT 2

Sequence 2, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:

COMPUTER READABLE FORM:

CURRENT APPLICATION DATA:

PRIOR APPLICATION DATA:

SEQUENCE DESCRIPTION:	SEQ ID NO:
2:	2:

QY 1 DIOMTQSSSSLSASVGDVITTCASAKTISIKLYAMYOQKKGKAPKLLITYSGTSLQSGVPS 60

Db 1 DIOMTQSSSSLSASVGRVITTCASAKTISIKLYAMYOQKKGKAPKLLITYSGTSLQSGVPS 60

QY 61 RPSGSGSGTDFTLLTSSIQPEDFATYYCOQHNEYPLTFQGGITKEIKR 108

Db 61 RPSGSGSGTDFTLLTSSIQPEDFATYYCOQHNEYPLTFQGGITKEIKR 108

RESULT 3
US-10-877-532-5
Sequence 5, Application us/108775322
Publication No. US20050038231A1
GENERAL INFORMATION:
APPLICANT: FAHNER, ROBERT L.
APPLICANT: LAVERIERE, AMY
APPLICANT: McDONALD, PAUL J.
APPLICANT: O'LEARY, RHONA M.

```

1 TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAPHY
2
3 FILE REFERENCE: P015R1
4
5 CURRENT APPLICATION NUMBER: US/10/877,532
6
7 CURRENT FILING DATE: 2004-06-24
8
9 PRIORITY APPLICATION NUMBER: US 60/490,500
10
11 PRIORITY FILING DATE: 2003-07-28
12
13 NUMBER OF SEQ ID NOS: 8
14

```

Query Match	100.0%;	Score 560;	DB 5;	length 108;
Best Local Similarity	100.0%;	Pred. No. 4e-39;		
Matches 108; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

RESULT 4
US-10-423-299-3

Query Match	100.0%;	Score 560;	DB 4;	Length 214;
Best Local Similarly	100.0%;	Pred. No. 7.8e-39;		
Matches 108;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

US-09-726-258-47
RESULT 5
Sequence 47, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Heel, Vanessa
APPLICANT: Koumanti, Iphigenia
APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.
APPLICANT: Shatrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-726-258-47

Query Match 97.6%; Score 546.5; DB 3; Length 109;
Best Local Similarity 98.2%; Pred. No. 5,4e-38;
Matches 107; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVDGVITTCRASTKISKYLAAYQOKRGAAPKLLI-YSGSTLQSGVP 59
DB 1 DIQMTQSPSSLSASVDGVITTCRASTKISKYLAAYQOKRGAAPKLLIYSGSTLQSGVP 60

QY 60 SRPSSGSGSTDPFTLTSSLOPEDFATYYCOQHNEVLTGGGKVEIKR 108
DB 61 SRPSSGSGSTDPFTLTSSLOPEDFATYYCOQHNEVLTGGGKVEIKR 109

RESULT 6
US-09-056-160B-12
Sequence 12, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Lowman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-056-160B-12

Query Match 90.4%; Score 506; DB 3; Length 108;
Best Local Similarity 89.8%; Pred. No. 1,2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVITTCRASTKISKYLAAYQOKRGAAPKLLIYSGSTLQSGVP 60
DB 1 DIQMTQSPSSLSASVDGVITTCRASTKISKYLAAYQOKRGAAPKLLIYSGSTLQSGVP 60

QY 61 SRPSSGSGSTDPFTLTSSLOPEDFATYYCOQHNEVLTGGGKVEIKR 108
DB 61 SRPSSGSGSTDPFTLTSSLOPEDFATYYCOQHNEVLTGGGKVEIKR 109

RESULT 7
US-09-795-798-3
Sequence 3, Application US/09795798
Publication No. US2003020736A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-795-798-3

Query Match 90.4%; Score 506; DB 3; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQKPKGAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASOSISNTLAWYQKPKGAPKLLIYASLSLSGVPS 60

QY 61 RFSSGSGTDFLTITSLQPEDFATYYCOQHNEYPITFGQGTKEIKR 108
DB 61 RFSSGSGTDFLTITSLQPEDFATYYCOQYNSLPMTFGQGTKEIKR 108

RESULT 8
US-10-234-671-12
Sequence 12, Application US/10234671
Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-Apr-1998
APPLICATION NUMBER: 60/1126446
FILING DATE: 07-Apr-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-Aug-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-234-671-12

Query Match 90.4%; Score 506; DB 4; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQKPKGAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASOSISNTLAWYQKPKGAPKLLIYASLSLSGVPS 60

QY 61 RFSSGSGTDFLTITSLQPEDFATYYCOQHNEYPITFGQGTKEIKR 108
DB 61 RFSSGSGTDFLTITSLQPEDFATYYCOQYNSLPMTFGQGTKEIKR 108

RESULT 9
US-10-727-737-3
Sequence 3, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-727-737-3

Query Match 90.4%; Score 506; DB 4; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAWYQKPKGAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASOSISNTLAWYQKPKGAPKLLIYASLSLSGVPS 60

QY 61 RFSSGSGTDFLTITSLQPEDFATYYCOQHNEYPITFGQGTKEIKR 108
DB 61 RFSSGSGTDFLTITSLQPEDFATYYCOQYNSLPMTFGQGTKEIKR 108

RESULT 10
US-10-861-049-38

Sequence 38, Application US/10861049
Publication No. US20050095243A1
GENERAL INFORMATION:
APPLICANT: Andrew Chan
APPLICANT: Qian Gong
APPLICANT: Flavius Martin
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P2040RIUS
CURRENT APPLICATION NUMBER: US/10/861,049
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: US 60/476,531
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR FILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US 60/476,414
PRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 145
SEQ ID NO 38
LENGTH: 108
TYPE: prt
ORGANISM: Homo sapiens
US-10-861-049-38

Query Match 90.4%; Score 506; DB 5; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCRASQISNTYLAWYQOKPGKAPKLLIYAASSLQSGVPS 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQHNEVPLTFGQTKVEIKR 108
DB 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQVNSLPWTFGQTKVEIKR 108

RESULT 11
US-10-974-591-12
Sequence 12, Application US/10974591
Publication No. US20050112126A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/974,591
FILING DATE: 26-Oct-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/723752
FILING DATE: 27-NOV-2000
APPLICATION NUMBER: 08/908469
FILING DATE: 06-AUG-1997
APPLICATION NUMBER: 08/833504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.

REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-974-591-12

Query Match 90.4%; Score 506; DB 5; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCRASQISNTYLAWYQOKPGKAPKLLIYAASSLQSGVPS 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQHNEVPLTFGQTKVEIKR 108
DB 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQVNSLPWTFGQTKVEIKR 108

RESULT 12
US-11-021-874-38
Sequence 38, Application US/11021874
Publication No. US20050163775A1
GENERAL INFORMATION:
APPLICANT: Andrew Chan
APPLICANT: Qian Gong
APPLICANT: Flavius Martin
TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
FILE REFERENCE: P2040R1P1
CURRENT APPLICATION NUMBER: US/11/021,874
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 10/861,049
PRIOR FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: US 60/476,531
PRIOR FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/476,481
PRIOR FILING DATE: 2003-06-05
PRIOR APPLICATION NUMBER: US 60/476,414
PRIOR FILING DATE: 2003-06-05
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 38
LENGTH: 108
TYPE: prt
ORGANISM: Homo sapiens
US-11-021-874-38

Query Match 90.4%; Score 506; DB 6; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTSPSSLSASVGDRTVITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCRASQISNTYLAWYQOKPGKAPKLLIYAASSLQSGVPS 60

QY 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQHNEVPLTFGQTKVEIKR 108
DB 61 RFSGSGSGTDFLTITSSLOPEDFATYYCOQVNSLPWTFGQTKVEIKR 108

RESULT 13
US-09-811-123-6
Sequence 6, Application US/09811123
Patent No. US20020001587A1
GENERAL INFORMATION:
APPLICANT: Sharon Erickson
APPLICANT: Ralph Schwall

```
APPLICANT: Mark Sliwowski
TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
FILE REFERENCE: GENEHT.073A2
CURRENT APPLICATION NUMBER: US/09/811,123
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/238,327
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 09/602,530
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized Antibody Sequence
US-09-811-123-6
```

```
Query Match          90.4%; Score 506; DB 3; Length 109;
Best Local Similarity 89.8%; Pred. No. 1.2e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHWYQKPKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHWYQKPKAPKLLIYSGSTLQSGVPS 60
QY 61 RFGSGSGTDFLTITISLQPEDPATYTCQGHNEYPPLTFGGTKVEIKR 108
DB 61 RFGSGSGTDFLTITISLQPEDPATYTCQGHNEYPPLTFGGTKVEIKR 108
```

```
RESULT 14
US-10-044-896-4
Sequence 4, Application US/10044896
Publication No. US20030166228A1
GENERAL INFORMATION:
APPLICANT: Chuncharapal, Anan
APPLICANT: Kim, Jin K.
APPLICANT: Stewart, Timothy
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: ANTI-INTERFERON-ALPHA ANTIBODIES
FILE REFERENCE: GENEHT.074A
CURRENT APPLICATION NUMBER: US/10/044,896
CURRENT FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: 60/270775
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
US-10-044-896-4
```

```
Query Match          90.4%; Score 506; DB 4; Length 110;
Best Local Similarity 89.8%; Pred. No. 1.3e-34;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHWYQKPKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHWYQKPKAPKLLIYSGSTLQSGVPS 60
QY 61 RFGSGSGTDFLTITISLQPEDPATYTCQGHNEYPPLTFGGTKVEIKR 108
DB 61 RFGSGSGTDFLTITISLQPEDPATYTCQGHNEYPPLTFGGTKVEIKR 108
```

```
RESULT 15
US-09-809-739-10
Sequence 10, Application US/09809739
Patent No. US20020106369A1
```

```
GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia B.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
FILE REFERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 127
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized light chain variable region with signal
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-09-809-739-10
```

```
Query Match          90.2%; Score 505; DB 3; Length 127;
Best Local Similarity 90.7%; Pred. No. 1.7e-34;
Matches 98; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHWYQKPKAPKLLIYSGSTLQSGVPS 60
DB 20 DIQMTQSPSSLSASVGRVTITCRASKTISKYLAHWYQKPKAPKLLIYSGSTLQSGVPS 79
QY 61 RFGSGSGTDFLTITISLQPEDPATYTCQGHNEYPPLTFGGTKVEIKR 108
DB 80 RFGSGSGTDFLTITISLQPEDPATYTCQGHNEYPPLTFGGTKVEIKR 127
```

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Search completed: January 17, 2006, 11:50:17
Job time : 53.821 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:44:33 ; Search time 5.18777 Seconds
(without alignments)
196.820 Million cell updates/sec

Title: US-10-665-658-2

Perfect score: 560
Sequence: 1 DIQMTQSPFSLASVGVDRVT.....QQHNEYPLTGGCTKVEIKR 108

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:
1: /cgn2_6/prodata/2/pubppaa/US08 NEW PUB.pep:*
2: /cgn2_6/prodata/2/pubppaa/US06 NEW PUB.pep:*
3: /cgn2_6/prodata/2/pubppaa/US07 NEW PUB.pep:*
4: /cgn2_6/prodata/2/pubppaa/PCT_NEW PUB.pep:*
5: /cgn2_6/prodata/2/pubppaa/US09 NEW PUB.pep:*
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8: /cgn2_6/prodata/2/pubppaa/US60_NEW_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560	100.0	108	6	US-10-665-658-2
2	555	99.1	107	7	US-11-107-028-49
3	506	90.4	108	6	US-10-665-658-3
4	506	90.4	108	7	US-11-120-338-3
5	506	90.4	109	7	US-11-096-046-5
6	501	89.5	108	7	US-11-106-820-3
7	501	89.5	109	6	US-10-834-397-28
8	501	89.5	109	6	US-10-834-397-43
9	497	88.8	108	6	US-10-771-257-77
10	497	88.8	108	7	US-11-127-677-75
11	496	88.6	107	7	US-11-051-453-32
12	495	88.6	129	7	US-11-051-453-46
13	495	88.4	109	7	US-11-127-932-14
14	495	88.4	109	7	US-11-127-932-18
15	495	88.4	109	7	US-11-127-903-14
16	495	88.4	109	7	US-11-127-903-18
17	493	88.0	108	6	US-10-834-397-14
18	493	87.5	107	6	US-11-051-453-30
19	490	87.5	108	6	US-10-925-366A-3
20	490	87.5	108	6	US-10-925-366A-6
21	490	87.5	129	7	US-11-051-453-44
22	490	87.5	240	6	US-10-925-366A-219
23	490	87.5	244	7	US-11-054-515-1881
24	490	87.5	363	7	US-11-000-463-335
25	489	87.3	107	7	US-11-084-554-1

26	489	87.3	108	6	US-10-771-257-4	Sequence 4, Appl1
27	489	87.3	108	7	US-11-127-677-4	Sequence 49, Appl1
28	489	87.3	108	7	US-11-127-932-11	Sequence 11, Appl1
29	489	87.3	108	7	US-11-127-903-11	Sequence 11, Appl1
30	489	87.3	109	7	US-11-127-932-16	Sequence 16, Appl1
31	489	87.3	109	7	US-11-127-932-17	Sequence 17, Appl1
32	489	87.3	109	7	US-11-127-932-20	Sequence 20, Appl1
33	489	87.3	109	7	US-11-127-903-17	Sequence 16, Appl1
34	489	87.3	109	7	US-11-127-903-17	Sequence 17, Appl1
35	489	87.3	109	7	US-11-127-903-20	Sequence 20, Appl1
36	488	87.1	107	7	US-11-051-453-4	Sequence 4, Appl1
37	488	87.1	108	7	US-11-127-932-19	Sequence 19, Appl1
38	488	87.1	108	7	US-11-127-903-19	Sequence 19, Appl1
39	488	87.1	129	7	US-11-051-453-43	Sequence 43, Appl1
40	488	87.1	244	7	US-11-054-515-82	Sequence 82, Appl1
41	488	87.1	244	7	US-11-054-515-261	Sequence 261, Appl1
42	487	87.0	107	7	US-11-051-453-33	Sequence 33, Appl1
43	487	87.0	108	6	US-10-771-257-36	Sequence 36, Appl1
44	487	87.0	108	7	US-11-127-677-36	Sequence 36, Appl1
45	487	87.0	129	7	US-11-051-453-47	Sequence 47, Appl1

ALIGNMENTS

RESULT 1
US-10-665-658-2
; Sequence 2, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-Oct-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-Feb-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9681
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-665-658-2

Query Match 100.0%; Score 560; DB 6; Length 108;
 Best Local Similarity 100.0%; Pred. No. 8.1e-40; Indels 0; Gaps 0;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIOMTSPSSLSASVGDRTITCRASKTISKYLAAYQKPKGAPKLLIYSGSTLQSGVPS 60
 |||||
 Db 1 DIOMTSPSSLSASVGDRTITCRASKTISKYLAAYQKPKGAPKLLIYSGSTLQSGVPS 60
 |||||
 Qy 61 RFSGSGGTDFLTITSSLOPEDPATYTCQONHEYPITFGQGTKEIKR 108
 |||||
 Db 61 RFSGSGGTDFLTITSSLOPEDPATYTCQONHEYPITFGQGTKEIKR 108
 |||||

RESULT 2

US-11-107-028-49
 ; Sequence 49, Application US/11107028
 ; Publication No. US20050276803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHAN, ANDREW C.
 ; APPLICANT: GONG, QIAN
 ; APPLICANT: MARTIN, FLAVIUS
 ; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
 ; FILE REFERENCE: P2112R1
 ; CURRENT APPLICATION NUMBER: US/11/107,028
 ; CURRENT FILING DATE: 2005-04-15
 ; PRIOR APPLICATION NUMBER: US 60/563,263
 ; PRIOR FILING DATE: 2004-04-16
 ; NUMBER OF SEQ ID NOS: 52
 ; SEQ ID NO 49
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: sequence is synthesized
 US-11-107-028-49

Query Match 99.1%; Score 555; DB 7; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2e-39; Indels 0; Gaps 0;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIOMTSPSSLSASVGDRTITCRASKTISKYLAAYQKPKGAPKLLIYSGSTLQSGVPS 60
 |||||
 Db 1 DIOMTSPSSLSASVGDRTITCRASKTISKYLAAYQKPKGAPKLLIYSGSTLQSGVPS 60
 |||||
 Qy 61 RFSGSGGTDFLTITSSLOPEDPATYTCQONHEYPITFGQGTKEIKR 107
 |||||
 Db 61 RFSGSGGTDFLTITSSLOPEDPATYTCQONHEYPITFGQGTKEIKR 107
 |||||

RESULT 3
 US-10-665-658-3
 ; Sequence 3, Application US/10665658
 ; Publication No. US20050276801A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jardieu, Paula M.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/665,658

; FILING DATE: 19-Sep-2003
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/031971
 ; FILING DATE: 27-NOV-1996
 ; APPLICATION NUMBER: 08/974899
 ; FILING DATE: 20-NOV-1997
 ; APPLICATION NUMBER: 09/420745
 ; FILING DATE: 20-OCT-1999
 ; APPLICATION NUMBER: 09/975798
 ; FILING DATE: 28-FEB-2001
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Tan, Lee K.
 ; REGISTRATION NUMBER: 39,447
 ; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-4462
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 108 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-665-658-3
 ; Sequence 3, Application US/11120338
 ; Publication No. US2005027658A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRUNETTA, PAUL G.
 ; APPLICANT: WALCKE, PATRICIA A.
 ; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
 ; FILE REFERENCE: P2079R2
 ; CURRENT APPLICATION NUMBER: US/11/120,338
 ; CURRENT FILING DATE: 2005-05-03
 ; PRIOR APPLICATION NUMBER: US 60/568,460
 ; PRIOR FILING DATE: 2004-05-05
 ; NUMBER OF SEQ ID NOS: 25
 ; SEQ ID NO 3
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: sequence is synthesized
 US-11-120-338-3

Query Match 90.4%; Score 506; DB 6; Length 108;
 Best Local Similarity 89.8%; Pred. No. 2e-35; Indels 0; Gaps 0;
 Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIOMTSPSSLSASVGDRTITCRASKTISKYLAAYQKPKGAPKLLIYSGSTLQSGVPS 60
 |||||
 Db 1 DIOMTSPSSLSASVGDRTITCRASKTISKYLAAYQKPKGAPKLLIYSGSTLQSGVPS 60
 |||||
 Qy 61 RFSGSGGTDFLTITSSLOPEDPATYTCQONHEYPITFGQGTKEIKR 108
 |||||
 Db 61 RFSGSGGTDFLTITSSLOPEDPATYTCQONHEYPITFGQGTKEIKR 108
 |||||

RESULT 4
 US-11-120-338-3
 ; Sequence 3, Application US/11120338
 ; Publication No. US2005027658A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRUNETTA, PAUL G.
 ; APPLICANT: WALCKE, PATRICIA A.
 ; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
 ; FILE REFERENCE: P2079R2
 ; CURRENT APPLICATION NUMBER: US/11/120,338
 ; CURRENT FILING DATE: 2005-05-03
 ; PRIOR APPLICATION NUMBER: US 60/568,460
 ; PRIOR FILING DATE: 2004-05-05
 ; NUMBER OF SEQ ID NOS: 25
 ; SEQ ID NO 3
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: sequence is synthesized
 US-11-120-338-3

Query Match 90.4%; Score 506; DB 7; Length 108;
 Best Local Similarity 89.8%; Pred. No. 2e-35; Indels 0; Gaps 0;
 Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DIOMTSPSSLSASVGDRTITCRASKTISKYLAAYQKPKGAPKLLIYSGSTLQSGVPS 60
 |||||
 Db 1 DIOMTSPSSLSASVGDRTITCRASKTISKYLAAYQKPKGAPKLLIYSGSTLQSGVPS 60
 |||||
 Qy 61 RFSGSGGTDFLTITSSLOPEDPATYTCQONHEYPITFGQGTKEIKR 108
 |||||
 Db 61 RFSGSGGTDFLTITSSLOPEDPATYTCQONHEYPITFGQGTKEIKR 108
 |||||

RESULT 5
US-11-096-046-5

; Sequence 5, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; PRIOR FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-5

Query Match 90.4%; Score 506; DB 7; Length 109;
Best Local Similarity 89.8%; Pred. No. 2e-35;
Matches 97; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTVITCRASKTISKYLAWYQOKRGKAPKLLIYSGSTLGSVPS 60
DB 1 DIOMTSPSSLSASVGDRTVITCRASQSI SNYLAWYQOKRGKAPKLLIYAASLSGSVPS 60
61 RSGSGSGTDFLTITSSLOPEDPATYCCQHNHYPLTFGQGTKEIKR 108
DB 61 RSGSGSGTDFLTITSSLOPEDPATYCCQYNSLPFTFGQGTKEIKR 108

RESULT 6
US-11-106-820-3
; Sequence 3, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-820-3

Query Match 89.5%; Score 501; DB 7; Length 108;
Best Local Similarity 88.9%; Pred. No. 5.2e-35;
Matches 96; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTVITCRASKTISKYLAWYQOKRGKAPKLLIYSGSTLGSVPS 60
DB 1 DIOMTSPSSLSASVGDRTVITCRASQSI SNYLAWYQOKRGKAPKLLIYAASLSGSVPS 60
61 RSGSGSGTDFLTITSSLOPEDPATYCCQHNHYPLTFGQGTKEIKR 108
DB 61 RSGSGSGTDFLTITSSLOPEDPATYCCQHNHYPLTFGQGTKEIKR 108

DB 61 RSGSGSGTDFLTITSSLOPEDPATYCCQYNSLPFTFGQGTKEIKR 108

RESULT 7

US-10-834-397-28
; Sequence 28, Application US/10834397
; Publication No. US20060003334A1
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/834,397
; FILING DATE: 29-Apr-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-Feb-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-834-397-28

Query Match 89.5%; Score 501; DB 6; Length 109;
Best Local Similarity 90.7%; Pred. No. 5.2e-35;
Matches 98; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIOMTSPSSLSASVGDRTVITCRASKTISKYLAWYQOKRGKAPKLLIYSGSTLGSVPS 60
DB 1 DIOMTSPSSLSASVGDRTVITCRASQSI SNYLAWYQOKRGKAPKLLIYAASLSGSVPS 60
61 RSGSGSGTDFLTITSSLOPEDPATYCCQHNHYPLTFGQGTKEIKR 108
DB 61 RSGSGSGTDFLTITSSLOPEDPATYCCQHYTTPFTFGQGTKEIKR 108

RESULT 8
US-10-834-397-43
; Sequence 43, Application US/10834397
; Publication No. US20060003334A1
; GENERAL INFORMATION:

APPLICANT: Knappik, Achim
Pack, Peter
Ilaq, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/834,397
FILING DATE: 29-Apr-2004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-834-397-43
Query Match 89.5%; Score 501; DB 6; Length 109;
Best Local Similarity 90.7%; Pred. No. 5.2e-35;
Matches 98; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCRASQGISSTYLAWYQOKPGKAPKLLIYASTLQSGVPS 60
QY 61 RFGSGSGTDFLTITSLQPEDFATYYCOQHNEYPLTFGQGTVEIKR 108
DB 61 RFGSGSGTDFLTITSLQPEDFATYYCOQHYYTTPFTFGQGTVEIKR 108
RESULT 9
US-10-771-257-77
Sequence 77, Application US/10771257
Publication No. US2005028864A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
APPLICANT: Cattaneo, Antonio
APPLICANT: Maritan, Amos
APPLICANT: Visintin, Michela
APPLICANT: Rabbitts, Terence H
APPLICANT: Settanni, Giovanni
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2272

CURRENT APPLICATION NUMBER: US/10/771, 257
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: PCT/GB02/03512
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: GB 0119004.0
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: GB 0121577.1
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: GB 0200928.0
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: GB 0203569.9
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: IT RM2001A000633
PRIOR FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.1
SEQ ID NO 77
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-10-771-257-77

Query Match 88.8%; Score 497; DB 6; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.1e-34;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCRASQGISSTYLAWYQOKPGKAPKLLIYASTLQSGVPS 60
QY 61 RFGSGSGTDFLTITSLQPEDFATYYCOQHNEYPLTFGQGTVEIKR 108
DB 61 RFGSGSGTDFLTITSLQPEDFATYYCOQLNSPTTFGQGTVEIKR 108
RESULT 10
US-11-127-677-75
Sequence 75, Application US/11127677
Publication No. US20050272107A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Rabbitts, Terence H
APPLICANT: Tanaka, Tomoyuki
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2462
CURRENT APPLICATION NUMBER: US/11/127,677
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: PCT/GB03/04942
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: GB 0226729.2
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin version 3.1
SEQ ID NO 75
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-75

Query Match 88.8%; Score 497; DB 7; Length 108;
Best Local Similarity 89.8%; Pred. No. 1.1e-34;
Matches 97; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTSPSSLSASVGDRTVITCRASKTISKYLAWYQOKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTSPSSLSASVGDRTVITCRASQGISSTYLAWYQOKPGKAPKLLIYASTLQSGVPS 60
QY 61 RFGSGSGTDFLTITSLQPEDFATYYCOQHNEYPLTFGQGTVEIKR 108
DB 61 RFGSGSGTDFLTITSLQPEDFATYYCOQLNSPTTFGQGTVEIKR 108


```
RESULT 11
US-11-051-453-32
; Sequence 32, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-PEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; FILE REFERENCE: MJI-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; PRIOR FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 32
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-32

Query Match      88.6%; Score 496; DB 7; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.3e-34;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVYITTCRASKTISKYLAHYQKPGKAPKLLIYSGSTLQSGVPS 60
DB 1 DIQMTQSPSSVSASVDGVYITTCRASQGISSTLAHYQHKGKAPKLLIYAAASLQSGVPS 60

QY 61 RFGSGSGTDFLTITISLQPEDPATYTCQAHNEYPLTFGQTKVEIK 107
DB 61 RFGSGSGTDFLTITISLQPEDPATYTCQAHNEYPLTFGQTKVEIK 107

RESULT 12
US-11-051-453-46
; Sequence 46, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-PEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; FILE REFERENCE: MJI-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; PRIOR FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 46
```

```
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-46

Query Match      88.6%; Score 496; DB 7; Length 129;
Best Local Similarity 88.8%; Pred. No. 1.5e-34;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVYITTCRASKTISKYLAHYQKPGKAPKLLIYSGSTLQSGVPS 60
DB 23 DIQMTQSPSSVSASVDGVYITTCRASQGISSTLAHYQHKGKAPKLLIYAAASLQSGVPS 82

QY 61 RFGSGSGTDFLTITISLQPEDPATYTCQAHNEYPLTFGQTKVEIK 107
DB 83 RFGSGSGTDFLTITISLQPEDPATYTCQAHNEYPLTFGQTKVEIK 129

RESULT 13
US-11-127-932-14
; Sequence 14, Application US/11127932
; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: anti-RAS intracellular scFv
US-11-127-932-14

Query Match      88.4%; Score 495; DB 7; Length 109;
Best Local Similarity 88.9%; Pred. No. 1.6e-34;
Matches 96; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVDGVYITTCRASKTISKYLAHYQKPGKAPKLLIYSGSTLQSGVPS 60
DB 2 DIQMTQSPSSLSASVDGVYITTCRASQGISSTLAHYQHKGKAPKLLIYAAASLQSGVPS 61

QY 61 RFGSGSGTDFLTITISLQPEDPATYTCQAHNEYPLTFGQTKVEIKR 108
DB 62 RFGSGSGTDFLTITISLQPEDPATYTCQAHNEYPLTFGQTKVEIKR 109

RESULT 14
US-11-127-932-18
; Sequence 18, Application US/11127932
; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
```


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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:38:06 ; Search time 75.559 Seconds
(without alignments)
703.621 Million cell updates/sec

Title: US-10-665-658-5
Perfect score: 656
Sequence: 1 EVQLVESGGGLVPGGSLRL.....FYGTYFDYWGQGLVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	656	100.0	121	2	AAW62013 Heavy cha
2	656	100.0	121	2	AAW63532 Humanised
3	656	100.0	121	3	AAV82336 Humanised
4	656	100.0	121	8	ADG38993 Humanised
5	656	100.0	121	8	ADRO3368 Humanised
6	656	100.0	121	8	ADM38458 CD11a hea
7	656	100.0	121	8	ADW80646 Humanized
8	656	100.0	451	8	ADP11670 anti-CD11
9	632	96.3	121	2	AAW62019 Rhesusise
10	632	96.3	121	2	AAW63542 Murine M
11	632	96.3	121	3	AAV82348 Rhesusise
12	632	96.3	121	8	ADG39012 Rhesusise
13	632	96.3	121	8	ADRO3380 Rhesusise
14	572.5	87.3	116	2	AAV29452 Human Igg
15	572.5	87.3	116	2	AAV77755 Human Igg
16	572.5	87.3	116	3	AAAB30312 Human Igg
17	572.5	87.3	116	6	ABU13789 Human Igg
18	572.5	87.3	116	6	ABU59502 Human Igg
19	572.5	87.3	116	6	AAE39085 Human Igg
20	534.5	81.5	122	8	ADM38454 CD11a hea
21	522.5	79.6	122	2	AAK30772 huXC3v9,
22	522.5	79.6	122	8	ADP79574 Humanised
23	522.5	79.6	122	8	ADG33302 Anti-CD20
24	522.5	79.6	122	9	ADM03408 Humanized

25	522.5	79.6	122	9	ADM21310 Mouse ant
26	522.5	79.6	122	9	ADX00803 Humanized
27	522.5	79.6	122	9	ADY62623 Humanized
28	522.5	79.6	122	9	AEb27726 Humanized
29	522.5	79.6	122	9	AEb17636 Variable
30	522.5	79.6	452	8	ADS33304 Anti-CD20
31	522.5	79.6	452	9	ADM03410 Humanized
32	522.5	79.6	452	9	ADM03411 Humanized
33	522.5	79.6	452	9	AEb27728 Humanized
34	522.5	79.6	452	9	AEb17638 Heavy Cha
35	522.5	79.6	471	8	ADP79584 2H7.v16 H
36	522.5	79.6	471	8	ADP79585 2H7.v31 L
37	522.5	79.6	471	9	ADM03389 Human ant
38	522.5	79.6	471	9	ADM03406 Human ant
39	522.5	79.6	471	9	ADM21319 Mouse ant
40	522.5	79.6	471	9	ADM21320 Mouse ant
41	522.5	79.6	471	9	ADX00805 Humanized
42	522.5	79.6	471	9	ADY62625 Humanized
43	521.5	79.5	253	2	AAV29444 Humanised
44	521.5	79.5	253	2	AAV29454 Humanised
45	521.5	79.5	253	3	AAV77757 Humanised

ALIGNMENTS

RESULT 1	
AAW62013	
ID	AAW62013 standard; peptide; 121 AA.
AC	AAW62013;
XX	
DT	01-OCT-1998 (first entry)
XX	
DE	Heavy chain variable region of humanised anti-CD11a antibody.
XX	
KW	Complementarity determining region; heavy chain variable region;
KW	humanised antibody; MEM24F(ab)-8; anti-CD11a antibody;
KW	human CD11a I domain; MEM24 epitope; alpha subunit;
KW	lymphocyte function-associated antigen 1; LFA-1; immunoassay;
KW	in vivo imaging; diagnosis; CD11a-associated disease.
OS	Mus sp.
OS	Homo sapiens.
PN	WO9823761-A1.
XX	
PD	04-JUN-1998.
XX	
PF	20-OCT-1997; 97WO-US019041.
XX	
PR	27-NOV-1996; 96US-00757205.
PA	(GETH) GENENTECH INC.
XX	
PI	Jardieu PM, Prestea LG;
XX	
DR	WPI; 1998-322737/28.
XX	
PT	New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
XX	also to treat conditions such as immunological or inflammatory disease.
PS	Claim 7; Page 50; 66pp; English.
XX	
CC	The present sequence represents the heavy chain variable region of a
CC	humanised anti-CD11a antibody that binds specifically to the human CD11a
CC	I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte
CC	function-associated antigen 1 (LFA-1) from any mammal. The humanised anti
CC	CD11a antibodies are used to determine presence of CD11a in usual
CC	immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-
CC	associated diseases (typically immune responses and inflammation such as
CC	psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
CC	leukaemia, etc

XX Sequence 121 AA; 100.0%; Score 656; DB 2; Length 121;
SQ Best Local Similarity 100.0%; Pred. No. 8e-52;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVROAPGKGLIEWGMHPSDESTRY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVROAPGKGLIEWGMHPSDESTRY 60
QY 61 NQKFDRTTISVDKSKNTLYLQMSLRADTAIVYVCARGIFYGTTYFDYWGQGLTVTVS 120
DB 61 NQKFDRTTISVDKSKNTLYLQMSLRADTAIVYVCARGIFYGTTYFDYWGQGLTVTVS 120
QY 121 S 121
DB 121 S 121

RESULT 2
AAW63532 standard; protein; 121 AA.
AAW63532;
AAW63532;
06-OCT-1998 (first entry)
Humanised MHM24 heavy chain.
Infectious; species-dependent antibody; malignancy;
infection; haematopoiesis; lymphocyte function-associated antigen-1;
intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
autoimmune disease; transplant rejection; tumour cell invasion;
human immune deficiency virus infection; heavy chain.
Synthetic.
WO9823746-A1.
04-JUN-1998.
29-OCT-1997; 97WO-US020169.
27-NOV-1996; 96US-00756150.
(GETH) GENENTECH INC.
Jardieu PM, Presta LG;
WPI; 1998-322726/28.
Mutants of species-dependent antibodies with affinity for non-human
mammalian antigen - greater than for parent antibody, particularly used
for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
directed against CD11a.
Disclosure; Page 55; 71pp; English.

This sequence represents the heavy chain of the humanised antibody MHM24,
and was used to produce a mutant of the invention. The mutants are of a
species-dependent antibody (Ab), and have an amino acid substitution in a
variable region of the Ab, and binding affinity for an antigen (Ag) from
a non-human mammal at least 10 times stronger than for the wild type Ab
against the Ag. The mutant antibodies are particularly intended for
administration to a non-human mammal in preclinical studies (e.g. of
infection, immunity, haematopoiesis or transplantation). They can also be
used diagnostically (to identify specific proteins) or therapeutically,
e.g. where directed against CD11a (lymphocyte function-associated antigen
-1) or intercellular adhesion molecule-1 against a wide variety of
inflammatory or autoimmune diseases, malignancies, transplant rejection,
CC human immune deficiency virus infection and tumour cell invasion.
Conversion to the mutant form allows useful antibodies to be produced

CC from antibodies which normally have affinity for non-human analogues of
CC the Ag too low to be of any use
XX

XX Sequence 121 AA; 100.0%; Score 656; DB 2; Length 121;
SQ Best Local Similarity 100.0%; Pred. No. 8e-52;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVROAPGKGLIEWGMHPSDESTRY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVROAPGKGLIEWGMHPSDESTRY 60
QY 61 NQKFDRTTISVDKSKNTLYLQMSLRADTAIVYVCARGIFYGTTYFDYWGQGLTVTVS 120
DB 61 NQKFDRTTISVDKSKNTLYLQMSLRADTAIVYVCARGIFYGTTYFDYWGQGLTVTVS 120
QY 121 S 121
DB 121 S 121

RESULT 3
AAW82336 standard; protein; 121 AA.
AAW82336;
AAW82336;
22-JUN-2000 (first entry)
Humanised anti-CD11a antibody heavy chain variable region SEQ ID NO:5.
Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
antitumour; antiviral; inflammation; immunological response; LFA-1;
lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
viral infection; transplant rejection; graft rejection.
Homo sapiens.
Mus sp.
US6037454-A.
14-MAR-2000.
20-NOV-1997; 97US-00974899.
27-NOV-1996; 96US-0031971P.
(GETH) GENENTECH INC.
Jardieu PM, Presta LG;
WPI; 2000-282241/24.
New humanised anti-CD11a antibody, useful for treating or preventing e.g.
inflammation and transplant rejection, contains human heavy variable
region complementarity determining regions.
Claim 1; Fig 1; 38pp; English.

The present invention describes a humanised anti-CD11a antibody (Ab) that
binds specifically to the human CD11a I-domain. The Ab has anti-
inflammatory, immunosuppressant, antitumour and antiviral activities. The
Ab blocks lymphocyte adhesion associated with inflammatory and
involved in leucocyte function-associated antigen (LFA-1) which is
CC immunological responses. The Ab are used: (i) optionally when coupled to
CC a cytotoxicin, to treat or prevent disorders mediated by lymphocyte
CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
CC thinitis, leukaemia, viral infections and many others, also for
CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs

CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine
 CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
 CC sequence represents the heavy chain variable region of the humanised anti-
 CC CD11a Ab
 CC
 SQ Sequence 121 AA;

Query Match 100.0%; Score 656; DB 3; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8e-52;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVQPGSLRLSCAASGYSFTGHMMNVRQAPKGLEWGMTHPSDSERY 60
 DB 1 EVQLVSGGGLVQPGSLRLSCAASGYSFTGHMMNVRQAPKGLEWGMTHPSDSERY 60

QY 61 NQKFDRTISVDKSKNTLYLQMNSLRAEDTAVVYVCARGIFYGTTYPDWGQGLTVTVS 120
 DB 61 NQKFDRTISVDKSKNTLYLQMNSLRAEDTAVVYVCARGIFYGTTYPDWGQGLTVTVS 120

QY 121 S 121
 DB 121 S 121

RESULT 4
 ADG38993
 ID ADG38993 standard; protein; 121 AA.
 XX
 AC ADG38993;
 XX
 DT 26-FEB-2004 (first entry)
 XX

DE Humanised Mouse anti-CD11a antibody heavy chain variable region.

XX Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
 KW VH; cluster of differentiation 11a; mixed lymphocyte response assay;
 KW Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 KW ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 KW psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; produg activating enzyme; humanised.

XX Synthetic.
 OS Mus sp.

XX US2003207336-A1.

XX 06-NOV-2003.

XX 28-FEB-2001; 2001US-00795798.

XX 27-NOV-1996; 96US-0031971P.

XX 20-NOV-1997; 97US-00974899.

XX 20-OCT-1999; 99US-00420745.

XX (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;

XX WPI; 2004-051511/05.

XX Humanized anti-CD11a antibody useful for treating lymphocyte function-
 PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

XX Claim 7; SEQ ID NO 5; 43pp; English.

XX The invention relates to a Humanised anti-cluster of differentiation

CC (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 CC a Kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The
 CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC produg activating enzyme, or as an affinity purification agent. The
 CC present sequence is the heavy chain variable region (VH) of the humanised
 CC mouse anti-CD11a I domain monoclonal antibody MHM24.

XX Sequence 121 AA;

Query Match 100.0%; Score 656; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8e-52;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVQPGSLRLSCAASGYSFTGHMMNVRQAPKGLEWGMTHPSDSERY 60
 DB 1 EVQLVSGGGLVQPGSLRLSCAASGYSFTGHMMNVRQAPKGLEWGMTHPSDSERY 60

QY 61 NQKFDRTISVDKSKNTLYLQMNSLRAEDTAVVYVCARGIFYGTTYPDWGQGLTVTVS 120
 DB 61 NQKFDRTISVDKSKNTLYLQMNSLRAEDTAVVYVCARGIFYGTTYPDWGQGLTVTVS 120

QY 121 S 121
 DB 121 S 121

RESULT 5
 ADR03368
 ID ADR03368 standard; protein; 121 AA.
 XX
 AC ADR03368;
 XX
 DT 21-OCT-2004 (first entry)
 XX

DE Humanised MHM24 F(ab)-8 antibody variable heavy chain protein.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 KW VH; murine; human; fusion protein.

XX Mus sp.
 OS Homo sapiens.
 OS Chimeric.

XX US2004146507-A1.

XX 29-JUL-2004.

XX 03-DEC-2003; 2003US-00727737.

XX 27-NOV-1996; 96US-0031945P.

```

PR 20-NOV-1997; 97US-00975329.
XX
XX (GETH ) GENENTECH INC.
XX
XX Jardiou PM, Preeta LG;
XX
XX WPI; 2004-552640/53.
XX
XX New antibody mutant of a species-dependent antibody, useful for treating
XX and preventing infectious diseases, psoriasis, inflammatory bowel
XX disease, allergic conditions, autoimmune diseases, or cancer.
XX
XX Example; SEQ ID NO 5; 54bp; English.
XX
XX The present invention relates to an antibody mutant of a species-
XX dependent antibody with beneficial properties. The invention is useful
XX for treating and preventing infectious diseases such as human
XX immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
XX disease such as psoriasis, inflammatory bowel diseases such as Crohn's
XX disease and ulcerative colitis, adult respiratory distress syndrome,
XX allergic diseases such as eczema and asthma, autoimmune diseases such as
XX rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
XX mellitus, Reynaud's syndrome, immunological diseases such as
XX tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
XX disease (COPD), CNS inflammatory disorder, skin hypersensitivity
XX disorders such as poison ivy and poison oak, B-cell malignancies such as
XX chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
XX disease and cancer. The invention is also useful in gene therapy. The
XX present sequence is humanised murine anti-human CD11a monoclonal antibody
XX (MH24) F(ab)-8 variable heavy chain protein. This sequence is used in
XX the exemplification of the invention.
XX
XX Sequence 121 AA;
XX
XX Query Match 100.0%; Score 656; DB 8; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 8e-52;
XX Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWRQAPGKGLRWGMTHPSDSERY 60
XX |||
XX DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWRQAPGKGLRWGMTHPSDSERY 60
XX
XX QY 61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAIVYVCARGIFYGTTYPDYWGQGLTVTVS 120
XX |||
XX DB 61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAIVYVCARGIFYGTTYPDYWGQGLTVTVS 120
XX
XX QY 121 S 121
XX |
XX DB 121 S 121
XX
XX RESULT 6
XX ADW38458
XX ID ADW38458 standard; protein; 121 AA.
XX
XX ADM38458;
XX
XX 24-MAR-2005 (first entry)
XX
XX CD11a heavy chain variable region #2.
XX
XX monoclonal antibody; CD11a; light-chain variable region;
XX heavy-chain variable region.
XX
XX Homo sapiens.
XX
XX CN1439651-A.
XX
XX 03-SEP-2003.
XX
XX 20-FEB-2002; 2002CN-00110866.
XX
XX 20-FEB-2002; 2002CN-00110866.
XX

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XX
XX (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
XX Wang H, Wang J;
XX
XX WPI; 2004-169719/17.
XX
XX Recombinant human CD11a monoclonal antibody and its preparation and
XX medicinal composition.
XX
XX Claim 1; Page 14-15; 16pp; Chinese.
XX
XX The present invention relates to a recombinant monoclonal antibody for
XX human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
XX No.5 in light-chain variable region and the amino acid sequence shown by
XX SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
XX bioactivity and the expression in host cell are greatly increased. The
XX DNA molecule for coding the antibody, its preparation process and the
XX medicinal composition containing it are also disclosed. The present
XX sequence represents a heavy chain variable region of human CD11a.
XX
XX Sequence 121 AA;
XX
XX Query Match 100.0%; Score 656; DB 8; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 8e-52;
XX Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWRQAPGKGLRWGMTHPSDSERY 60
XX |||
XX DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWRQAPGKGLRWGMTHPSDSERY 60
XX
XX QY 61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAIVYVCARGIFYGTTYPDYWGQGLTVTVS 120
XX |||
XX DB 61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAIVYVCARGIFYGTTYPDYWGQGLTVTVS 120
XX
XX QY 121 S 121
XX |
XX DB 121 S 121
XX
XX RESULT 7
XX ADX80646
XX ID ADX80646 standard; protein; 121 AA.
XX
XX ADX80646;
XX
XX 05-MAY-2005 (first entry)
XX
XX Humanized CD11a variable heavy chain amino acid sequence, seq id 6.
XX
XX Protein purification; leaching; protein A affinity chromatography; CD11a;
XX antibody.
XX
XX Synthetic.
XX
XX US2005038231-A1.
XX
XX 17-FEB-2005.
XX
XX 24-JUN-2004; 2004US-00877532.
XX
XX 28-JUL-2003; 2003US-0490500P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Fahrner RJ, Laverdiere A, McDonald PJ, O'leary RM;
XX
XX WPI; 2005-172327/18.
XX
XX Purifying a protein, e.g. antibody or immunoadhesin, comprises reducing
XX the temperature of a composition subjected to protein A affinity
XX chromatography to 3-20 degrees C, where protein A leaching is reduced.
XX

```

PS Disclosure; SEQ ID NO 6; 27pp; English.
XX
CC The invention relates to a method of purifying a protein which comprises
CC a CH2/CH3 region by protein A affinity chromatography. The method
CC involves reducing the temperature of a composition comprising the protein
CC and one or more impurities subjected to protein A affinity chromatography
CC to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably
CC the protein is antibody. The antibody is selected from Trastuzumab,
CC humanized 2C4, humanized CD1a antibody, and humanized VEGF antibody.
CC Preferably, the antibody binds HER2 antigen, where the antibody is
CC Trastuzumab or humanized 2C4. The protein is an immunoadhesin.
CC Specifically a TNF receptor immunoadhesin. The methods are useful for
CC purifying a protein, which comprises a CH2/CH3 region by protein A
CC affinity chromatography and for reducing leaching of protein A during
CC protein A affinity chromatography. The current sequence represents the
CC variable heavy chain amino acid sequence of CD1a.
XX
SQ Sequence 121 AA;
XX
Query Match 100.0%; Score 656; DB 9; Length 121;
Best Local Similarity 100.0%; Pred. No. 86-52;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVPGGSLRLSCAASGYSFTGHMMNWVROAPGKLEWVGMIHPSDSETRY 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGYSFTGHMMNWVROAPGKLEWVGMIHPSDSETRY 60
QY 61 NQKFKDRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIYFGTTYFDYWGQGLTVTVS 120
DB 61 NQKFKDRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIYFGTTYFDYWGQGLTVTVS 120
QY 121 S 121
DB 121 S 121
XX
RESULT 8
ADP11670 standard; protein; 451 AA.
XX
AC ADF11670;
XX
DT 26-FEB-2004 (first entry)
XX
DE anti-CD11a rhumab heavy chain amino acid sequence #SEQ ID 4.
XX
KW Purifying; target protein; non-affinity purification;
KM high-performance tangential flow filtration; HPRFF; pharmaceutical;
KW diagnostic; therapeutic; antibody.
XX
OS Synthetic.
XX
PN WO2003102132-A2.
XX
PD 11-DEC-2003.
XX
PE 25-APR-2003; 2003WO-US013054.
XX
PR 26-APR-2002; 2002US-0375953P.
XX
PA (GETH) GENENTECH INC.
XX
PI Fahner RI, Follman D, Lebreton B, Van Reis R;
XX
DR WPI; 2004-043096/04.
XX
PT Purifying target protein from mixture containing host cell protein
PT involves subjecting mixture to non-affinity purification, high-
PT performance tangential flow filtration and isolating purified protein.
XX
PS Disclosure; SEQ ID NO 4; 77pp; English.
XX
CC The invention relates to a method for purifying a target protein from a

CC mixture containing a host cell protein. This method comprises subjecting
CC the mixture to a non-affinity purification followed by high-performance
CC tangential flow filtration (HPRFF) and isolating the protein in a purity
CC containing less than 100 parts/million (ppm) of the host cell protein,
CC where the method of the invention includes no affinity purification
CC process. The method of the invention is useful for purifying a target
CC protein from a mixture containing a host cell protein, and is useful for
CC incorporating the isolated protein into a pharmaceutical formulation.
CC Protein purified using the method of the invention are useful in a
CC pharmaceutical respect, and are also useful in various diagnostic and
CC therapeutic purposes. The method of the invention is efficient in
CC purifying a target protein from a mixture containing a host cell protein,
CC and may also be effectively performed at low cost. The current sequence
CC represents the anti-CD1a rhumab heavy chain amino acid sequence. This
CC particular protein was used to demonstrate the method of the invention.
XX
SQ Sequence 451 AA;
XX
Query Match 100.0%; Score 656; DB 8; Length 451;
Best Local Similarity 100.0%; Pred. No. 3.2e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVPGGSLRLSCAASGYSFTGHMMNWVROAPGKLEWVGMIHPSDSETRY 60
DB 1 EVQLVESGGGLVPGGSLRLSCAASGYSFTGHMMNWVROAPGKLEWVGMIHPSDSETRY 60
QY 61 NQKFKDRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIYFGTTYFDYWGQGLTVTVS 120
DB 61 NQKFKDRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIYFGTTYFDYWGQGLTVTVS 120
QY 121 S 121
DB 121 S 121
XX
RESULT 9
AAW62019 standard; peptide; 121 AA.
XX
AC AAW62019;
XX
DT 01-OCT-1998 (first entry)
XX
DE Rhesusised heavy chain of humanised anti-CD11a antibody.
XX
KW Complementarity determining region; heavy chain variable region;
KM humanised antibody; MM24F(ab)-8; anti-CD11a antibody;
KM human CD11a I domain; MM24 epitope; alpha subunit;
KM lymphocyte function-associated antigen 1; LFA-1; immunoassay;
KM in vivo imaging; diagnosis; CD11a-associated disease.
XX
OS Unidentified.
XX
PN WO9823761-A1.
XX
PD 04-JUN-1998.
XX
PE 20-OCT-1997; 97WO-US019041.
XX
PR 27-NOV-1996; 96US-00757205.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 1998-322737/28.
XX
PT New humanised anti-CD1a antibody - used in immunoassays for CD1a, and
PT also to treat conditions such as immunological or inflammatory disease.
XX
PS Disclosure; Page 56; 66pp; English.
XX
CC The present sequence represents the heavy chain of a "rhesusised" (sic)

CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 CC involved in leucocyte adhesion associated with inflammatory and
 CC immunological responses. The Ab are used: (i) optionally when coupled to
 CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
 CC rhinitis, leukemia, viral infections and many others, also for
 CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine
 CC anti-CD11a antibody MM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing ICAM-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MM24 had IC50 0.13 nM. The present
 CC sequence represents the amino acid sequence of a rhesusised antibody
 CC mutant heavy chain, which is used in the exemplification of the present
 CC invention

CC Sequence 121 AA;

Query Match 96.3%; Score 632; DB 3; Length 121;
 Best Local Similarity 96.7%; Pred. No. 1.2e-49;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVOLVSSGGGLVPGGSLRLSCAASGYSFTGHMMNWRQAPGKGLMWGMIAPASSSTRY 60
 DB 1 EVOLVSSGGGLVPGGSLRLSCAASGYSFTGHMMNWRQAPGKGLMWGMIAPASSSTRY 60

QY 61 NQKFKRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIFYGTTYFDYWGQGITLVTS 120
 DB 61 NQKFKRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIFYGTTYFDYWGQGITLVTS 120

QY 121 S 121
 DB 121 S 121

RESULT 12
 ADG39012
 ID ADG39012 standard; protein; 121 AA.

AC ADG39012;

DT 26-FEB-2004 (first entry)

DE Rhesusised mouse anti-CD11a I-domain antibody VL.

XX Mouse; CD11a; I-domain; monoclonal antibody;
 KM cluster of differentiation 11a; mixed lymphocyte response assay;
 KM Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 KM ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 KM psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 KM rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KM diabetes mellitus; prodrug activating enzyme.

XX Synthetic.
 OS Mus sp.

XX US2003207336-A1.

XX 06-NOV-2003.

XX 28-FEB-2001; 2001US-00795798.

XX 27-NOV-1996; 96US-0031971P.

XX 20-NOV-1997; 97US-00974899.

XX 20-OCT-1999; 99US-00420745.

XX (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG;
 XX PI

XX WPI; 2004-051511/05.

DR Humanized anti-CD11a antibody useful for treating lymphocyte function-
 XX associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

XX Example; SEQ ID NO 24; 43pp; English.

XX The invention relates to a Humanised anti-cluster of differentiation
 CC (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 CC a Kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MM24 on CD11a. The
 CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is the light chain of a rhesusised anti-CD11a antibody of
 CC the invention.

CC Sequence 121 AA;

Query Match 96.3%; Score 632; DB 8; Length 121;
 Best Local Similarity 96.7%; Pred. No. 1.2e-49;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVOLVSSGGGLVPGGSLRLSCAASGYSFTGHMMNWRQAPGKGLMWGMIAPASSSTRY 60
 DB 1 EVOLVSSGGGLVPGGSLRLSCAASGYSFTGHMMNWRQAPGKGLMWGMIAPASSSTRY 60

QY 61 NQKFKRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIFYGTTYFDYWGQGITLVTS 120
 DB 61 NQKFKRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIFYGTTYFDYWGQGITLVTS 120

QY 121 S 121
 DB 121 S 121

RESULT 13
 ADR03380
 ID ADR03380 standard; protein; 121 AA.

AC ADR03380;

DT 21-OCT-2004 (first entry)

DE Rhesusised MM24 antibody variable heavy chain mutant protein.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 XX rhinovirus infection; inflammatory skin disease; psoriasis;
 KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculosis; sarcoidosis; polymyositis;
 KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KM skin hypersensitivity disorder; poison ivy; poison oak;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD11a monoclonal antibody; MM24; variable heavy chain;
 KM VH; murine; rhesus macaque; fusion protein; mutant; mutein.

XX Mus sp.

OS Macaca mulatta.
 OS Chimeric.
 XX US2004146507-A1.
 XX PD 29-JUL-2004.
 XX 03-DEC-2003; 2003US-00727737.
 XX 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX (GETH) GENENTECH INC.
 XX Jardiou PM, Preesta LG;
 P1 WPI; 2004-552640/53.
 DR
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 17; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polyomyelitis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is the substituted murine anti-human CD11a monoclonal
 CC antibody (MHM24) variable heavy chain protein. This sequence is used in
 CC the exemplification of the invention.
 CC
 SQ Sequence 121 AA;
 QY Query Match 96.3%; Score 632; DB 8; Length 121;
 Best Local Similarity 96.7%; Pred. No. 1.2e-49;
 Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EVOLVSSGGGLVOPGSLRLSCAASGYFTGHMMNMMVROAPGKGLWVGMIHPSDSETRY 60
 Db 1 EVOLVSSGGGLVOPGSLRLSCAASGYFTGHMMNMMVROAPGKGLWVGMIHPSDSETRY 60
 QY 61 NQKFKDRFTISVDKSKNTLYLQMSLRAEDTAVVYCAARGIFYGTTFFDYWGQGT 120
 Db 61 NQKFKDRFTISVDKSKNTLYLQMSLRAEDTAVVYCAARGIFYGTTFFDYWGQGT 120
 QY 121 S 121
 Db 121 S 121
 Db 121 S 121
 RESULT 14
 ID AAY29452 standard; protein; 116 AA.
 XX AAY29452;
 AC AAY29452;
 XX
 DT 05-OCT-1999 (first entry)
 XX
 DE Human IgG1 subgroup III heavy chain variable domain.
 XX
 XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
 KW diagnosis; inflammatory disorder; conjugate; immunoglobulin;

KW fusion protein.
 XX
 XX Homo sapiens.
 XX WO9937779-A1.
 XX PD 29-JUL-1999.
 XX 19-JAN-1999; 99WO-US001081.
 XX
 XX 22-JAN-1998; 98US-00012116.
 PR 20-FEB-1998; 98WO-US003337.
 PR 24-JUL-1998; 98US-00121952.
 PR 24-JUL-1998; 98US-00122513.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Hseil V, Koumenis I, Leong SJ, Preesta LG, Shahrokh Z, Zapata GA;
 P1 WPI; 1999-469134/39.
 DR
 XX
 PT New conjugates of nonproteaceous polymers with antibody fragments, used
 PT for treating inflammatory disorders.
 XX
 PS Disclosure; Fig 29; 360pp; English.
 XX
 CC The present invention describes a novel conjugate having one or more
 CC antibody fragments covalently attached to one or more nonproteaceous
 CC polymer molecules, where the apparent size of the conjugate is at least
 CC about 500 kDa. Conjugates of antibody fragments which bind the human
 CC interleukin (IL) 8 with a nonproteaceous polymer can be used for
 CC treating inflammatory disorders e.g. acute lung injury, ischaemic
 CC reperfusion disorder, and autoimmune diseases including psoriasis and atopic
 CC dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases.
 CC The conjugates can also be used as reagents in an animal model system for
 CC in vivo study of the biological functions of the antigen recognised by
 CC the conjugate. The present sequence represents the human IgG1 subgroup
 CC III heavy chain variable domain form the present invention
 CC
 SQ Sequence 116 AA;
 QY Query Match 87.3%; Score 572.5; DB 2; Length 116;
 Best Local Similarity 92.2%; Pred. No. 2.9e-44;
 Matches 107; Conservative 1; Mismatches 7; Indels 1; Gaps 1;
 QY 1 EVOLVSSGGGLVOPGSLRLSCAASGYFTGHMMNMMVROAPGKGLWVGMIHPSDSETRY 60
 Db 1 EVOLVSSGGGLVOPGSLRLSCAASGYFTGHMMNMMVROAPGKGLWVGMIHPSDSETRY 60
 QY 61 NQKFKDRFTISVDKSKNTLYLQMSLRAEDTAVVYCAARGIFYGTTFFDYWGQGT 115
 Db 61 ADSVKGKFTISVDKSKNTLYLQMSLRAEDTAVVYCAARGIFYGTTFFDYWGQGT 116
 RESULT 15
 ID AAY77755 standard; protein; 116 AA.
 XX AAY77755;
 AC AAY77755;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Human IgG1 subgroup III heavy chain variable domain.
 XX
 XX Interleukin-8; IL-8; monoclonal antibody; Mab; anti-IL-8; 664.2.5V1IN35A;
 KW inflammatory disorder; adult respiratory distress syndrome; chimeric;
 KW affinity purification; 664.2.5.
 XX
 XX Homo sapiens.
 XX
 XX US6025158-A.
 XX

```

PD 15-FEB-2000.
XX
XX
PF 20-FEB-1998; 98US-00027449.
XX
PR 21-FEB-1997; 97US-0038664P.
PR 22-JAN-1998; 98US-0074330P.
XX
XX
PA (GETH ) GENENTECH INC.
PI Presta LG, Leong SR, Gonzalez TN;
XX
XX
DR MPI; 2000-181809/16.
XX
XX
PT New nucleic acid molecule encodes a polypeptide which is an anti-
PT interleukin-8 monoclonal antibody or antibody fragment useful for the
PT production of anti-interleukin-8 monoclonal antibodies or fragments.
XX
XX
PS Example; Fig 29; 188pp; English.
XX
XX
CC The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
CC (MAB). The anti-IL-8 MAB comprises a sequence containing the CDRs
CC (complementarity determining regions) of the humanized anti-IL-8
CC 6G4.2.5V1IN35A light chain; and amino acids 24-253 of the humanized anti-
CC IL-8 6G4.2.5V1IN35A heavy chain. The anti-IL-8 MABs and fragments can be
CC used in diagnosis, for affinity purification of IL-8 from recombinant
CC cell culture or natural sources and for the treatment of inflammatory
CC disorders e.g. adult respiratory distress syndrome. Nucleic acids
CC encoding the anti-IL-8 MAb can be associated in a vector with another
CC gene encoding another protein or protein fragment to produce a fusion
CC protein which can make isolation and/or purification of the protein an
CC easier process
XX
XX
SQ Sequence 116 AA;

```

Query Match 87.3%; Score 572.5; DB 3; Length 116;
 Best Local Similarity 92.2%; Pred. No. 2.9e-44;
 Matches 107; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

```

QY 1 EVQLVDSGGGLVQPGGSLRLISCAASGYSFTGHMMNWVROAPGKGLEWVGMIHPSDSETRY 60
   |||||
DB 1 EVQLVDSGGGLVQPGGSLRLISCAASGFSFTGHMMNWVROAPGKGLEWVGMIHPSDSETRY 60
   |||||
QY 61 NQKFKDRFTISVSKSKNTLYLQNMNSLAEDPTAVYYC-ARGIVFYGTTFPDYMGQGT 115
   |||||
DB 61 ADSVKGKRFITSRDMSKNTLYLQNMNSLAEDPTAVYYCAARGIVFYGTTFPDYMGQGT 116
   |||||

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Best Local Similarity	73.0%;	Pred. No. 1.1e-34;		
Matches 89; Conservative		9; Mismatches 23;	Indels 1;	Gaps 1;

RESULT 14
S19666
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19666
R:Mark, J.D.; Hooogenboom, H.R.; Bonmert, T.D.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991
A:title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage
A:reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19666
A:Molecule type: mRNA
A:Residues: 1-121 <MR>
A:Cross-references: UNIPARC:UPI0000115FE5; EMBL:X61646; NID:g37688; PIDD:CAA3827.1; PIDD:CAA3827.1
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match	68.0%;	Score 446;	DB 2;	Length 121;
Best Local Similarity	71.9%;	Pred NO 1	3e-34.	

Matches 87; Conservative 10; Mismatches 24; Indels

Matches 87; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGSLRLSCAASGYSFTGHWMMNVRQAPGKGLEWVGMIHPSDSETRY 60

Db 1 QVQLVQSGGKVQPGSLRLSCAASGFTFS SYGMHWVRQAPGKGLEWVAVISYDGSNKY 60

QY 61 N0KFKDRFTISVDKSKNTLYLQMNSLRAEDTAVVYCARGIYFYGTTYEDYWGQGLVTVS 120

Db 61 ADSVKGRFTISRDN SKNTLYLQMSLR AEDTAVYCAKTGYSSG WGYFDYWGQGLTVS 120

QY 121 S 121

Db 121 S 121

RESULT 15

S23624

Ig heavy chain V region - human (Fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence 13-Jan-1995 #text_change 23-Jul-1999

C;Accession: S23624

R/Olee, T.; Lu, B.W.; Huang, D.F.; Soto-Gil, R.W.; Dellos, M.; Kozin, F.; Carson, D.A.;
T. Eng. Mod. 175 821-842 1993

J. Exp. Med. 175, 8

A; title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

A; Reference number: S23623; MUID:92156804; PMID:1/40665
B; Accession: S23624

A;Accession: 523624
A:Status: preliminaryA: Molecule type: DNA
A: status: preliminary

A:Residues: 1-143 <OLE>

A:Cross-references: UNIT

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <I

[illegible]

Query Match 68.0%; Score 446; DB 2; Length 143;

Best Local Similarity 74.4%; Pred. No. 1.5e-34;

Matches 90; Conservative 6; Mismatches 21; Indels 4; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMMNWVRQAPCKGLEWVGMIHPDSETRY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSNYSMNWVRQAPEGKLEWVSYSISSTIYY 600

61 NOKFKDRFTISVDKSKNTLYLOMNSLRAEDTAVVYCARGIYFYGTTYFDYWGQTLTVS 120

Db 61 ADSVKGRFTISRDNAKNSLYLQNSLRADTAVYCARSGYRG---DYWGQGLTVS 116

121 S 121

117 — 117

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Job time : 12.6812 secs

Job time : 12.6812 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 17, 2006, 11:39:01 ; Search time 69.7467 Seconds
(without alignments)
1223.985 Million cell updates/sec

Title: US-10-665-658-5
Perfect score: 656
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....FYGTYFDYMGGLVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	442	67.4	493	2	Q6GMX2_HUMAN
2	441.5	67.3	119	2	HV37_MOUSE
3	441	67.2	470	2	Q6PJA4_HUMAN
4	440	67.1	478	2	Q6P181_HUMAN
5	439.5	67.0	119	1	HV40_MOUSE
6	438.5	66.8	467	2	Q4VBR1_RAT
7	438.5	66.8	597	2	Q6GMV2_HUMAN
8	438	66.8	597	2	Q6GBB9_HUMAN
9	436.5	66.5	119	1	HV38_MOUSE
10	435	66.3	479	2	Q5PQK9_RAT
11	430	65.5	113	2	Q9UI90_HUMAN
12	429.5	65.5	469	2	Q569F4_HUMAN
13	428	65.2	121	2	Q9UI71_HUMAN
14	425	64.8	118	1	HV39_MOUSE
15	425	64.8	616	2	Q504M7_MOUSE
16	424.5	64.7	118	2	Q9UI72_HUMAN
17	424.5	64.7	118	2	Q9UI91_HUMAN
18	422.5	64.4	613	2	Q8WUK1_HUMAN
19	422	64.3	464	2	Q6MZU6_HUMAN
20	420.5	64.1	465	2	Q6PEC4_HUMAN
21	419.5	63.9	114	2	Q9UI81_MOUSE
22	419.5	63.9	473	2	Q6MZV7_HUMAN
23	419	63.9	131	2	Q9UI88_HUMAN
24	419	63.9	240	2	Q6S2C9_HUMAN
25	419	63.9	466	2	Q6N096_HUMAN
26	417.5	63.6	139	1	HV07_MOUSE
27	417.5	63.6	145	2	Q924Q7_MOUSE
28	417	63.6	117	1	HV41_MOUSE
29	416.5	63.5	475	2	Q6MZQ6_HUMAN
30	415.5	63.3	119	2	Q5F218_MOUSE
31	415.5	63.3	487	2	Q6ZVX0_HUMAN

32	415	63.3	146	2	Q924Q3_MOUSE
33	415	63.3	476	2	Q4V924_MOUSE
34	414.5	63.2	494	2	Q96K68_HUMAN
35	414	63.1	116	2	Q9UI93_HUMAN
36	414	63.1	479	2	Q5BK12_RAT
37	413.5	63.0	122	1	HV3G_HUMAN
38	413.5	63.0	483	2	Q6MZK9_HUMAN
39	411.5	62.7	486	2	Q5H2Y6_MOUSE
40	411	62.7	466	2	Q6IN78_HUMAN
41	410	62.5	115	1	HV3D_HUMAN
42	410	62.5	146	2	Q924R8_MOUSE
43	410	62.5	472	2	Q6N089_HUMAN
44	409	62.3	119	2	Q9GY22_MOUSE
45	408.5	62.3	147	2	Q9Y509_HUMAN

ALIGNMENTS

RESULT 1
Q6GMX2_HUMAN
ID Q6GMX2_HUMAN PRELIMINARY; PRT; 493 AA.
AC Q6GMX2_HUMAN
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHAI protein.
GN Name=IGHAI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeck S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RC NIH MGC Project;
RC Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
RL EMBL; BC073771; AAH73771.1; -, mRNA.
DR SMR; Q6GMX2; 263-471.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGv; 1.

DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG MHC; UNKNOWN 1.
 DR SEQUENCE 493 AA, 52865 MW, 558993058286203 CRC64;

Query Match 67.4%; Score 442; DB 2; Length 493;
 Best Local Similarity 70.2%; Pred. No. 5, 2e-38;
 Matches 85; Conservative 8; Mismatches 28; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNMYVQAQPGKGLIEWYGMTHPSDSERY 60
 DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFLPSSYMMHWVQAQPGKGLVWVRINSDDSTSY 79
 QY 61 NQKFKDRFTISVDKSKNTLYLQNMNSLRAPDVAIVYCARGIYFGTYTDPYWGQGLTVTVS 120
 DB 80 ADSVGRFTISRDNKNTLYLQNMNSLRGDAIVYCARGFVSLPRSTLDIWGQGLTVTVS 139
 QY 121 S 121
 DB 140 S 140

RESULT 2

HV37 MOUSE STANDARD; PRT; 119 AA.
 AC P01807;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ig heavy chain V region X44.
 OS Mus musculus (Mouse).
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]

PROTEIN SEQUENCE.
 MEDLINE=79223895; PubMed=111245;
 RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
 RT "Structural evidence for independent joining region gene in
 RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
 RT its potential role in generating diversity in complementarity-
 RT determining regions.";
 RT Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).

CC [2]
 CC NUCLEOTIDE SEQUENCE OF 1-118
 CC MEDLINE=90064531; PubMed=2555519;
 CC Miller A. III, Glasel J.A.;
 CC "Comparative sequence and immunochemical analyses of murine monoclonal
 CC anti-morphine antibodies.";
 CC J. Mol. Biol. 209:763-778 (1989).
 CC -1- MISCELLANEOUS: This chain was isolated from an IGA myeloma protein
 CC that binds galactan.
 CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC PIR: A02077; AVMSX4.
 CC HSSP: P01810; 2FBJ.
 CC SMR: P01807; 1-119.
 CC DR Ensembl: ENSMUSG0000003483; Mus musculus.
 CC DR InterPro: IPR007110; Ig-like.
 CC DR InterPro: IPR003596; Ig_V.
 CC DR SMART: SM00406; IGV; 1.
 CC DR PROSITE: PS50835; IG LIKE; 1.
 CC DR Direct protein sequencing: Immunoglobulin domain;
 CC Immunoglobulin V region.
 CC KW DOMAIN 1 117 Ig-like.
 CC FT NON TER 119 119
 CC SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;

Query Match 67.3%; Score 441.5; DB 1; Length 119;
 Best Local Similarity 66.9%; Pred. No. 1, 1e-38;
 Matches 81; Conservative 19; Mismatches 18; Indels 3; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNMYVQAQPGKGLIEWYGMTHPSDSERY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGDFPSRMYMSWVQAQPGKGLIEWYGMTHPSDSERY 60
 QY 61 NQKFKDRFTISVDKSKNTLYLQNMNSLRAPDVAIVYCARGIYFGTYTDPYWGQGLTVTVS 120
 DB 61 TPSLKDFTISRDNKNTLYLQNMNSLRKVSSEDTALYYCAR-LHYTG--YAAVWGQGLTVTVS 117
 QY 121 S 121
 DB 118 A 118

RESULT 3

Q6PUA4 HUMAN PRELIMINARY; PRT; 470 AA.
 ID Q6PUA4;
 DT 05-JUL-2004 (TRMBLrel. 27, Created)
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RP TISSUE=Primary B-Cells;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

CC NUCLEOTIDE SEQUENCE.
 CC TISSUE=Primary B-Cells;
 CC RG NIH GGC Project;
 CC DR Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC DR EMBL: BC018747; AAH18747.1; -, mRNA.
 CC DR HSSP: P01861; IADO.
 CC DR SMR: Q6PUA4; 20-470.
 CC DR InterPro: IPR003599; Ig.
 CC DR InterPro: IPR007110; Ig-like.
 CC DR InterPro: IPR003597; Ig_C1.
 CC DR InterPro: IPR003006; IG_MHC.
 CC DR InterPro: IPR003596; IG_V.
 CC DR Pfam: PF07654; C1-set; 3.
 CC DR SMART: SM00409; IG; 2.
 CC DR SMART: SM00407; IGH1; 3.
 CC DR SMART: SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 470 AA; 51716 MW; 78495656A1FD7D9 CRC64;

Query Match 67.2%; Score 441; DB 2; Length 470;
 Best Local Similarity 71.1%; Pred. No. 6.2e-38;

Matches 86; Conservative 9; Mismatches 26; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKLEWYGMIPHSDETRY 60
 DB 20 EVQLVESGGGLVQPGGSLRLSCVSGFTSSYTMNSWVRQAPGKLEWYANIKQDSEKYY 79
 QY 61 NQKFPDRFTISVDKSKNTLYLQMSLRADTAIVYVCARGIYYGTYPDYWGQGLTVTVS 120
 DB 80 VDSVKGRTTISRDNKNSLYLQMSLRADTAIVYVCARGDSSWYRDMFPMGQGLTVTVS 139
 QY 121 S 121
 DB 140 S 140

RESULT 4

Q6PI81_HUMAN PRELIMINARY; PRT; 478 AA.

AC Q6PI81;
 DT 05-JUL-2004 (TRMBLrel. 27, Created)
 DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE IGHM protein.
 GN Name=IGHM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grusec L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollany S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S., Schein J.E., Jones S.J.M., Skaleka U., Smallos D.E.,
 RA Scherch A., Scherch J.E., Jones S.J.M., Maria M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC041037; AAH41037.1; -, mRNA.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; Cl-sect.3.
 DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 478 AA; 52667 MW; 17BED38D917970D6 CRC64;

Query Match 67.1%; Score 440; DB 2; Length 478;
 Best Local Similarity 67.2%; Pred. No. 8.1e-38;

Matches 88; Conservative 9; Mismatches 22; Indels 12; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKLEWYGMIPHSDETRY 60
 DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSSYTMNSWVRQAPGKLEWYANIKQDSEKYY 79
 QY 61 NQKFPDRFTISVDKSKNTLYLQMSLRADTAIVYVCARGI-----YFGTYPDY 110
 DB 80 VDSVKGRTTISRDNKNSLYLQMSLRADTAIVYVCANEPSTMTTVNADYY--FYMDV 137
 QY 111 WGQGLTVTVSS 121
 DB 138 WGKGTTVTVSS 148

RESULT 5

HV40_MOUSE STANDARD; PRT; 119 AA.

AC HV40_MOUSE
 DT 21-JUL-1966 (Rel. 01, Created)
 DT 21-JUL-1966 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region J539.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP PRELIMINARY PROTEIN SEQUENCE.
 RC MEDLINE=79223895; PubMed=111245;
 RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
 RT "Structural evidence for independent joining region gene in
 immunoglobulin heavy chains from anti-galactan myeloma proteins and
 its potential role in generating diversity in complementarity-
 determining regions.";
 RT Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
 RL [2]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=88217852; PubMed=3449853; DOI=10.1002/prot.340010112;
 RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
 RA Davies D.R.;
 RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
 study at 2.6-A resolution.";
 RL Proteins 1:74-80(1986).
 CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein that
 binds galactan.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC PIR; A02080; AVMSJ5.
 DR PDB; 2PB1; X-ray; H=1-119.
 DR Ensembl; ENSMUSG00000003483; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
 FT Immunoglobulin V region.
 FT NON_TER 119 119

```

FT STRAND 3 7
FT STRAND 10 12
FT TURK 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 34 39
FT TURK 41 42
FT STRAND 45 51
FT TURK 53 54
FT STRAND 58 60
FT TURK 62 67
FT STRAND 68 72
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 100
FT TURK 101 103
FT STRAND 104 108
FT STRAND 112 116
SQ SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;

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Query Match 67.0%; Score 439.5; DB 1; Length 119;
 Best Local Similarity 66.1%; Pred. No. 1.8e-38;
 Matches 80; Conservative 19; Mismatches 19; Indels 3; Gaps 2;

```

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLWVGMHPDSETRY 60
DB 1 EVKLEESGGGLVOPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLWVGMHPDSETRY 60
QY 61 NOKPDRFTISVDKSKNTLYLQMSLRADTAIVYCARGIYGYGTYTFFDYWGQGLTVTV 120
DB 61 TSLKDKFTISRDNAMNSLYLQMSKVRSDTALYYCAR-LHYYG--YNAVMGQGLTVTVS 117
QY 121 S 121
DB 118 A 118

```

RESULT 6

Q4VBH1_RAT PRELIMINARY; PRT; 467 AA.

AC Q4VBH1; 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE LOC2939354 protein.
 GN Name=LOC2939354;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 NCBI_TaxId=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smolins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
 CC histocompatibility complex class I molecules (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC EMBL, BC095846; AA095846.1; -. mRNA.
 DR InterPro; IPR003599; IG_1-like.
 DR InterPro; IPR007110; IG_1-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR Immunoglobulin domain; Repeat.
 SQ SEQUENCE 467 AA; 51651 MW; 1FF0328F50160ED3 CRC64;

Query Match 66.8%; Score 438.5; DB 2; Length 467;
 Best Local Similarity 66.4%; Pred. No. 1.1e-37;
 Matches 81; Conservative 15; Mismatches 25; Indels 1; Gaps 1;

```

QY 1 EVOLVESGGGLVOPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLWVGMHPDSETRY 60
DB 20 EVOLVETGGGLVOPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLWVGMHPDSETRY 79
QY 61 NOKPDRFTISVDKSKNTLYLQMSLRADTAIVYCARGIYGYGTYTFFDYWGQGLTVTV 119
DB 80 PDSVKGRTTISRDNAMNSLYLQMSLRSDTATYVYCARGEYGYGTYTFFDYWGQGLTVTV 139
QY 120 SS 121
DB 140 SS 141

```

RESULT 7

Q6GMV2_HUMAN PRELIMINARY; PRT; 606 AA.

AC Q6GMV2; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE LOC2939354 protein.
 GN Name=IGHM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Mullahy S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butcherfield V.S.N., Krzywniak M.J., Skalska U., Smalhus D.E.,
RA Schnerber A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -, mRNA.
DR SMR; O6GM2; 20-256.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sect; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 606 AA; 66185 MW; B6B3B85114B4C55 CRC64;

Query Match 66.8%; Score 438.5; DB 2; Length 606;
Best Local Similarity 63.5%; Pred. No. 1.5e-37;
Matches 87; Conservative 12; Mismatches 19; Indels 19; Gaps 2

QY 1 EVQLVESGGGLVQPQGSRLTSCAASGYSFTGIMNWNVRAQPKGLEWYGMHPSDSETRY 60
DB 20 QVQLVESGGGLVPGGSLRLTSCAASGFTSDYMSIRQAPKGLKLEWYVYSSSSYTRY 79
QY 61 NQKFDRLFTISVDKSKNTLYLQWNSLRADTAIVYVCARG-----IIFYG 104
DB 80 ADSVAGRFTISRDNAKNSLYLQWNSLRADTAIVYVCARGNGIAAGRVYVADYVYVYG 139
QY 105 TTPDYWGQGLTVTVSS 121
DB 140 --MDVWGQGTITVTVSS 153

RESULT 8
Q96BB9 HUMAN PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.Q., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murthy D.M., Sodegryen B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,
RA Scherch A., Schein J.B., Jones S.J.M., Merra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH Mcg Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2500644;
RA Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
RT "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
RT chains of a human monoclonal antibody with broad reactivity to
RT malignant tumor cells";
RL Nucleic Acids Res. 17:4385-0(1989).
DR EMBL, BC015760; AAH15760.1; -, mRNA.
DR PIR, S05271, S05271.
DR PIR, S24260, S24260.
DR HSSP, P01861, IADQ.
DR Ensemble, ENSG00000130076; Homo sapiens.
DR InterPro, IPR007110, Ig-like.
DR InterPro, IPR003597, Ig_C1.
DR InterPro, IPR003006, Ig_MHC.
DR InterPro, IPR003596, Ig_V.
DR Pfam, PF07654, C1-set; 4.
DR SMART, SM00406; IGV, 1.
DR PROSITE, PS50835, IG_LIKE; 5.
DR PROSITE, PS00290, IG_MHC; UNKNOWN_3.
RW Immunoglobulin domain.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3ADBCE263D9 CRC64;

Query Match 66.8%; Score 438; DB 2; Length 597;
Best Local Similarity 72.8%; Pred. No. 1.7e-37;
Matches 91; Conservative 6; Mismatches 24; Indels 4; Gaps 2

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSGFTGMNWVRQAPRGKLEWYGMTHPSDSETRY 60
DB 20 EVQLLEGGGGLVQGGSLRLSCAASGSPFSFYANWVRQAPRGKLEWVSALSGSGSTYY 79
QY 61 NQKFKDRFTISVDKSKNTLYIQNNSLRAEDPAVYYCA--RGIFYGCI-TYFDYGGQGL 116
DB 80 ADSYKGFRTISRDNSRDTLYIQNNSLRAEDPAVYYCACKDPGYSASGNYTRDYWGQGL 139
QY 117 VTSS 121
DB 140 VTSS 144

RESULT 9
ID HV38_MOUSE STANDARD; PRT; 119 AA.
AC P01808;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Kruttsch H., Poter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in complementarity-
```

RT determining regions."
 RL Proc Natl Acad Sci U S A. 76:2890-2894(1979).
 CC -I- MISCELLANEOUS: This chain was isolated from an Iga myeloma protein
 CC that binds galactan.
 CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC PIR: A02078; AWMST6.
 DR HSSP: P01810; 2FBJ.
 DR SMR: P01808; 1-119.
 DR Ensembl: ENSMUSG0000003483; Mus musculus.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin domain;
 KM Immunoglobulin V region.
 KM DOMAIN 1 112 IG-like.
 FT NON TER 119 119
 SQ SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;

 Query Match 66.5%; Score 436.5; DB 1; Length 119;
 Best Local Similarity 66.9%; Pred. No. 3.8e-38;
 Matches 81; Conservative 17; Mismatches 20; Indels 3; Gaps 2;

 QY 1 EVOLVESGGGLVOPGGSRLRLSCAAGYSFTGHMMWVROAPGKGLIEWGMIPDSSETRY 60
 DB 1 EVKLSSGGGLVOPGGSRLRLSCAAGSFPDSRYRMWVRAAPGKGLIEWGMIPDSSTINY 60
 QY 61 NQKFRDFTISVDKSKNTLYIQMNSLRADTAIVYICARGIYFGTTFDYWGQGLTVYS 120
 DB 61 TSLDKKFTISRDNKNTLYIQMNSKVRSDTALYYCAR-IGYGG--YFDVWGAGTVTVYS 117
 QY 121 S 121
 DB 118 S 118

 RESULT 10
 Q5POK9 RAT PRELIMINARY; PRT; 479 AA.
 AC Q5POK9;
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Igha protein.
 GN Name=Igha;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OK NCBI_TaxId=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenken C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grilwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherzer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RG NIH MGC Project;
 RL Submitted (DEC-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC087137; AA87137.1; -; mRNA.
 DR GO: GO:0003823; F:antigen binding; IEA.
 DR InterPro: IPR003599; IG-like.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG_c1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; CI-set; 2.
 DR SMART: SM00409; IG; 3.
 DR SMART: SM00407; IGC1; 3.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 479 AA; 52354 MW; 1632EF3457BE686E CRC64;

 Query Match 66.3%; Score 435; DB 2; Length 479;
 Best Local Similarity 66.9%; Pred. No. 2.7e-37;
 Matches 81; Conservative 11; Mismatches 29; Indels 0; Gaps 0;

 QY 1 EVOLVESGGGLVOPGGSRLRLSCAAGYSFTGHMMWVROAPGKGLIEWGMIPDSSETRY 60
 DB 20 EVKLSSGGGLVOPGGSRLRLSCAAGSFPDSRYRMWVRAAPGKGLIEWGMIPDSSTINY 79
 QY 61 NQKFRDFTISVDKSKNTLYIQMNSLRADTAIVYICARGIYFGTTFDYWGQGLTVYS 120
 DB 80 PDSVKGFTISRDNKNTLYIQMNSLRSDTATYCTRAAHVWGPYFAVWGQGLTVYS 139
 QY 121 S 121
 DB 140 S 140

 RESULT 11
 Q9UL90 HUMAN PRELIMINARY; PRT; 113 AA.
 AC Q9UL90;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OK NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=1730252;
 RX Raapport F.M., Timmers E., Kenter M.J., Van Tol M.J., Voosen J.M.,
 RA Schuurman R.K.;
 RT "Restricted utilization of germ-line VH3 genes and short diverse third

RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
 RT Immunoglobulin heavy chain rearrangements.";
 RL Eur. J. Immunol. 22:247-251 (1992).
 DR EMBL: AF035024; AAD56260.1; -, mRNA.
 DR F1R; S78486; S78486.
 DR HSP; P01772; 2F84.
 DR SMR; Q9UL90; 1-113.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1_v.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT 113 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
 Query Match 65.5%; Score 430; DB 2; Length 113;
 Best Local Similarity 70.2%; Pred. No. 1.8e-37;
 Matches 85; Conservative 9; Mismatches 19; Indels 8; Gaps 1;
 QY 1 EVOLVSSGGGLVOPGGSRLRLSCAASGYSTFGHMNMVROAPGKLEWGMHPSDSETRY 60
 DB 1 EVOLVSSGGGVOPGGSRLRLSCAASGFTBSYGMHVROAPGKLEWVAFIRYDSNKTY 60
 QY 61 NQFKDRTISVDKSNITLYLQNSLRADPTAVYCA-RGIYFGTTYFDYWGQGLTVV 120
 DB 61 ADVKGRFTISRDNKNSLYLQNSLRADPTAVYCAKDL-----NYWGQGLTVV 112
 QY 121 S 121
 QY 113 S 113
 DB 113 S 113
 RESULT 12
 Q569F4 HUMAN PRT; 469 AA.
 ID Q569F4 HUMAN PRELIMINARY;
 AC 0569F4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;

RG NIH MGC Project;
 RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092518; AAH92518.1; -, mRNA.
 SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
 Query Match 65.5%; Score 429.5; DB 2; Length 469;
 Best Local Similarity 72.1%; Pred. No. 1e-36;
 Matches 88; Conservative 8; Mismatches 23; Indels 3; Gaps 2;
 QY 1 EVOLVSSGGGLVOPGGSRLRLSCAASGYSTFGHMNMVROAPGKLEWGMHPSDSETRY 60
 DB 20 EVOLVSSGGGVOPGGSRLRLSCAASGFTDVTAMHVROAPGKLEWVLSMDGSSTY 79
 QY 61 NQFKDRTISVDKSNITLYLQNSLRADPTAVYCA-RGIYFGTTYFDYWGQGLTVV 119
 DB 80 ADVKGRFTISRDNKNSLYLQNSLRADPTAVYCATRG--GYSTAGFDYWGQGLTVV 137
 QY 120 SS 121
 QY 117 SS 119
 DB 117 SS 119
 RESULT 13
 Q9UL71 HUMAN PRT; 121 AA.
 ID Q9UL71 HUMAN PRELIMINARY;
 AC Q9UL71;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive Immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RP MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cclin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035043; AAD56279.1; -, mRNA.
 DR HSP; P01852; INPD.
 DR SMR; Q9UL71; 1-121.
 DR InterPro; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR SMART; SM00406; IGV; 1_v.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON TER 1
 FT 121 121
 SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFASD50736 CRC64;
 Query Match 65.2%; Score 428; DB 2; Length 121;
 Best Local Similarity 68.8%; Pred. No. 3.1e-37;
 Matches 86; Conservative 10; Mismatches 21; Indels 8; Gaps 2;
 QY 1 EVOLVSSGGGLVOPGGSRLRLSCAASGYSTFGHMNMVROAPGKLEWGMHPSDSETRY 60
 DB 1 EVOLVSSGGGVOPGGSRLRLSCAASGFTDVTAMHVROAPGKLEWVLSMDGSSTY 60
 QY 61 NQFKDRTISVDKSNITLYLQNSLRADPTAVYCA-RGIYFGTTYFDYWGQGLTVV 116
 DB 61 ADVKGRFTISRDNKNSLYLQNSLRADPTAVYCAKAKKVTITY---DRPDWQGT 116
 QY 117 VTVSS 121
 DB 117 VTVSS 121

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RESULT 14
HV39_MOUSE STANDARD; PRT; 118 AA.
AC P01809;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE I3 heavy chain V region X24.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
PROTEIN SEQUENCE.
MEDLINE=79223895; PubMed=111245.
RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in complementarity-
RT determining regions";
RT Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
[2]
NUCLEOTIDE SEQUENCE OF 103-117.
MEDLINE=92355114; PubMed=1644448; DOI=10.1007/BF00215659;
RA Solin M.L., Kaartinen M.;
RT "Allelic polymorphism of mouse Igh-J locus, which encodes
RT immunoglobulin heavy chain joining (JH) segments.";
RL Immunogenetics 36:306-313(1992).
CC -I- MISCELANEOUS: This chain was isolated from an IGA myeloma protein
CC that binds galactan.
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
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CC
DR EMBL; X63164; -, NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; P10394; AVMSX2.
DR HSSP; P01810; 2FBJ.
DR SMR; P01809; 1-118.
DR Ensembl; ENSMUSG00000003483; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 111 Ig-like.
FT NON_TER 118 118
FT SEQUENCE 118 AA; 13105 MW; B16A2DB677E717F CRC64;
SQ
Query Match 64.8%; Score 425; DB 1; Length 118;
Best local Similarity 66.1%; Pred. No. 6.3e-37;
Matches 80; Conservative 17; Mismatches 20; Indels 4; Gaps 3;
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ID Q504M7_MOUSE PRELIMINARY; PRT; 616 AA.
AC Q504M7;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalski U., Smalios D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RC NIH MGC Project;
RG Submitted (May-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC094936; AAH94936.1; -, mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-rec; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein
KW SEQUENCE 616 AA; 67919 MW; 0FF4532BCD596A52 CRC64;
SQ
Query Match 64.8%; Score 425; DB 2; Length 616;
Best local Similarity 61.2%; Pred. No. 4.2e-36;
Matches 74; Conservative 23; Mismatches 24; Indels 0; Gaps 0;
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Wed Jan 18 11:47:47 2006

us-10-665-658-5.rup

Page 9

Job time : 70.7467 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: January 17, 2006, 11:40:17 ; Search time 21.638 Seconds
(without alignments)
461.774 Million cell updates/sec

Title: US-10-665-658-5

Perfect score: 656
Sequence: 1 EVOLVSGGGLVPGGSLRL.....FYGTTFDYMGQGLVTVSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
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2: /cgn2_6/prodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/RX_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	656	100.0	121	2	US-08-974-899-5	Sequence 5, Appl
2	656	100.0	121	2	US-09-795-798-5	Sequence 5, Appl
3	632	96.3	121	2	US-08-974-899-24	Sequence 24, Appl
4	632	96.3	121	2	US-09-795-798-24	Sequence 24, Appl
5	572.5	87.3	116	2	US-09-027-449-50	Sequence 50, Appl
6	572.5	87.3	116	2	US-08-804-444A-50	Sequence 50, Appl
7	572.5	87.3	116	2	US-09-026-985-50	Sequence 50, Appl
8	572.5	87.3	116	2	US-09-121-952A-50	Sequence 50, Appl
9	572.5	87.3	116	2	US-09-234-340A-50	Sequence 50, Appl
10	572.5	87.3	116	2	US-09-355-014-50	Sequence 50, Appl
11	522.5	79.6	122	1	US-07-934-373C-20	Sequence 20, Appl
12	522.5	79.6	122	2	US-08-477-642B-20	Sequence 20, Appl
13	522.5	79.6	122	2	US-08-146-206C-20	Sequence 20, Appl
14	522.5	79.6	122	2	US-09-705-686-20	Sequence 20, Appl
15	522.5	79.6	122	2	US-09-705-392A-20	Sequence 20, Appl
16	522.5	79.6	122	2	US-09-705-398-20	Sequence 20, Appl
17	522.5	79.6	122	2	PCT-US93-07832-20	Sequence 20, Appl
18	521.5	79.5	253	2	US-08-027-449-52	Sequence 52, Appl
19	521.5	79.5	253	2	US-09-027-449-55	Sequence 55, Appl
20	521.5	79.5	253	2	US-08-804-444A-52	Sequence 52, Appl
21	521.5	79.5	253	2	US-08-804-444A-55	Sequence 55, Appl
22	521.5	79.5	253	2	US-09-026-985-52	Sequence 52, Appl
23	521.5	79.5	253	2	US-09-026-985-55	Sequence 55, Appl
24	521.5	79.5	253	2	US-08-121-952A-52	Sequence 52, Appl
25	521.5	79.5	253	2	US-08-121-952A-55	Sequence 55, Appl
26	521.5	79.5	253	2	US-09-234-340A-55	Sequence 55, Appl
27	521.5	79.5	253	2	US-09-234-340A-55	Sequence 55, Appl

28	521.5	79.5	253	2	US-09-355-014-52	Sequence 52, Appl
29	521.5	79.5	253	2	US-09-355-014-55	Sequence 55, Appl
30	521.5	79.5	256	2	US-09-027-449-70	Sequence 70, Appl
31	521.5	79.5	256	2	US-09-026-985-70	Sequence 70, Appl
32	521.5	79.5	256	2	US-09-121-952A-70	Sequence 70, Appl
33	521.5	79.5	256	2	US-09-234-340A-70	Sequence 70, Appl
34	521.5	79.5	256	2	US-09-355-014-70	Sequence 70, Appl
35	521.5	79.5	298	2	US-09-027-449-60	Sequence 60, Appl
36	521.5	79.5	298	2	US-08-804-444A-60	Sequence 60, Appl
37	521.5	79.5	298	2	US-09-026-985-60	Sequence 60, Appl
38	521.5	79.5	298	2	US-09-121-952A-60	Sequence 60, Appl
39	521.5	79.5	298	2	US-09-234-340A-60	Sequence 60, Appl
40	521.5	79.5	298	2	US-09-355-014-60	Sequence 60, Appl
41	521.5	79.5	452	2	US-09-027-449-71	Sequence 71, Appl
42	521.5	79.5	452	2	US-09-026-985-71	Sequence 71, Appl
43	521.5	79.5	452	2	US-09-121-952A-71	Sequence 71, Appl
44	521.5	79.5	452	2	US-09-234-340A-71	Sequence 71, Appl
45	521.5	79.5	452	2	US-09-355-014-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-08-974-899-5
; Sequence 5, Application US/08974899
; Patent No. 6037454

GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899

; FILING DATE:
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971

; FILING DATE: 11/27/96

; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P1014R1

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 121 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-974-899-5

Query Match 100.0%; Score 656; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.4e-57;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EVOLVSGGGLVPGGSLRLSCAASGYSFTGMNVRQAPEGKLEWVGTHPSDESTRY 60

QY 61 NQKQKRFETISVNDKSNKNTLYLQMSLRADDAVYVCARGIYFGTTPDYDVGOSTLVTS 120
Db 61 NQKQKRFETISVNDKSNKNTLYLQMSLRADDAVYVCARGIYFGTTPDYDVGOSTLVTS 120
QY 121 S 121
Db 121 S 121

RESULT 2
US-09-795-798-5

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1      Sequence 5, Application US/09795798
2      Patent No. 6703018
3
4      GENERAL INFORMATION:
5      APPLICANT: Prestea, Leonard G.
6      Jardiaeu, Paula M.
7      TITLE OF INVENTION: Humanized Anti-CD14 Antibodies
8      NUMBER OF SEQUENCES: 24
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: Genentech, Inc.
11     STREET: 1 DNA Way
12     CITY: South San Francisco
13     STATE: California
14     COUNTRY: USA
15     ZIP: 94080
16
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: WinPatIn (Genentech)
22
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/09795,798
25     FILING DATE: 28-Feb-2001
26     CLASSIFICATION: <unknown>
27
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: 08/974,899
30     FILING DATE: <unknown>
31
32     ATTORNEY/AGENT INFORMATION:
33     NAME: Lee, Wendy M.
34     REGISTRATION NUMBER: 40,378
35     REFERENCE/DOCKET NUMBER: P1014R1
36
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: 650/225-1994
39     TELEFAX: 650/952-9881
40
41     INFORMATION FOR SEQ ID NO: 5:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 121 amino acids
44     TYPE: Amino Acid
45     TOPOLOGY: Linear
46
47     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
48     US-09-795-798-5

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				Gaps	0;
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Db	1	EVQLVESGGGLVQPGGSLRLTCAASGYSFTGMHWVRQAPGKGLIEWYGMIHPSDSETRY	60		
QY	61	NQKFDRLFTISVDKSKNTLLYLOMNSLRADIAVYYCARGIYYGTTTFDYMGQGLTVYS	120		
Db	61	NQKFDRLFTISVDKSKNTLLYLOMNSLRADIAVYYCARGIYYGTTTFDYMGQGLTVYS	120		
QY	121	S	121		
Db	121	S	121		

RESULT 3
US-08-974-899-24
; Sequence 24, Application US/08974899
; Patent No. 6037454

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1 GENERAL INFORMATION:
2 APPLICANT: Presta, Leonard G.
3 APPLICANT: Jardieu, Paula M.
4 TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
5 NUMBER OF SEQUENCES: 24
6 CORRESPONDENCE ADDRESS:
7 ADDRESSSEE: Genentech, Inc.
8 STREET: 1 DNA Way
9 CITY: South San Francisco
10 STATE: California
11 COUNTRY: USA
12
13 ZIP: 94080
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: 3.5 inch, 1.44 Mb Floppy disk
17
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Winpatin (Genentech)
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/974,899
24
25 FILING DATE:
26 CLASSIFICATION: 536
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: 60/031971
29 FILING DATE: 11/27/96
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Lee, Wendy M.
32 REGISTRATION NUMBER: 40,378
33 REFERENCE/DOCKET NUMBER: P1014RI
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 650/225-1994
36 TELEFAX: 650/952-9881
37 INFORMATION FOR SEQ ID NO: 24:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 121 amino acids
40 TYPE: Amino Acid
41 TOPOLOGY: Linear
42
43 US-08-974-899-24

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Query Match	96.3%	Score 632;	DB 2;	Length 121;
Best Local Similarity	96.7%	Pred. No. 3,4e-55;		
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QY	1	EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNMYRQAPGKGLIEWGMTHPSDET	RY	60
DB	1	EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNMYRQAPGKGLIEWGMTHPSDET	RY	60
QY	61	NQKFDRLFTISVDSKNTLYLQMSNLSRAEDTAIVYVCARGIYFGTYYEDYMGQGITLVTS	RY	120
DB	61	NQKFDRLFTISVDSKNTLYLQMSNLSRAEDTAIVYVCARGIYFGTYYEDYMGQGITLVTS	RY	120
QY	121	S 121	RY	
	121	121		
DB	121	S 121	RY	
	121	121		

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1  RESULT 4
2  US-09-795-798-24
3  ; Sequence 24, Application US/09795798
4  ; Patent No. 6,703,018
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Prestea, Leonard G.
7  ; Jarden, Paul M.
8  ; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
9  ; NUMBER OF SEQUENCES: 24
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Genentech, Inc.
12 ; STREET: 1 DNA Way
13 ; CITY: South San Francisco
14 ; STATE: California
15 ; COUNTRY: USA
16 ; ZIP: 94080
17 ;
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
20 ;

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COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-795-798-24

Query Match
Best Local Similarity 96.3%; Score 632; DB 2; Length 121;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGMNMMVWVROAPGKLEWGMIHPSDETRY 60
QY 61 NQKFDKRTISVDKSKNTLYLQNNSLRAEDTAVYYCAARGIFYGTTYPDYWGQGT 120
DB 61 NQKFDKRTISVDKSKNTLYLQNNSLRAEDTAVYYCAARGIFYGTTYPDYWGQGT 120
QY 121 S 121
DB 121 S 121

RESULT 5
US-09-027-449-50
Sequence 50, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leon, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-50

Query Match
Best Local Similarity 87.3%; Score 572.5; DB 2; Length 116;
Matches 107; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGMNMMVWVROAPGKLEWGMIHPSDETRY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGMNMMVWVROAPGKLEWGMIHPSDETRY 60
QY 61 NQKFDKRTISVDKSKNTLYLQNNSLRAEDTAVYYCAARGIFYGTTYPDYWGQGT 115
DB 61 ADVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCAARGIFYGTTYPDYWGQGT 116
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RESULT 6
US-08-804-444A-50
Sequence 50, Application US/0880444A
Patent No. 611980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leon, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-804-444A-50
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Query Match
Best Local Similarity 87.3%; Score 572.5; DB 2; Length 116;
Matches 107; Conservative 1; Mismatches 7; Indels 1; Gaps 1;
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Db 1 EVCLVVEGGGLVVGCGSLRLSCAAGVSPFGHMMNMYRQAPGKGLPMVMIHPSSETRY 60
QY 61 NQKFRDRTISVDSKNTLYLQNSLAEETAVYYC-ARGITYYGTTTYPDWQGT 115
QY 61 ADVSKGPTTISRDSKNTLYLQNSLAEETAVYYCAARITYYGTTTYPDWQGT 116

RESULT 7
US-09-026-985-50

APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:

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; ADDRESS: Genentech, Inc
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
;

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: WinPatIn (Genentech)

CONSENT APPLICATION DATED: 02/20/1998
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B

REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
FOR FURTHER INFORMATION:

TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881

SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids

US-09-026-985-50

Query Match	87.3%	Score 572.5;	DB 2;	length 116;
Best Local Similarity	92.2%	Pred. No. 2.5e-49;		
Matches 107; Conservative	1;	Mismatches 7;	Indels 1;	Gaps 1

QY 1 EVQLVESGGGLVQPGSSRLRLSCAASGYSTFTMMNWVRQAPGKLELVWGMIHSDSTR 6
 Db 1 EVQLVESGGGLVQPGSSRLRLSCAASGFTFTMMNWVRQAPGKLELVWGMIHSDSTR 6
 QY 61 NQKFDRTTISVDKSKNTLYIQNMSLRADPTAVYCC-ARGITYFPTTYPDYWGQT 115
 Db 61 ADVSGRFTTISRDKSKNTLYIQNMSLRADPTAVYCCARGITYFPTTYPDYWGQT 116

RESULT 8
US-09-121-952A-50
: Sequence 50, Application US/09121952A

GENERAL INFORMATION:
 APPLICANT: Genetech, Inc., Hesi, Vanness
 APPLICANT: Koumenis, Iphigenia
 APPLICANT: Leong, Steven R.
 APPLICANT: Presta, Leonard G.
 APPLICANT: Shahrokh, Zahra

1 APPLICANT: Zapata, Gerardo A.
 2 TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
 3 TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
 4
 5 NUMBER OF SEQUENCES: 72
 6
 7 CORRESPONDENCE ADDRESS:
 8
 9 ADDRESSEE: Genentech, Inc.
 10 STREET: 1 DNA Way
 11 CITY: South San Francisco
 12 STATE: California
 13 COUNTRY: USA
 14 ZIP: 94080

COUNTRY: USA
ZIP: 94080

```

? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: WinPatIn (Genetech)
?
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/121,952
? FILING DATE: 24-Jul-1998
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/074130

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; APPLICATION NUMBER: 60/074
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075
; FILING DATE: 20-FEB-1998
; PUBLICATION INFORMATION

```

```

; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
;

```

TELECOMMUNICATION INFORMATION
TELEPHONE: 650/225-5530

```

; INFORMATION FOR SEQ ID NO: 50
;
; SEQUENCE CHARACTERISTICS:
;

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TYPE: Amino Acid
TOPOLOGY: Linear

Query Match

Best Local	Simultaneously	Seq. No.	2, 3, 5, 7, 11
Matches 107; Conservative 1; Mismatches 7; Indels 1; Gaps 1	52.20%	52.20%	52.20%

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01 I EVOLVESGGGIVLPQSSLRKLS CASGISLTGHMWNVNRQAFGLGLEWGNLTFPSIDINI   60  
02 QY      ||||| :|||||  
03 |||||
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61 NQKFDRTISVDKSKNTLYLQNSLRADTAVYYC-ARGIYEVGTTYFDYWGQGT 115

Db 61 ADSVGRFTISRDN SKNTLYLQNMNLSLR AEDTAVVYCAARGIYFVGITTFEDYWGOST 116

US-09-234-340A-50
; Sequence 50, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumentsis, Iphigenia
; APPLICANT: Leong, Steven K.

APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES

; CORRESPONDENCE Address:
 ; ADDRESSEE: Genentech, Inc
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-50

Query Match 87.3%; Score 572.5; DB 2; Length 116;
Best Local Similarity 92.2%; Pred. No. 2.5e-49;
Matches 107; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 EVQLVDSGGGLVQPGSRLRSCAASGYSFTGHMMNVRQAPGKGLFWGMTHPSDSETRY 60
DB 1 EVQLVDSGGGLVQPGSRLRSCAASGYSFTGHMMNVRQAPGKGLFWGMTHPSDSETRY 60
QY 61 NQKFKRFTISVDKSKNTLYLQMSLRADPTAVYYC-ARGIYFGTTYPDYWGQGT 115
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAARGIYFGTTYPDYWGQGT 116

RESULT 10
US-09-355-014-50
Sequence 50, Application US/09355014
Patent No. 6870033
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hael, Vanessa
Kounenis, Iphigenia
Leong, Steven K.
Presta, Leonard G.
Shahrokh, Zahra
Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014

FILING DATE: 21-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-355-014-50

Query Match 87.3%; Score 572.5; DB 2; Length 116;
Best Local Similarity 92.2%; Pred. No. 2.5e-49;
Matches 107; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 EVQLVDSGGGLVQPGSRLRSCAASGYSFTGHMMNVRQAPGKGLFWGMTHPSDSETRY 60
DB 1 EVQLVDSGGGLVQPGSRLRSCAASGYSFTGHMMNVRQAPGKGLFWGMTHPSDSETRY 60
QY 61 NQKFKRFTISVDKSKNTLYLQMSLRADPTAVYYC-ARGIYFGTTYPDYWGQGT 115
DB 61 ADSVKGRFTISRDNKNTLYLQMSLRADPTAVYYCAARGIYFGTTYPDYWGQGT 116

RESULT 11
US-07-934-373C-20
Sequence 20, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-07-934-373C-20

Query Match	79.6%;	Score 522.5;	DB 1;	Length 122;
Best Local Similarity	83.7%;	Pred. No. 2.3e-44;		
Matches 103; Conservative	5;	Mismatches 12;	Indels 3;	Gaps 2

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QY      1 EVQLVESGGGLVQPGRSLRLSCAASGYSFTGHIMNNWVRQAAPKGLEWMGIHSDSEIRY 60
        ||||| :||| :|
DB      1 EVQLVESGGGLVQPGRSLRLSCAASGSFTGYTMNWRQAAPKGLEWALLINPKGVSTY 60
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Oy      61 NQKFD RFTLSVD KSKNTLYIQMNSLRAEDTAVYYCARGIYFGTT--YFDVWGQGTLTV 118
        |||||
Db      61 NQKFD RFTLSVD KSKNTALYIQMNSLRAEDTAVYYCARSGY-YGDSIDWYFDVWGQGLTV 119
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Qy	119	VSS	121
Db	120	VSS	122

RESULT 12
US-08-437

; Sequence 20, Application US/08437642E
; Patent No. 6054297

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437, 642B
FILING DATE: 09-May-1995

Query Match	79.6%	Score 522.5;	DB 2;	Length 122;
Best Local Similarity	83.7%	Pred. NO. 2.3e-44;		
Matches 103; Conservative	5;	Mismatches 12;	Indels 3;	Gaps 2

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Qy      I EVQLVESGGGIVQPGGSLRLSCAASGYSFTGHMMNWRQAPEGKLEWVGNIHPDSSETRY 600
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Db      1 EVQLVESGGGIVQPGGSLRLSCAASGYSFTGYTMNWRQAPEGKLEWVALINPYKGVSTY 600
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QY      61 NQKKDRFTISVDKSKNTLYLQMSLRAPETAVVYCARGIIFYGTT--YFDWVGQGLTIVT 118
        |||||
DB       61 NQKKDRFTISVDKSKNTAYLQMSLRAPETAVVYCARSGY-YGDSDMYFDWVGQGLTIVT 119
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QY	119	VSS	121
Db	120	VSS	122

RESULT 13
US-08-146

; Sequence 20, Application US/08146206C
; Patent No. 6407213

? GENERAL INFORMATION:
 ? APPLICANT: Carter, Paul J.
 ? APPLICANT: Presta, Leonard G.
 ? TITLE OF INVENTION: Method for Making Humanized Antibodies
 ? NUMBER OF SEQUENCES: 26
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Genentech, Inc.
 ? STREET: 1 DNA Way
 ? CITY: South San Francisco
 ? STATE: California
 ? COUNTRY: USA
 ?

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-NO. 6407213-1993

/ CLASSIFICATION: 550
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 07/715272
 / FILING DATE: 14-JUN-1991
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Lee, Wendy M.
 / REGISTRATION NUMBER: 40,378
 / REFERENCE/DOCKET NUMBER: P0709P1
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 650/225-1994
 / TELEFAX: 650/952-9881
 / INFORMATION FOR SEQ ID NO: 20:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 122 amino acids
 / TYPE: Amino Acid
 / TOPOLOGY: Linear
 /

Query Match	79.6%	Score 522.5;	DB 2;	Length 122;
Best Local Similarity	83.7%	Pred.No. 2.3e-44;		
Matches 103; Conservative	5;	Mismatches 12;	Indels 3;	Gaps 2

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QY      1 EVQLVESGGGIVQPQGSRLRLSCAASGYSFTGHMMNTVRQAPKGLGVNMGIMHPSDSETRY 60
      |||||
DB      1 EVQLVESGGGIVQPQGSRLRLSCAASGYSFTGYTMNNTVRQAPKGLGVNALLINPKGVSTY 60

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QY	61	NQFKDF
Db	61	NQFKDF

RESULT 14
US-09-705-686-20
Sequence 20, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709PID3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-705-686-20
Query Match 79.6%; Score 522.5; DB 2; Length 122;
Best Local Similarity 83.7%; Pred. No. 2.3e-44;
Matches 103; Conservative 5; Mismatches 12; Indels 3; Gaps 2;
QY 1 EVOLVESGGGLVPGGSLRLSQAAGYSFTGHMMNWRQAPGKGLIEWGMIHPSDSETRY 60
Db 1 EVOLVESGGGLVPGGSLRLSQAAGYSFTGYTMNWRQAPGKGLIEWVALINPKGVSTY 60
QY 61 NQFKKRFITISVDKSKNTLYLQNNSLRAEDTAVYYCARGIFYGTT--YFDYWGQGLVT 118
Db 61 NQFKKRFITISVDKSKNTLYLQNNSLRAEDTAVYYCARGSY-YGDSMDYFDVWGQGLVT 119
QY 119 VSS 121
Db 120 VSS 122

RESULT 15
US-09-705-392A-20
Sequence 20, Application US/09705392A
Patent No. 6719971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-No. 6719971-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709PID1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-705-392A-20
Query Match 79.6%; Score 522.5; DB 2; Length 122;
Best Local Similarity 83.7%; Pred. No. 2.3e-44;
Matches 103; Conservative 5; Mismatches 12; Indels 3; Gaps 2;
QY 1 EVOLVESGGGLVPGGSLRLSQAAGYSFTGHMMNWRQAPGKGLIEWGMIHPSDSETRY 60
Db 1 EVOLVESGGGLVPGGSLRLSQAAGYSFTGYTMNWRQAPGKGLIEWVALINPKGVSTY 60
QY 61 NQFKKRFITISVDKSKNTLYLQNNSLRAEDTAVYYCARGIFYGTT--YFDYWGQGLVT 118
Db 61 NQFKKRFITISVDKSKNTLYLQNNSLRAEDTAVYYCARGSY-YGDSMDYFDVWGQGLVT 119
QY 119 VSS 121
Db 120 VSS 122

Search completed: January 17, 2006, 11:48:15
Job time : 22.6538 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:42:07 ; Search time 59.179 Seconds
(without alignments)
854.312 Million cell updates/sec

Title: US-10-6665-658-5

Perfect score: 656
Sequence: 1 EVQLVESGGGLVQPGSLRL...FYGTTYFDYWGQGLVTSS 121

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 18675655

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	45 summaries

```
Database : Published Applications AA Main:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	656	100.0	121	3	US-09-795-798-5	Sequence 5, Appl1
2	656	100.0	121	4	US-10-727-737-5	Sequence 5, Appl1
3	656	100.0	121	5	US-10-877-532-6	Sequence 6, Appl1
4	656	100.0	451	4	US-10-423-399-4	Sequence 4, Appl1
5	632	96.3	121	3	US-09-795-798-24	Sequence 24, Appl1
6	632	96.3	121	4	US-10-727-737-17	Sequence 17, Appl1
7	572.5	87.3	116	3	US-09-726-258-50	Sequence 50, Appl1
8	523.5	79.6	122	4	US-10-818-765-2	Sequence 2, Appl1
9	523.5	79.6	122	5	US-10-835-641-20	Sequence 20, Appl1
10	522.5	79.6	122	5	US-10-877-363-2	Sequence 2, Appl1
11	522.5	79.6	122	5	US-10-922-651-2	Sequence 2, Appl1
12	522.5	79.6	122	5	US-10-861-049-14	Sequence 14, Appl1
13	522.5	79.6	122	6	US-11-021-874-14	Sequence 14, Appl1
14	523.5	79.6	122	6	US-11-005-677-2	Sequence 2, Appl1
15	522.5	79.6	122	6	US-11-006-136-2	Sequence 2, Appl1
16	522.5	79.6	452	4	US-10-818-765-4	Sequence 4, Appl1
17	522.5	79.6	452	5	US-10-861-049-16	Sequence 16, Appl1
18	522.5	79.6	452	5	US-10-861-049-17	Sequence 17, Appl1
19	522.5	79.6	452	5	US-10-861-049-20	Sequence 20, Appl1
20	523.5	79.6	452	5	US-10-861-049-22	Sequence 22, Appl1
21	522.5	79.6	452	6	US-11-021-874-16	Sequence 16, Appl1
22	522.5	79.6	452	6	US-11-021-874-17	Sequence 17, Appl1
23	522.5	79.6	452	6	US-11-021-874-20	Sequence 20, Appl1
24	522.5	79.6	452	6	US-11-021-874-22	Sequence 22, Appl1
25	522.5	79.6	452	6	US-11-005-677-4	Sequence 4, Appl1
26	522.5	79.6	452	6	US-11-005-136-4	Sequence 4, Appl1
27	522.5	79.6	471	5	US-10-877-363-4	Sequence 4, Appl1

28	522.5	79.6	471.5	US-10-922-651-4	Sequence 4, April 11
29	522.5	79.6	471.5	US-10-861-049-4	Sequence 4, April 11
29	522.5	79.6	471.5	US-10-861-049-4	Sequence 4, April 11
30	522.5	79.6	471.5	US-10-861-049-4	Sequence 11, April 1
31	522.5	79.6	471.6	US-11-021-874-1	Sequence 4, April 1
32	522.5	79.6	471.6	US-11-021-874-1	Sequence 11, April 1
33	521.5	79.5	253.3	US-09-726-258-52	Sequence 52, April 1
33	521.5	79.5	253.3	US-09-726-258-52	Sequence 55, April 1
34	521.5	79.5	253.3	US-09-726-258-52	Sequence 55, April 1
35	521.5	79.5	256.3	US-09-726-258-70	Sequence 70, April 1
36	521.5	79.5	298.3	US-09-726-258-60	Sequence 60, April 1
37	521.5	79.5	452.3	US-09-726-258-71	Sequence 71, April 1
38	519.5	79.2	452.5	US-10-861-049-6	Sequence 46, April 1
39	519.5	79.2	452.6	US-11-021-874-6	Sequence 46, April 1
40	513	78.2	121.3	US-09-795-798-4	Sequence 4, April 1
41	513	78.2	121.4	US-10-727-737-4	Sequence 49, April 1
42	496	75.6	117.3	US-09-726-258-49	Sequence 49, April 1
43	494.5	75.4	122.5	US-10-835-641-26	Sequence 26, April 1
44	489	74.5	119.4	US-09-811-123-2	Sequence 2, April 1
45	489	74.5	119.4	US-10-266-501-4	Sequence 4, April 1

ALIGNMENTS

```

1 RESULT 1
2 US-09-795-798-5
3 : Sequence 5, Application US/09795798
4 : Publication No. US20030207336A1
5 : GENERAL INFORMATION:
6 : APPLICANT: Presta, Leonard G.
7 : Jardieu, Paula M.
8 : TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
9 : NUMBER OF SEQUENCES: 24
10 : CORRESPONDENCE ADDRESS:
11 : ADDRESSEE: Genentech, Inc.
12 : STREET: 1 DNA Way
13 : CITY: South San Francisco
14 : STATE: California
15 : COUNTRY: USA
16 : ZIP: 94080
17 :
18 : COMPUTER READABLE FORM:
19 : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
20 : COMPUTER: IBM PC compatible
21 : OPERATING SYSTEM: PC-DOS/MS-DOS
22 : SOFTWARE: Winpatin (Genentech)
23 : CURRENT APPLICATION DATA:
24 : APPLICATION NUMBER: US/09/795,798
25 : FILING DATE: 28-Feb-2001
26 : CLASSIFICATION: <Unknown>
27 : PRIOR APPLICATION DATA:
28 : APPLICATION NUMBER: 08/974,899
29 : FILING DATE: <Unknown>
30 : ATTORNEY/AGENT INFORMATION:
31 : NAME: Lee, Wendy M.
32 : REGISTRATION NUMBER: 40,378
33 : REFERENCE/DOCKET NUMBER: P1014R1
34 : TELECOMMUNICATION INFORMATION:
35 : TELEPHONE: 650/225-1994
36 : TELEFAX: 650/352-9861
37 : INFORMATION FOR SEQ ID NO: 5:
38 : SEQUENCE CHARACTERISTICS:
39 : LENGTH: 121 amino acids
40 : TYPE: Amino Acid
41 : TOPOLOGY: Linear
42 :
43 : SEQUENCE DESCRIPTION: SEQ ID NO: 5:
44 :
45 : US-09-795-798-5
46 :
47 : Query Match 100.0%; Score 656; DB 3; Length 121;
48 : Best Local Similarity 100.0%; Prid. No. 2.2e-52;
49 : Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
50 :
51 :
52 : 1 EVQLVESGGGLVQPGSGRLSCASGYSFPTGHMMNWVRQAPGKGLIEWYGMTHPSDSETRY 60
53 : |||||
54 : 1 EVQLVESGGGLVQPGSGRLSCASGYSFTGHMMNWVRQAPGKGLIEWYGMTHPSDSETRY 60

```

OY		61	NOKFDRPTISVDKSNITLYLOMNSLRADPAVYYCARGLTFYGGTTPPYMGCGTLVWTS	120
Dd		61	NOKFDRPTISVDKSNITLYLOMNSLRADPAVYYCARGLTFYGGTTPPYMGCGTLVWTS	120
OY		121	S	121
Dd		121	S	121

RESULT 2

```

US10-727-737-5
1 / Sequence 5, Application US/10727737
2 / Publication No. US20040146507A1
3 /
4 / GENERAL INFORMATION:
5 / APPLICANT: Presta, Leonard G.
6 / Jardiou, Paula M.
7 / TITLE OF INVENTION: Antibody Mutants
8 / NUMBER OF SEQUENCES: 79
9 / CORRESPONDENCE ADDRESS:
10 / ADDRESSEE: Genentech, Inc.
11 / STREET: 1 DNA Way
12 / CITY: South San Francisco
13 / STATE: California
14 / COUNTRY: USA
15 / ZIP: 94080
16 /
17 / COMPUTER READABLE FORM:
18 / MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
19 / COMPUTER: IBM PC compatible
20 / OPERATING SYSTEM: PC-DOS/MS-DOS
21 / SOFTWARE: winpatin (Genentech)
22 /
23 / CURRENT APPLICATION DATA:
24 / APPLICATION NUMBER: US/10727,737
25 / FILING DATE: 03-Dec-2003
26 /
27 / CLASSIFICATION: <Unknown>
28 /
29 / PRIOR APPLICATION DATA:
30 / APPLICATION NUMBER: US/08/975,329B
31 / FILING DATE: 20-Nov-1997
32 / APPLICATION NUMBER: 60/031945
33 / FILING DATE: 27-Nov-1996
34 /
35 / ATTORNEY/AGENT INFORMATION:
36 / NAME: Lee, Wendy M.
37 / REGISTRATION NUMBER: 40,378
38 / REFERENCE/DOCKET NUMBER: P1064R1
39 / TELECOMMUNICATION INFORMATION:
40 / TELEPHONE: 650/225-1994
41 / TELEFAX: 650/952-9881
42 /
43 / INFORMATION FOR SEQ ID NO: 5:
44 / SEQUENCE CHARACTERISTICS:
45 / LENGTH: 121 amino acids
46 / TYPE: Amino Acid
47 / TOPOLOGY: Linear
48 /
49 / SEQUENCE DESCRIPTION: SEQ ID NO: 5:
50 /
51 /
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100 /

```

Query Match 100.0%; Score 656; DB 4; Length 121;

Best Local Similarity 100.0%; Pred. No. 2.2e-52;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVOLVESGGGLVOPGGSLRLSCAAGSYFTGHMMNWTQAPKGLKLEWYGMIHSDSETRY 60

Db 1 EVOLVESGGGLVOPGGSLRLSCAAGSYFTGHMMNWTQAPKGLKLEWYGMIHSDSETRY 60

Qy 61 NQKFKRFTISVDKSKNTLYLQMNLSLAEDTAVYYCARGIYEGTTYFDYWGQGLTVTS 120

Dh 61 NQKFKRFTISVDKSKNTLYLQMNLSLAEDTAVYYCARGIYEGTTYFDYWGQGLTVTS 120

Qy	121	S	121
Db	121	S	121

RESULT 3

```

US-10-877-532-6
; Sequence 6, Application US/10877532
; Publication No. US20050038231A1
; GENERAL INFORMATION:
; APPLICANT: FAHRNER, ROBERT L.
; APPLICANT: LAVERDIERE, AMY
; APPLICANT: McDONALD, PAUL J.
; APPLICANT: O'LEARY, RHONA M.
; TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAPHY
; FILE REFERENCE: P2015R1
; CURRENT APPLICATION NUMBER: US/10/877,532
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US 60/490,500
; PRIOR FILING DATE: 2003-07-28
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 6
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-877-532-6

```

Query Match	100.0%;	Score 656;	DB 5;	Length 121;
Best Local Similarity	100.0%;	Pred. No. 2.2e-52;		
Matches 121; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNWVRQAPGKGLEWVGMIHPDSETRY 60

QY 1 EVQLVDSGGGLVQPGGSLRLSCAAGYSPFTGMNMMVRAAPKGLIEWVMGHIHPSSEETFF 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAAGYSPFTGMNMMVRAAPKGLIEWMGINHPSDETFF 60
QY 61 NQKFDREFTISVDKSKNTLLYLOMNSIRAEADIAVYYCARGIYFGTTFPDYMGGSLVTVS 120
DB 61 NQKFDREFTISVDKSKNTLLYLOMNSIRAEADIAVYYCARGIYFGTTFPDYMGGSLVTVS 120

Qy	121	S	121
Db	121	S	121

RESULT 4

```

US-10-423-299-4
; Sequence 4, Application US/104232299
; Publication No. US20030229212A1
; GENERAL INFORMATION:
; APPLICANT: FAHNER, ROBERT
; APPLICANT: FOLLMAN, DEBORAH
; APPLICANT: LEBERTON, BENEDICTE
; APPLICANT: VAN REIS, ROBERT
; TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
; FILE REFERENCE: 39766-0121A
; CURRENT APPLICATION NUMBER: US/10/423,299
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/375,953
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-423-299-4

```

Query Match	100.0%	Score 656	DB 4	Length 451
-------------	--------	-----------	------	------------

Best Local Similarity 100.0%; Pred. No. 8.5e-52;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVOPGGSRLRLSCAAGSYFTGHNWNTVROAPGKGLENVGMIHPSDSERY 60

Db 1 EVLVESGGGLVOPGGSRLRLSCAAGSYFTGHNWNTVROAPGKGLENVGMIHPSDSERY 60

61 NQKFKDRFTISVDKSKNTLYLQMSLRADTAVVYCARGIYFYGTTYFDYWGGLTVS 120

Db 61 NOKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCCARGIYFGTTYFDYWGQGLTVVS 120
QY 121 S 121
Db 121 S 121

RESULT 5
US-09-795-798-24

/ Sequence 24, Application US/09795798
/ Publication No. US20030207336A1
/ GENERAL INFORMATION:
/ APPLICANT: Presta, Leonard G.
/ Jardiou, Paula M.
/ TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/795,798
/ FILING DATE: 28-Feb-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/974,899
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P1014R1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1994
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 121 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-795-798-24

Query Match 96.3%; Score 632; DB 3; Length 121;
Best Local Similarity 96.7%; Pred. No. 3.5e-50;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVQPGSLRLSCAASGYSFTGHMMNWVROAPGKGLEWGMIHPSDSETRY 60
Db 1 EVQLVSGGGLVQPGSLRLSCAASGYSFTGHMMNWVROAPGKGLEWGMIA PASSTRY 60
QY 61 NOKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCCARGIYFGTTYFDYWGQGLTVVS 120
Db 61 NOKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCCARGIYFGTTYFDYWGQGLTVVS 120
QY 121 S 121
Db 121 S 121

RESULT 6
US-10-727-737-17
/ Sequence 17, Application US/10727737
/ Publication No. US20040146507A1
/ GENERAL INFORMATION:

/ APPLICANT: Presta, Leonard G.
/ Jardiou, Paula M.
/ TITLE OF INVENTION: Antibody Mutants
/ NUMBER OF SEQUENCES: 79
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/727,737
/ FILING DATE: 03-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/975,329B
/ FILING DATE: 20-Nov-1997
/ APPLICATION NUMBER: 60/031945
/ FILING DATE: 27-Nov-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P1064R1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1994
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 121 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-727-737-17

Query Match 96.3%; Score 632; DB 4; Length 121;
Best Local Similarity 96.7%; Pred. No. 3.5e-50;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVQLVSGGGLVQPGSLRLSCAASGYSFTGHMMNWVROAPGKGLEWGMIHPSDSETRY 60
Db 1 EVQLVSGGGLVQPGSLRLSCAASGYSFTGHMMNWVROAPGKGLEWGMIA PASSTRY 60
QY 61 NOKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCCARGIYFGTTYFDYWGQGLTVVS 120
Db 61 NOKFKDRFTISVDKSKNTLYLQMNLSRAEDTAVVYCCARGIYFGTTYFDYWGQGLTVVS 120
QY 121 S 121
Db 121 S 121

RESULT 7
US-09-726-258-50

/ Sequence 50, Application US/09726258
/ Publication No. US20030021790A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc., Heel, Vanessa
/ APPLICANT: Koumenis, Iphigenia
/ APPLICANT: Leong, Steven R.
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Shatrokh, Zahra
/ APPLICANT: Zapata, Gerardo A.
/ TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
/ TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
/ NUMBER OF SEQUENCES: 72
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.

```

: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/726,258
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/234,182
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/094003
: FILING DATE: 24-JUL-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P1085R4-1A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 116 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: US-09-726-258-50
:
: Query Match      87.3%; Score 572.5; DB 3; Length 116;
: Best Local Similarity 92.2%; Pred. No. 9.4e-45;
: Matches 107; Conservative 1; Mismatches 7; Indels 1; Gaps 1;
:
: QY      1 EVOLVESGGGLVQPGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDSETRY 60
:         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
: DB      1 EVOLVESGGGLVQPGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDSETRY 60
:
: QY      61 NQKFKDRFTISVDKSKNTLYLQNNSLRAEDTAVYYC-ARGIFYGTYFDYWGGLT 115
:         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
: DB      61 ADSVKGRFTISRDNSKNTLYLQNNSLRAEDTAVYYCAAGIIFYGTYFDYWGGLT 116
:
: RESULT 8
: US-10-818-765-2
: Sequence 2, Application US/10818765
: Publication No. US20040202658A1
: GENERAL INFORMATION:
: APPLICANT: Benyunes, Mark C.
: TITLE OF INVENTION: THERAPY OF AUTOIMMUNE DISEASE IN A PATIENT WITH AN
: TITLE OF INVENTION: INADEQUATE RESPONSE TO A TNF- $\alpha$  INHIBITOR
: FILE REFERENCE: P2027R1-US
: CURRENT APPLICATION NUMBER: US/10/818,765
: CURRENT FILING DATE: 2004-04-06
: PRIOR APPLICATION NUMBER: US 60/461,4819
: PRIOR FILING DATE: 2003-04-09
: NUMBER OF SEQ ID NOS: 4
: SEQ ID NO 2
: LENGTH: 122
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: humanized sequence
:
: US-10-818-765-2
:
: Query Match      79.6%; Score 522.5; DB 4; Length 122;
: Best Local Similarity 82.0%; Pred. No. 3.8e-40;
: Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

```

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: QY      1 EVOLVESGGGLVQPGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDSETRY 60
:         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
: DB      1 EVOLVESGGGLVQPGSLRLSCAASGYTFTSYNNHWVRQAPGKLEWVAIYPNGDTSY 60
:
: QY      61 NQKFKDRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIFYGT--TFPDYWGGLT 119
:         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
: DB      61 NQKFKGRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARVYVNSYTFDVGGLT 120
:
: QY      120 SS 121
:         ||
: DB      121 SS 122
:
: RESULT 9
: US-10-835-641-20
: Sequence 20, Application US/10835641
: Publication No. US20040236078A1
: GENERAL INFORMATION:
: APPLICANT: Carter, Paul J.
: Presta, Leonard G.
: TITLE OF INVENTION: Method for Making Humanized Antibodies
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESS: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/835,641
: FILING DATE: 30-Apr-2004
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/705,398
: FILING DATE: 02-Nov-2000
: APPLICATION NUMBER: 08/146206
: FILING DATE: 17-Nov-1993
: APPLICATION NUMBER: 07/715272
: FILING DATE: 14-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P0709P1D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-1994
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 122 amino acids
: TYPE: Amino Acid
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 20:
:
: US-10-835-641-20
:
: Query Match      79.6%; Score 522.5; DB 5; Length 122;
: Best Local Similarity 83.7%; Pred. No. 3.8e-40;
: Matches 103; Conservative 5; Mismatches 12; Indels 3; Gaps 2;
:
: QY      1 EVOLVESGGGLVQPGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDSETRY 60
:         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
: DB      1 EVOLVESGGGLVQPGSLRLSCAASGYFTGYTNMVRQAPGKLEWVALINPYGVSTY 60
:
: QY      61 NQKFKDRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIFYGT--YFDYWGGLT 118
:         |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
: DB      61 NQKFKDRFTISVDKSKNTLYLQNNSLRAEDTAVYYCAASGY- YGDSMYTFDVGGLT 119
:
: QY      119 VSS 121

```


Db 120 VSS 122

RESULT 10

US-10-877-363-2
; Sequence 2, Application US/10877363
; Publication No. US20050032130A1
; GENERAL INFORMATION:
; APPLICANT: BERESINI, MAUREN
; APPLICANT: SONG, AN
; TITLE OF INVENTION: NEUTRALIZING ANTIBODY ASSAY AND USES THEREFOR
; FILE REFERENCE: P2032R1
; CURRENT APPLICATION NUMBER: US/10/877,363
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US 60/490,678
; PRIOR FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-877-363-2

Query Match 79.6%; Score 522.5; DB 5; Length 122;
Best Local Similarity 82.0%; Pred. No. 3.8e-40;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

Qy 1 EVOLVESGGGLVOPGSGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDESTRY 60

Db 1 EVOLVESGGGLVOPGSGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDESTRY 60

Qy 61 NOFKGRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIYFGT-TYFDYWGQGLTVTV 119

Db 61 NOFKGRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARVYYSNSYTFDVGQGLTVTV 120

Qy 120 SS 121

Db 121 SS 122

RESULT 11

US-10-922-651-2
; Sequence 2, Application US/10922651
; Publication No. US20050053602A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; TITLE OF INVENTION: Therapy of Ocular Disorders
; FILE REFERENCE: P2029R1
; CURRENT APPLICATION NUMBER: US/10/922,651
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/498,791
; PRIOR FILING DATE: 2003-08-29
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-922-651-2

Query Match 79.6%; Score 522.5; DB 5; Length 122;
Best Local Similarity 82.0%; Pred. No. 3.8e-40;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

Qy 1 EVOLVESGGGLVOPGSGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDESTRY 60

Db 1 EVOLVESGGGLVOPGSGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDESTRY 60

Qy 61 NOFKGRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIYFGT-TYFDYWGQGLTVTV 119

Db 61 NOFKGRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARVYYSNSYTFDVGQGLTVTV 120

RESULT 12

US-10-861-049-14
; Sequence 14, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-861-049-14

Query Match 79.6%; Score 522.5; DB 5; Length 122;
Best Local Similarity 82.0%; Pred. No. 3.8e-40;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

Qy 1 EVOLVESGGGLVOPGSGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDESTRY 60

Db 1 EVOLVESGGGLVOPGSGSLRLSCAASGYSFTGHMMNVRQAPGKLEWVGMIHPSDESTRY 60

Qy 61 NOFKGRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARGIYFGT-TYFDYWGQGLTVTV 119

Db 61 NOFKGRFTISVDKSKNTLYLQNNSLRAEDTAVYYCARVYYSNSYTFDVGQGLTVTV 120

Qy 120 SS 121

Db 121 SS 122

RESULT 13

US-11-021-874-14
; Sequence 14, Application US/11021874
; Publication No. US20050163775A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1P1
; CURRENT APPLICATION NUMBER: US/11/021,874
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/861,049
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 165

```
; SEQ ID NO 14
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-021-874-14
```

```
Query Match      79.6%; Score 522.5; DB 6; Length 122;
Best Local Similarity 82.0%; Pred. No. 3.8e-40;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
```

```
QY      1 EVQLVESGGGLVQPQGSRLSCAASGYSTFGHMNVRQAPGKLEWGMIHPSDESTRY 60
      |||
      1 EVQLVESGGGLVQPQGSRLSCAASGYSTFGHMNVRQAPGKLEWGMIHPSDESTRY 60
DB      1 EVQLVESGGGLVQPQGSRLSCAASGYSTFGHMNVRQAPGKLEWGMIHPSDESTRY 60
      |||
      61 NQKFKGRFTISVDKSKNTLYLQMSLRADTAIVYCARVYYNSYWFVDWGGGLTVTV 119
      |||
      61 NQKFKGRFTISVDKSKNTLYLQMSLRADTAIVYCARVYYNSYWFVDWGGGLTVTV 120
QY      120 SS 121
      ||
DB      121 SS 122
```

```
RESULT 14
US-11-005-677-2
; Sequence 2, Application US/11005677
; Publication No. US20050186206A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; TITLE OF INVENTION: DETECTION OF CD20 IN THERAPY OF AUTOIMMUNE DISEASES
; FILE REFERENCE: P2061R1
; CURRENT APPLICATION NUMBER: US/11/005,677
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US 60/531,363
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-11-005-677-2
```

```
Query Match      79.6%; Score 522.5; DB 6; Length 122;
Best Local Similarity 82.0%; Pred. No. 3.8e-40;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
```

```
QY      1 EVQLVESGGGLVQPQGSRLSCAASGYSTFGHMNVRQAPGKLEWGMIHPSDESTRY 60
      |||
      1 EVQLVESGGGLVQPQGSRLSCAASGYSTFGHMNVRQAPGKLEWGMIHPSDESTRY 60
DB      1 EVQLVESGGGLVQPQGSRLSCAASGYSTFGHMNVRQAPGKLEWGMIHPSDESTRY 60
      |||
      61 NQKFKGRFTISVDKSKNTLYLQMSLRADTAIVYCARVYYNSYWFVDWGGGLTVTV 119
      |||
      61 NQKFKGRFTISVDKSKNTLYLQMSLRADTAIVYCARVYYNSYWFVDWGGGLTVTV 120
QY      120 SS 121
      ||
DB      121 SS 122
```

```
RESULT 15
US-11-006-136-2
; Sequence 2, Application US/11006136
; Publication No. US20050191297A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; TITLE OF INVENTION: DETECTION OF CD20 IN TRANSPLANT REJECTION
; FILE REFERENCE: P2062R1
; CURRENT APPLICATION NUMBER: US/11/006,136
; CURRENT FILING DATE: 2004-12-07
```

```
; PRIOR APPLICATION NUMBER: US 60/531,594
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-11-006-136-2
```

```
Query Match      79.6%; Score 522.5; DB 6; Length 122;
Best Local Similarity 82.0%; Pred. No. 3.8e-40;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
```

```
QY      1 EVQLVESGGGLVQPQGSRLSCAASGYSTFGHMNVRQAPGKLEWGMIHPSDESTRY 60
      |||
      1 EVQLVESGGGLVQPQGSRLSCAASGYSTFGHMNVRQAPGKLEWGMIHPSDESTRY 60
DB      1 EVQLVESGGGLVQPQGSRLSCAASGYSTFGHMNVRQAPGKLEWGMIHPSDESTRY 60
      |||
      61 NQKFKGRFTISVDKSKNTLYLQMSLRADTAIVYCARVYYNSYWFVDWGGGLTVTV 119
      |||
      61 NQKFKGRFTISVDKSKNTLYLQMSLRADTAIVYCARVYYNSYWFVDWGGGLTVTV 120
QY      120 SS 121
      ||
DB      121 SS 122
```

```
Search completed: January 17, 2006, 11:50:18
Job time : 60.179 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 11:44:33 ; Search time 5.81223 Seconds
(without alignments)
196.820 Million cell updates/sec

Title: US-10-665-658-5

Perfect score: 656
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....FYGTYFPDWGQGLTVVSS 121

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications_AA_New:*

1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppaa/BCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	656	100.0	121	6	US-10-665-658-5
2	656	100.0	121	7	US-11-107-028-50
3	632	96.3	121	6	US-10-665-658-24
4	523.5	79.8	122	7	US-11-120-338-24
5	523.5	79.8	122	7	US-11-120-338-25
6	523.5	79.8	122	7	US-11-120-338-17
7	523.5	79.8	122	7	US-11-107-028-47
8	523.5	79.8	122	7	US-11-106-820-45
9	523.5	79.6	122	7	US-11-120-338-8
10	523.5	79.6	122	7	US-11-107-028-30
11	522.5	79.6	122	7	US-11-106-820-8
12	522.5	79.6	122	7	US-11-120-338-22
13	522.5	79.6	122	7	US-11-120-338-14
14	522.5	79.6	122	7	US-11-120-338-15
15	522.5	79.6	122	7	US-11-107-028-32
16	522.5	79.6	122	7	US-11-107-028-33
17	522.5	79.6	122	7	US-11-106-820-26
18	522.5	79.6	122	7	US-11-106-820-28
19	522.5	79.6	122	7	US-11-106-820-25
20	522.5	79.6	122	7	US-11-106-820-27
21	519.5	79.2	122	7	US-11-107-028-43
22	519.5	79.2	122	7	US-11-107-028-45
23	519.5	79.2	122	7	US-11-107-028-46
24	519.5	79.2	122	7	US-11-106-820-30
25	513	78.2	121	6	US-10-665-658-4

26	513	78.2	121	7	US-11-107-028-52	Sequence 52, Appl
27	494	75.3	667	7	US-11-096-046-25	Sequence 25, Appl
28	494	75.3	695	7	US-11-096-046-26	Sequence 26, Appl
29	487	74.2	124	7	US-11-096-046-4	Sequence 4, Appl
30	487	74.2	667	7	US-11-096-046-28	Sequence 28, Appl
31	487	74.2	667	7	US-11-096-046-30	Sequence 30, Appl
32	486	74.1	666	7	US-11-096-046-27	Sequence 27, Appl
33	484	73.8	248	7	US-11-106-820-16	Sequence 16, Appl
34	472.5	72.0	232	7	US-11-025-712-10	Sequence 10, Appl
35	472.5	72.0	450	7	US-11-025-712-12	Sequence 12, Appl
36	463	70.6	117	7	US-11-127-903-44	Sequence 44, Appl
37	460.5	70.2	116	6	US-10-925-366A-223	Sequence 223, App
38	460.5	70.2	249	7	US-11-054-535-1856	Sequence 1856, Ap
39	460	70.1	126	6	US-10-923-327-16	Sequence 16, Appl
40	459.5	70.0	126	7	US-11-127-932-5	Sequence 5, Appl
41	459.5	70.0	126	7	US-11-127-903-5	Sequence 5, Appl
42	459	70.0	125	7	US-11-127-903-21	Sequence 21, Appl
43	459	70.0	129	6	US-10-850-635-12	Sequence 12, Appl
44	458	69.8	118	6	US-10-648-816-12	Sequence 12, Appl
45	458	69.8	118	6	US-10-648-816-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-10-665-658-5
Sequence 5, Application US/10665658

Publication No. US20050276801A1

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996

APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997

APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999

APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.

REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014RIC1D1C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids

TYPE: Amino Acid
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-665-658-5

Query Match 100.0%; Score 656; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 4e-47;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPQGSRLRLSCAASGYSTFGHMNMVVRQAPGKGLRWGMHPSDSETRY 60
|
1 EVQLVESGGGLVQPQGSRLRLSCAASGYSTFGHMNMVVRQAPGKGLRWGMHPSDSETRY 60

DB 61 NQKFKDRFTISVDKSKNTLYLQWNSLRADPTAVVYCARGIYFGTTYPDYWGQGLTVVS 120
|
61 NQKFKDRFTISVDKSKNTLYLQWNSLRADPTAVVYCARGIYFGTTYPDYWGQGLTVVS 120

QY 121 S 121
|
121 S 121

DB 121 S 121
|
121 S 121

RESULT 2
US-11-107-028-50
; Sequence 50, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 50
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-50

Query Match 100.0%; Score 656; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 4e-47;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPQGSRLRLSCAASGYSTFGHMNMVVRQAPGKGLRWGMHPSDSETRY 60
|
1 EVQLVESGGGLVQPQGSRLRLSCAASGYSTFGHMNMVVRQAPGKGLRWGMHPSDSETRY 60

DB 61 NQKFKDRFTISVDKSKNTLYLQWNSLRADPTAVVYCARGIYFGTTYPDYWGQGLTVVS 120
|
61 NQKFKDRFTISVDKSKNTLYLQWNSLRADPTAVVYCARGIYFGTTYPDYWGQGLTVVS 120

QY 121 S 121
|
121 S 121

DB 121 S 121
|
121 S 121

RESULT 3
US-10-665-658-24
; Sequence 24, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447

REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-665-658-24

Query Match 96.3%; Score 632; DB 6; Length 121;
Best Local Similarity 96.7%; Pred. No. 3.5e-45;
Matches 117; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPQGSRLRLSCAASGYSTFGHMNMVVRQAPGKGLRWGMHPSDSETRY 60
|
1 EVQLVESGGGLVQPQGSRLRLSCAASGYSTFGHMNMVVRQAPGKGLRWGMHPSDSETRY 60

DB 61 NQKFKDRFTISVDKSKNTLYLQWNSLRADPTAVVYCARGIYFGTTYPDYWGQGLTVVS 120
|
61 NQKFKDRFTISVDKSKNTLYLQWNSLRADPTAVVYCARGIYFGTTYPDYWGQGLTVVS 120

QY 121 S 121
|
121 S 121

DB 121 S 121
|
121 S 121

RESULT 4
US-11-120-338-24
; Sequence 24, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IORAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 24
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-24

```
Query Match          79.8%; Score 523.5; DB 7; Length 122;
Best Local Similarity 82.8%; Pred. No. 2.1e-36;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 1 EVOLVSSGGGLVOPGSLRLSCAASGYSTFGHMMNVRQAPGKGLEWGMHPSDSERY 60
    |||
DB 1 EVOLVSSGGGLVOPGSLRLSCAASGYSTFGHMMNVRQAPGKGLEWGMHPSDSERY 60
    |||
QY 61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYF-YGTFYFDYWGQGLTVTV 119
    |||
DB 61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVIYSRYWYFDWVGQGLTVTV 120
    |||
QY 120 SS 121
    ||
DB 121 SS 122

RESULT 5
US-11-120-338-25
; Sequence 25, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: WALLICE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 25
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-25

Query Match          79.8%; Score 523.5; DB 7; Length 451;
Best Local Similarity 82.8%; Pred. No. 6.2e-36;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 1 EVOLVSSGGGLVOPGSLRLSCAASGYSTFGHMMNVRQAPGKGLEWGMHPSDSERY 60
    |||
DB 1 EVOLVSSGGGLVOPGSLRLSCAASGYSTFGHMMNVRQAPGKGLEWGMHPSDSERY 60
    |||
QY 61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYF-YGTFYFDYWGQGLTVTV 119
    |||
DB 61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVIYSRYWYFDWVGQGLTVTV 120
    |||
QY 120 SS 121
    ||
DB 121 SS 122

RESULT 6
US-11-120-338-17
; Sequence 17, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: WALLICE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
```

```
; SEQ ID NO 17
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-17

Query Match          79.8%; Score 523.5; DB 7; Length 452;
Best Local Similarity 82.8%; Pred. No. 6.2e-36;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 1 EVOLVSSGGGLVOPGSLRLSCAASGYSTFGHMMNVRQAPGKGLEWGMHPSDSERY 60
    |||
DB 1 EVOLVSSGGGLVOPGSLRLSCAASGYSTFGHMMNVRQAPGKGLEWGMHPSDSERY 60
    |||
QY 61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYF-YGTFYFDYWGQGLTVTV 119
    |||
DB 61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVIYSRYWYFDWVGQGLTVTV 120
    |||
QY 120 SS 121
    ||
DB 121 SS 122

RESULT 7
US-11-107-028-47
; Sequence 47, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 47
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-47

Query Match          79.8%; Score 523.5; DB 7; Length 452;
Best Local Similarity 82.8%; Pred. No. 6.2e-36;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 1 EVOLVSSGGGLVOPGSLRLSCAASGYSTFGHMMNVRQAPGKGLEWGMHPSDSERY 60
    |||
DB 1 EVOLVSSGGGLVOPGSLRLSCAASGYSTFGHMMNVRQAPGKGLEWGMHPSDSERY 60
    |||
QY 61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYF-YGTFYFDYWGQGLTVTV 119
    |||
DB 61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVIYSRYWYFDWVGQGLTVTV 120
    |||
QY 120 SS 121
    ||
DB 121 SS 122

RESULT 8
US-11-106-820-45
; Sequence 45, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: SEMEL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
```

```
FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 45
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-45
```

```
Query Match      79.8%; Score 523.5; DB 7; Length 452;
Best Local Similarity 82.8%; Pred. No. 6.2e-36;
Matches 101; Conservative 7; Mismatches 13; Indels 1; Gaps 1;
```

```
QY      1 EVOLVESGGGLVQPGSRLRLSCAASGYFTGHMMNVRQAPGKLEWVGMIHPDSETRY 60
        |||
        1 EVOLVESGGGLVQPGSRLRLSCAASGYFTSYNMHWVRQAPGKLEWVGAIYPGNGDTSY 60
DB
QY      61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFGT-TYFDYWGQGLTVTV 119
        |||
        61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVYYSYNRYFDYWGQGLTVTV 120
DB
QY      120 SS 121
        ||
        121 SS 122
DB
```

```
RESULT 9
US-11-120-338-8
; Sequence 8, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 8
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-8
```

```
Query Match      79.6%; Score 522.5; DB 7; Length 122;
Best Local Similarity 82.0%; Pred. No. 2.5e-36;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
```

```
QY      1 EVOLVESGGGLVQPGSRLRLSCAASGYFTGHMMNVRQAPGKLEWVGMIHPDSETRY 60
        |||
        1 EVOLVESGGGLVQPGSRLRLSCAASGYFTSYNMHWVRQAPGKLEWVGAIYPGNGDTSY 60
DB
QY      61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFGT-TYFDYWGQGLTVTV 119
        |||
        61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVYYSYNRYFDYWGQGLTVTV 120
DB
QY      120 SS 121
        ||
        121 SS 122
DB
```

```
RESULT 10
US-11-107-028-30
; Sequence 30, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 30
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-30
```

```
Query Match      79.6%; Score 522.5; DB 7; Length 122;
Best Local Similarity 82.0%; Pred. No. 2.5e-36;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
```

```
QY      1 EVOLVESGGGLVQPGSRLRLSCAASGYFTGHMMNVRQAPGKLEWVGMIHPDSETRY 60
        |||
        1 EVOLVESGGGLVQPGSRLRLSCAASGYFTSYNMHWVRQAPGKLEWVGAIYPGNGDTSY 60
DB
QY      61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFGT-TYFDYWGQGLTVTV 119
        |||
        61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVYYSYNRYFDYWGQGLTVTV 120
DB
QY      120 SS 121
        ||
        121 SS 122
DB
```

```
RESULT 11
US-11-106-820-8
; Sequence 8, Application US/11106820
; Publication No. US2006002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: SEMELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 8
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-8
```

```
Query Match      79.6%; Score 522.5; DB 7; Length 122;
Best Local Similarity 82.0%; Pred. No. 2.5e-36;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
```

```
QY      1 EVOLVESGGGLVQPGSRLRLSCAASGYFTGHMMNVRQAPGKLEWVGMIHPDSETRY 60
        |||
        1 EVOLVESGGGLVQPGSRLRLSCAASGYFTSYNMHWVRQAPGKLEWVGAIYPGNGDTSY 60
DB
QY      61 NOKFKRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFGT-TYFDYWGQGLTVTV 119
```

Db 61 NQFKGRFTISVDKSKNTLYLQNMNSLRABDTAVYYCARVYYNSYWFVWGQGLTVTV 120
QY 120 SS 121
Db 121 SS 122

RESULT 12
US-11-120-338-22

/ Sequence 22, Application US/11120338
/ Publication No. US20050271658A1
/ GENERAL INFORMATION:
/ APPLICANT: BRUNETTA, PAUL G.
/ APPLICANT: GREWAL, IOBAL S.
/ APPLICANT: WALICKE, PATRICIA A.
/ TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
/ FILE REFERENCE: P2079R2
/ CURRENT APPLICATION NUMBER: US/11/120,338
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: US 60/568,460
/ PRIOR FILING DATE: 2004-05-05
/ NUMBER OF SEQ ID NOS: 25
/ SEQ ID NO 22
/ LENGTH: 451
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-120-338-22

Query Match 79.6%; Score 522.5; DB 7; Length 451;

Best Local Similarity 82.0%; Pred. No. 7.5e-36;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLEWVGMIHPSDSETRY 60
1 EVOLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYRGNIDTSTY 60
Db 61 NQFKDRFTISVDKSKNTLYLQNMNSLRABDTAVYYCARGYIFYGT-TYFDYWGQGLTVTV 119
61 NQFKGRFTISVDKSKNTLYLQNMNSLRABDTAVYYCARVYYNSYWFVWGQGLTVTV 120
QY 120 SS 121
Db 121 SS 122

RESULT 13
US-11-120-338-14

/ Sequence 14, Application US/11120338
/ Publication No. US20050271658A1
/ GENERAL INFORMATION:
/ APPLICANT: BRUNETTA, PAUL G.
/ APPLICANT: GREWAL, IOBAL S.
/ APPLICANT: WALICKE, PATRICIA A.
/ TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
/ FILE REFERENCE: P2079R2
/ CURRENT APPLICATION NUMBER: US/11/120,338
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: US 60/568,460
/ PRIOR FILING DATE: 2004-05-05
/ NUMBER OF SEQ ID NOS: 25
/ SEQ ID NO 14
/ LENGTH: 452
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-120-338-14

Query Match 79.6%; Score 522.5; DB 7; Length 452;
Best Local Similarity 82.0%; Pred. No. 7.5e-36;

Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLEWVGMIHPSDSETRY 60
1 EVOLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYRGNIDTSTY 60
Db 61 NQFKDRFTISVDKSKNTLYLQNMNSLRABDTAVYYCARGYIFYGT-TYFDYWGQGLTVTV 119
61 NQFKGRFTISVDKSKNTLYLQNMNSLRABDTAVYYCARVYYNSYWFVWGQGLTVTV 120
QY 120 SS 121
Db 121 SS 122

RESULT 14
US-11-120-338-15

/ Sequence 15, Application US/11120338
/ Publication No. US20050271658A1
/ GENERAL INFORMATION:
/ APPLICANT: BRUNETTA, PAUL G.
/ APPLICANT: GREWAL, IOBAL S.
/ APPLICANT: WALICKE, PATRICIA A.
/ TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
/ FILE REFERENCE: P2079R2
/ CURRENT APPLICATION NUMBER: US/11/120,338
/ CURRENT FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: US 60/568,460
/ PRIOR FILING DATE: 2004-05-05
/ NUMBER OF SEQ ID NOS: 25
/ SEQ ID NO 15
/ LENGTH: 452
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-120-338-15

Query Match 79.6%; Score 522.5; DB 7; Length 452;

Best Local Similarity 82.0%; Pred. No. 7.5e-36;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

QY 1 EVOLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNVRQAPGKGLEWVGMIHPSDSETRY 60
1 EVOLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYRGNIDTSTY 60
Db 61 NQFKDRFTISVDKSKNTLYLQNMNSLRABDTAVYYCARGYIFYGT-TYFDYWGQGLTVTV 119
61 NQFKGRFTISVDKSKNTLYLQNMNSLRABDTAVYYCARVYYNSYWFVWGQGLTVTV 120
QY 120 SS 121
Db 121 SS 122

RESULT 15
US-11-107-028-32

/ Sequence 32, Application US/11107028
/ Publication No. US20050276803A1
/ GENERAL INFORMATION:
/ APPLICANT: CHAN, ANDREW C.
/ APPLICANT: GONG, QIAN
/ APPLICANT: MARTIN, FLAVIUS
/ TITLE OF INVENTION: Method for Augmenting B Cell Depletion
/ FILE REFERENCE: P2112R1
/ CURRENT APPLICATION NUMBER: US/11/107,028
/ CURRENT FILING DATE: 2005-04-15
/ PRIOR APPLICATION NUMBER: US 60/563,263
/ PRIOR FILING DATE: 2004-04-16
/ NUMBER OF SEQ ID NOS: 52
/ SEQ ID NO 32
/ LENGTH: 452
/ TYPE: PRT

```

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-32

```

```

Query Match          79.6%; Score 522.5; DB 7; Length 452;
Best Local Similarity 82.0%; Pred. No. 7.5e-36;
Matches 100; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

```

```

Oy      1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHMMNMVROAPGKGLIEWVGMTHPSDSETRY 60
         |||||
Db       1 EVQLVESGGGLVQPGGSLRLSCAASGYFTSYNMHWROAPGKGLIEWGAIYPGNGDTSY 60
         |||||
Oy      61 NQKFDKPTISYDKSKNTLYIQMNSLRADPTAVYYCARGIYFGT-TYEDVWGQGLIVTV 119
         |||||
Db       61 NQKFKGRPTISYDKSKNTLYIQMNSLRADPTAVYYCARVYVYSNSIYIFDVWGQGLIVTV 120
         |||||
Oy      120 SS 121
         ||
Db       121 SS 122

```

Search completed: January 17, 2006, 11:50:39
Job time : 5.81223 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2006, 11:46:53 : Search time 62.5758 Seconds
(without alignments)
70.215 Million cell updates/sec

Title: US-10-665-658-10
Perfect score: 64
Sequence: 1 GVSFTGHMMN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq.21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	10	2	AAW62010 Heavy cha
2	64	100.0	10	3	AAW62010 Heavy cha
3	64	100.0	10	8	ADG38998 Humanised
4	64	100.0	10	8	ADG38998 Humanised
5	64	100.0	121	2	AAW62013 Heavy cha
6	64	100.0	121	2	AAW62013 Heavy cha
7	64	100.0	121	2	AAW62019 Rhesusise
8	64	100.0	121	2	AAW63542 Murine MH
9	64	100.0	121	2	AAW63551 Murine MH
10	64	100.0	121	3	AAW63552 Humanised
11	64	100.0	121	3	AAW63552 Humanised
12	64	100.0	121	3	AAW63552 Humanised
13	64	100.0	121	3	AAW63552 Humanised
14	64	100.0	121	3	AAW63552 Humanised
15	64	100.0	121	3	AAW63552 Humanised
16	64	100.0	121	3	AAW63552 Humanised
17	64	100.0	121	3	AAW63552 Humanised
18	64	100.0	121	3	AAW63552 Humanised
19	64	100.0	121	3	AAW63552 Humanised
20	64	100.0	121	3	AAW63552 Humanised
21	64	100.0	121	3	AAW63552 Humanised
22	64	100.0	121	3	AAW63552 Humanised
23	64	100.0	121	3	AAW63552 Humanised
24	64	100.0	121	3	AAW63552 Humanised

25	60	93.8	116	3	AAB30312 Human Igg
26	60	93.8	116	6	ABU13789 Human Igg
27	60	93.8	116	6	ABU59502 Human Igg
28	60	93.8	116	7	AAE39085 Human Igg
29	59	92.2	10	8	ADRO3385 Humanised
30	58	90.6	10	8	ADRO3385 Humanised
31	55	85.9	122	8	ADW38454 CD11a hea
32	54	84.4	10	8	ADRO3387 Humanised
33	52	81.2	66	6	ABU56835 BONT/A Hc
34	52	81.2	66	6	ABU56835 BONT/A Hc
35	52	81.2	66	6	ABU56835 BONT/A Hc
36	52	81.2	66	6	ABU56835 BONT/A Hc
37	52	81.2	117	5	AAE22192 Murine MC
38	52	81.2	118	2	AAW01576 Lead bind
39	52	81.2	118	2	AAW01576 Lead bind
40	52	81.2	118	9	ADZ21535 Anti-Muc-
41	52	81.2	121	8	ADZ21535 Anti-Muc-
42	52	81.2	121	8	ADZ21535 Anti-Muc-
43	52	81.2	121	8	ADZ21535 Anti-Muc-
44	52	81.2	121	8	ADZ21535 Anti-Muc-
45	52	81.2	125	8	ADZ21535 Anti-Muc-
46	52	81.2	125	8	ADZ21535 Anti-Muc-
47	52	81.2	125	8	ADZ21535 Anti-Muc-
48	52	81.2	125	8	ADZ21535 Anti-Muc-
49	52	81.2	125	8	ADZ21535 Anti-Muc-
50	51	79.7	120	8	AAW45442 Sequence
51	51	79.7	120	8	AAW45442 Sequence
52	51	79.7	120	8	AAW45442 Sequence
53	51	79.7	120	8	AAW45442 Sequence
54	51	79.7	120	8	AAW45442 Sequence
55	51	79.7	120	8	AAW45442 Sequence
56	51	79.7	120	8	AAW45442 Sequence
57	51	79.7	120	8	AAW45442 Sequence
58	51	79.7	120	8	AAW45442 Sequence
59	51	79.7	120	8	AAW45442 Sequence
60	51	79.7	120	8	AAW45442 Sequence
61	51	79.7	120	8	AAW45442 Sequence
62	51	79.7	120	8	AAW45442 Sequence
63	51	79.7	120	8	AAW45442 Sequence
64	51	79.7	120	8	AAW45442 Sequence
65	51	79.7	120	8	AAW45442 Sequence
66	51	79.7	120	8	AAW45442 Sequence
67	51	79.7	120	8	AAW45442 Sequence
68	51	79.7	120	8	AAW45442 Sequence
69	51	79.7	120	8	AAW45442 Sequence
70	51	79.7	120	8	AAW45442 Sequence
71	51	79.7	120	8	AAW45442 Sequence
72	51	79.7	120	8	AAW45442 Sequence
73	51	79.7	120	8	AAW45442 Sequence
74	51	79.7	120	8	AAW45442 Sequence
75	51	79.7	120	8	AAW45442 Sequence
76	51	79.7	120	8	AAW45442 Sequence
77	51	79.7	120	8	AAW45442 Sequence
78	51	79.7	120	8	AAW45442 Sequence
79	51	79.7	120	8	AAW45442 Sequence
80	51	79.7	120	8	AAW45442 Sequence
81	51	79.7	120	8	AAW45442 Sequence
82	51	79.7	120	8	AAW45442 Sequence
83	51	79.7	120	8	AAW45442 Sequence
84	51	79.7	120	8	AAW45442 Sequence
85	51	79.7	120	8	AAW45442 Sequence
86	51	79.7	120	8	AAW45442 Sequence
87	51	79.7	120	8	AAW45442 Sequence
88	51	79.7	120	8	AAW45442 Sequence
89	51	79.7	120	8	AAW45442 Sequence
90	51	79.7	120	8	AAW45442 Sequence
91	51	79.7	120	8	AAW45442 Sequence
92	51	79.7	120	8	AAW45442 Sequence
93	51	79.7	120	8	AAW45442 Sequence
94	51	79.7	120	8	AAW45442 Sequence
95	51	79.7	120	8	AAW45442 Sequence
96	51	79.7	120	8	AAW45442 Sequence
97	51	79.7	120	8	AAW45442 Sequence

98	49	76.6	260	9	ADZ21542	Adz21542	Anti-Muc-	171	46	71.9	120	8	ADQ92339	Adq92339	Human A10
99	49	76.6	263	2	AAW90226	Aaw90226	Anti-B7.2	172	46	71.9	120	8	ADQ80528	Adq80528	Human A10K heav
100	49	76.6	268	2	AAW90222	Aaw90222	Anti-B7.2	173	46	71.9	120	8	ADR38650	Adr38650	Mouse hea
101	49	76.6	276	2	AAW90227	Aaw90227	Anti-B7.1	174	46	71.9	121	2	AAW53584	Aaw53584	Heavy cha
102	49	76.6	277	2	AAW96342	Aaw96342	sFVMHC-1-	175	46	71.9	124	2	AAE03750	Aae03750	Murine ps
103	49	76.6	277	2	AAW96343	Aaw96343	sFVMHC-1-	176	46	71.9	128	7	ADD28334	Add28334	Human het
104	49	76.6	281	2	AAW90223	Aaw90223	Anti-B7.1	177	46	71.9	137	9	AEA89783	Aea89783	Anti-body
105	49	76.6	447	9	AEB13531	Aeb13531	Mature ch	178	46	71.9	138	9	ADM44425	Adm44425	CP3a mono
106	49	76.6	477	8	ADQ14477	Adq14477	Mature ant	179	46	71.9	140	2	AAE27051	Aae27051	Reshaped
107	49	76.6	470	8	ADM72031	Adm72031	Chimeric	180	46	71.9	140	3	AAV56712	Aav56712	Anti-acti
108	49	76.6	507	5	AAU72858	Aau72858	8G7C10x4-	181	46	71.9	254	4	AEA44057	Aea44057	Anti-TPO
109	49	76.6	556	2	AAW90218	Aaw90218	Bispecific	182	46	71.9	288	2	AAW82743	Aaw82743	Fusion pr
110	49	76.6	580	2	AAW90217	Aaw90217	Bispecific	183	46	71.9	445	2	AAE76085	Aae76085	MAB 55.1
111	49	76.6	709	3	ADR43337	Adr43337	Anti-NKG2	184	46	71.9	466	4	AAE76088	Aae76088	Chimeric
112	48	75.0	98	2	AAE00038	Aae00038	Human sec	185	46	71.9	466	4	AAE03755	Aae03755	Chimeric
113	48	75.0	98	2	AAE27008	Aae27008	Hypercalc	186	46	71.9	524	9	AEA44228	Aea44228	Anti-TPO
114	48	75.0	115	2	AAE21267	Aae21267	Murine VH	187	46	71.9	524	9	AEA44189	Aea44189	Anti-TPO
115	48	75.0	115	2	AEA44083	Aea44083	Anti-TPO	188	46	71.9	524	9	AEA44199	Aea44199	Anti-TPO
116	48	75.0	116	2	AAE27010	Aae27010	Hypercalc	189	46	71.9	524	9	AEA44222	Aea44222	Anti-TPO
117	48	75.0	117	8	ADP47094	Adp47094	Human pho	190	46	71.9	524	9	AEA43937	Aea43937	Anti-TPO
118	48	75.0	118	8	ADP47116	Adp47116	Human pho	191	46	71.9	524	9	AEA44195	Aea44195	Anti-TPO
119	48	75.0	118	8	ADP47102	Adp47102	Human pho	192	46	71.9	673	2	AAW82742	Aaw82742	Plasmid P
120	48	75.0	119	8	ADP25815	Adp25815	Anti-alph	193	45	70.3	10	8	ADM78114	Adm78114	Human SJB
121	48	75.0	119	8	ADG25812	Adg25812	Anti-CD30	194	45	70.3	10	8	ADM78132	Adm78132	Human SJB
122	48	75.0	120	2	AAE47491	Aae47491	Humanised	195	45	70.3	10	8	ADQ92371	Adq92371	Human hui
123	48	75.0	120	2	AAE47493	Aae47493	Murine an	196	45	70.3	10	8	ADQ80560	Adq80560	TNF-alpha
124	48	75.0	120	4	AAE62860	Aae62860	Anti-SAF-	197	45	70.3	10	8	ADU07226	Adu07226	Human 4D4
125	48	75.0	120	9	ADM13533	Adm13533	Anti-anti-	198	45	70.3	10	8	ADT88293	Adt88293	Human IL-
126	48	75.0	232	9	ADM13531	Adm13531	Anti-anti-	199	45	70.3	10	8	ADV14584	Adv14584	CDR1 pept
127	48	75.0	315	4	AAH70843	Aah70843	SNV-env 1	200	45	70.3	11	8	ADM78108	Adm78108	Human SJB
128	47	73.4	10	8	ADQ92367	Adq92367	Human hui	201	45	70.3	99	2	AAE30771	Aae30771	Murine an
129	47	73.4	98	2	AAE80556	Aae80556	TNF-alpha	202	45	70.3	110	5	ABE71522	Abe71522	Mouse ant
130	47	73.4	98	2	AAE33701	Aae33701	SP2, IgG V	203	45	70.3	112	5	ABE07356	Abe07356	22A5 IGM
131	47	73.4	106	2	AAE91365	Aae91365	Anti-proc	204	45	70.3	112	8	ADG25838	Adg25838	Anti-CD30
132	47	73.4	118	7	ADH80431	Adh80431	Hybrid hu	205	45	70.3	113	2	AAW93480	Aaw93480	mAb TRC8
133	47	73.4	118	7	ADH80435	Adh80435	Hybrid hu	206	45	70.3	113	9	ABE21717	Abe21717	Anti-NOGO
134	47	73.4	118	9	ADY85026	Ady85026	Monoclon	207	45	70.3	113	9	ABE08751	Abe08751	Anti-NOGO
135	47	73.4	119	7	ADH80432	Adh80432	Hybrid hu	208	45	70.3	114	8	ADG64770	Adg64770	CI mouse
136	47	73.4	119	7	ADH80434	Adh80434	Hybrid hu	209	45	70.3	114	8	ADQ32164	Adq32164	Mouse ant
137	47	73.4	119	8	ADP25822	Adp25822	Anti-alph	210	45	70.3	115	6	ABE57379	Abe57379	Human des
138	47	73.4	120	7	ADP57801	Adp57801	Monoclon	211	45	70.3	115	6	ABE40167	Abe40167	Humanised
139	47	73.4	120	7	ADP57803	Adp57803	Monoclon	212	45	70.3	115	6	ADP57801	Adp57801	H2V1 Hea
140	47	73.4	120	7	ADP57802	Adp57802	Monoclon	213	45	70.3	115	9	AEA44071	Aea44071	Anti-TPO
141	47	73.4	120	7	ADP57804	Adp57804	Monoclon	214	45	70.3	117	8	ADM78075	Adm78075	Human SJA
142	47	73.4	120	8	ADQ92335	Adq92335	Human hui	215	45	70.3	118	8	ADU07232	Adu07232	Human 4D4
143	47	73.4	120	8	ADH80524	Adh80524	Hui heavy	216	45	70.3	118	8	ADT88299	Adt88299	Human IL-
144	47	73.4	127	9	AEA88769	Aea88769	Murine SA	217	45	70.3	119	2	AAE25730	Aae25730	Humanised
145	47	73.4	141	9	ADY16604	Ady16604	PRO polyP	218	45	70.3	119	4	AAE69680	Aae69680	Humanised
146	47	73.4	226	9	AEA88770	Aea88770	Murine SA	219	45	70.3	119	4	AAE69692	Aae69692	Human WOI
147	47	73.4	250	5	ABP45150	Abp45150	Human Bly	220	45	70.3	119	5	ABJ10403	Abj10403	Anti-meso
148	47	73.4	250	7	ADG95977	Adg95977	Single ch	221	45	70.3	119	8	ADQ47793	Adq47793	Mutant an
149	47	73.4	462	2	AAW14933	Aaw14933	2A2 (Chim	222	45	70.3	119	8	ADQ47727	Adq47727	Humanised
150	47	73.4	462	2	AAW14934	Aaw14934	2A2 (Chim	223	45	70.3	119	8	ADQ47727	Adq47727	Humanised
151	47	73.4	463	2	AAW14932	Aaw14932	Murine an	224	45	70.3	120	8	ADG25803	Adg25803	Anti-CD30
152	47	73.4	463	2	AAW14935	Aaw14935	2A2 Human	225	45	70.3	120	8	ADU07242	Adu07242	Human 4D4
153	46	71.9	10	8	ADQ92369	Adq92369	Human hui	226	45	70.3	120	8	ADT88309	Adt88309	Human IL-
154	46	71.9	10	8	ADQ92373	Adq92373	Human hui	227	45	70.3	120	9	ABE21359	Abe21359	Mouse ant
155	46	71.9	10	8	ADQ80558	Adq80558	TNF-alpha	228	45	70.3	120	9	ABE31117	Abe31117	Anti-body
156	46	71.9	10	8	ADQ80562	Adq80562	TNF-alpha	229	45	70.3	121	7	ADH80426	Adh80426	Hybrid hu
157	46	71.9	10	8	ADQ80562	Adq80562	TNF-alpha	230	45	70.3	121	8	ADQ60451	Adq60451	Human B43
158	46	71.9	66	6	ABU56854	Abu56854	BoNT/A Hc	231	45	70.3	121	8	ADU39746	Adu39746	Human SLC
159	46	71.9	96	3	AAV56647	Aav56647	Partial P	232	45	70.3	121	9	ADY85053	Ady85053	Human HMG
160	46	71.9	108	8	ADT74981	Adt74981	Heavy cha	233	45	70.3	121	9	ABE24603	Abe24603	Human B43
161	46	71.9	115	3	AAH12169	Aah12169	Humanised	234	45	70.3	122	2	AAE30772	Aae30772	huxCD3v9,
162	46	71.9	118	8	ADU39748	Adu39748	Human SLC	235	45	70.3	122	7	ADG75545	Adg75545	Humanised
163	46	71.9	118	8	AEA89798	Aea89798	Anti-body	236	45	70.3	122	7	ADG75551	Adg75551	Human H2
164	46	71.9	118	9	AEA44164	Aea44164	Anti-TPO	237	45	70.3	122	7	ADG75540	Adg75540	Humanised
165	46	71.9	118	9	AEA44053	Aea44053	Anti-TPO	238	45	70.3	122	7	ABR40164	Abra40164	Human H1
166	46	71.9	118	9	AEA44191	Aea44191	Anti-TPO	239	45	70.3	123	6	ABR40163	Abra40163	Humanised
167	46	71.9	118	9	AEA44224	Aea44224	Anti-TPO	240	45	70.3	123	6	ABR40166	Abra40166	Humanised
168	46	71.9	118	9	AEA44085	Aea44085	Anti-TPO	241	45	70.3	123	6	ABR40165	Abra40165	Humanised
169	46	71.9	118	9	AEA44230	Aea44230	Anti-TPO	242	45	70.3	123	6	ADG64769	Adg64769	CI mouse
170	46	71.9	118	9	AEA44197	Aea44197	Anti-TPO	243	45	70.3	123	8			

244	45	70.3	123	8	ADG64767	Adg64767 C1 mouse	317	45	70.3	498	9	ADZ83709	Adz83709 CD3 speci
245	45	70.3	123	8	ADG64768	Adg64768 C1 mouse	318	45	70.3	498	9	ADZ83721	Adz83721 CD3 speci
246	45	70.3	123	8	ADX39143	Adx39143 Humanized	319	45	70.3	498	9	ADZ83578	Adz83578 Vector pE
247	45	70.3	124	8	ADU07234	Adu07234 Human 4D4	320	45	70.3	498	9	ADZ83749	Adz83749 CD3 speci
248	45	70.3	124	8	ADT88301	Adt88301 Human IL-	321	45	70.3	498	9	ADZ83562	Adz83562 Vector pE
249	45	70.3	124	9	ADV21421	Adv21421 Human ant	322	45	70.3	498	9	ADZ83705	Adz83705 CD3 speci
250	45	70.3	124	9	ADV14591	Adv14591 VH(CD19)	323	45	70.3	498	9	ADZ83717	Adz83717 CD3 speci
251	45	70.3	124	9	ADX58344	Adx58344 Variable	324	45	70.3	498	9	ADZ83729	Adz83729 CD3 speci
252	45	70.3	124	9	ADZ83492	Adz83492 CD19 VH.	325	45	70.3	498	9	ADZ83773	Adz83773 CD3 speci
253	45	70.3	127	8	ADM78063	Adm78063 Human SKB	326	45	70.3	498	9	ADZ83785	Adz83785 Vector pE
254	45	70.3	127	8	ADY22015	Ady22015 Antibody	327	45	70.3	498	9	ADZ83560	Adz83560 Vector pE
255	45	70.3	127	9	ADY22019	Ady22019 Antibody	328	45	70.3	498	9	ADZ83582	Adz83582 Non-deinum
256	45	70.3	130	8	ADM78059	Adm78059 Human SKB	329	45	70.3	498	9	ADZ83767	Adz83767 CD3 speci
257	45	70.3	136	2	AAR14153	Aar14153 Ig heavy	330	45	70.3	498	9	ADZ83779	Adz83779 CD3 speci
258	45	70.3	139	2	AAR38259	Aar38259 Chimeric	331	45	70.3	498	9	ADZ83737	Adz83737 CD3 speci
259	45	70.3	151	5	ABE31602	Aeb31602 Murine in	332	45	70.3	498	9	ADZ83745	Adz83745 CD3 speci
260	45	70.3	164	5	ABG71533	Abg71533 Mouse ant	333	45	70.3	499	9	ADZ83715	Adz83715 CD3 speci
261	45	70.3	209	6	ABP67712	Abp67712 TSH recep	334	45	70.3	499	9	ADZ83775	Adz83775 CD3 speci
262	45	70.3	209	6	ABP67711	Abp67711 TSH recep	335	45	70.3	499	9	ADZ83743	Adz83743 CD3 speci
263	45	70.3	209	6	ABP6752	Abp6752 TSH recep	336	45	70.3	499	9	ADZ83763	Adz83763 CD3 speci
264	45	70.3	209	6	ABP6751	Abp6751 TSH recep	337	45	70.3	499	9	ADZ83787	Adz83787 CD3 speci
265	45	70.3	233	2	AAR41710	Aar41710 Murine 12	338	45	70.3	499	9	ADZ83707	Adz83707 CD3 speci
266	45	70.3	233	2	AAR41707	Aar41707 Murine 12	339	45	70.3	499	9	ADZ83747	Adz83747 CD3 speci
267	45	70.3	235	2	AAR41682	Aar41682 Cimeric a	340	45	70.3	499	9	ADZ83765	Adz83765 CD3 speci
268	45	70.3	235	2	AAR41715	Aar41715 Murine 12	341	45	70.3	499	9	ADZ83731	Adz83731 CD3 speci
269	45	70.3	241	2	AAW09435	Aaw09435 Anti-CD19	342	45	70.3	499	9	ADZ83771	Adz83771 CD3 speci
270	45	70.3	241	2	ABW76197	Abw76197 Anti-mero	343	45	70.3	499	9	ADZ83739	Adz83739 CD3 speci
271	45	70.3	241	4	ABW50019	Abw50019 Antimeosc	344	45	70.3	499	9	ADZ83753	Adz83753 CD3 speci
272	45	70.3	243	2	AAW09444	Aaw09444 Modified	345	45	70.3	499	9	ADZ83759	Adz83759 CD3 speci
273	45	70.3	243	7	ADG30408	Adg30408 Human GMB	346	45	70.3	499	9	ADZ83775	Adz83775 CD3 speci
274	45	70.3	244	2	ADX39104	Adx39104 Humanized	347	45	70.3	499	9	ADZ83783	Adz83783 CD3 speci
275	45	70.3	246	2	AAW09434	Aaw09434 Anti-CD19	348	45	70.3	499	9	ADZ83757	Adz83757 CD3 speci
276	45	70.3	246	8	ADG64766	Adg64766 C1 mouse	349	45	70.3	499	9	ADZ83711	Adz83711 CD3 speci
277	45	70.3	247	2	AAW09443	Aaw09443 Modified	350	45	70.3	499	9	ADZ83727	Adz83727 CD3 speci
278	45	70.3	249	7	ABP45946	Abp45946 Human Bly	351	45	70.3	499	9	ADZ83719	Adz83719 CD3 speci
279	45	70.3	249	7	ADG96773	Adg96773 Single ch	352	45	70.3	499	9	ADZ83777	Adz83777 CD3 speci
280	45	70.3	250	9	ADV14571	Adv14571 VH(CD19) -	353	45	70.3	499	9	ADZ83777	Adz83777 CD3 speci
281	45	70.3	250	9	ADV14575	Adv14575 VL(CD19) -	354	45	70.3	499	9	ADZ83735	Adz83735 CD3 speci
282	45	70.3	271	5	ABG31022	Abg31022 Mouse sin	355	45	70.3	499	9	ADZ83751	Adz83751 CD3 speci
283	45	70.3	271	7	ADD25451	Add25451 Binding d	356	45	70.3	499	9	ADZ83781	Adz83781 CD3 speci
284	45	70.3	271	7	ADM42726	Adm42726 Synthetic	357	45	70.3	502	9	ADV14530	Adv14530 Bispecifici
285	45	70.3	271	7	ABE95394	Aeb95394 Mouse HD3	358	45	70.3	503	9	ADV21509	Adv21509 Mature fo
286	45	70.3	271	9	ABE94428	Aeb94428 Mouse ant	359	45	70.3	503	9	ADV21499	Adv21499 Mature fo
287	45	70.3	272	7	ADB29203	Adb29203 Multivale	360	45	70.3	503	9	ADV14538	Adv14538 Bispecifici
288	45	70.3	273	9	ADY22017	Ady22017 Single ch	361	45	70.3	503	9	ADV14532	Adv14532 Bispecifici
289	45	70.3	273	9	ADY22021	Ady22021 Antibody	362	45	70.3	503	9	ADV14540	Adv14540 Bispecifici
290	45	70.3	281	2	AAW82314	Aaw82314 Human SCF	363	45	70.3	503	9	AEA52452	Aea52452 Human CD3
291	45	70.3	288	2	AAW82482	Aaw82482 Mouse bis	364	45	70.3	504	9	AEA52450	Aea52450 Bispecifici
292	45	70.3	466	9	ADX39100	Adx39100 Mouse mon	365	45	70.3	504	9	ADV14534	Adv14534 Bispecifici
293	45	70.3	466	9	ADX39137	Adx39137 Mouse mon	366	45	70.3	504	9	ADV14556	Adv14556 Bispecifici
294	45	70.3	473	9	ADX39139	Adx39139 Humanized	367	45	70.3	504	9	ADV14536	Adv14536 Bispecifici
295	45	70.3	483	2	AAW82315	Aaw82315 Chimeric	368	45	70.3	504	9	AEA52451	Aea52451 Human CD3
296	45	70.3	496	9	ADV21501	Adv21501 Mature fo	369	45	70.3	504	9	AEA52449	Aea52449 Human CD3
297	45	70.3	496	9	ADV21511	Adv21511 Mature fo	370	45	70.3	504	9	AEA52449	Aea52449 Human CD3
298	45	70.3	497	9	ADV21497	Adv21497 Mature fo	371	45	70.3	505	9	ADV14528	Adv14528 Antibody
299	45	70.3	497	9	ADY21507	Ady21507 Mature fo	372	45	70.3	505	9	ADY22027	Ady22027 Antibody
300	45	70.3	498	8	ADW38798	Adw38798 Single ch	373	45	70.3	505	9	ADY22025	Ady22025 Antibody
301	45	70.3	498	8	ADW21503	Adw21503 Mature fo	374	45	70.3	505	9	AEA52448	Aea52448 Human CD3
302	45	70.3	498	9	ADV21513	Adv21513 Mature fo	375	45	70.3	506	9	ADV21505	Adv21505 Mature fo
303	45	70.3	498	9	ADZ83558	Adz83558 Vector pE	376	45	70.3	506	9	ADV21515	Adv21515 Mature fo
304	45	70.3	498	9	ADZ83761	Adz83761 CD3 speci	377	45	70.3	521	9	ADY22023	Ady22023 Antibody
305	45	70.3	498	9	ADZ83574	Adz83574 Vector pE	378	45	70.3	531	3	AAV43749	Aav43749 Amino aci
310	45	70.3	498	9	ADZ83564	Adz83564 Vector pE	384	45	70.3	601	6	ABG72265	Abg72265 Recombina
311	45	70.3	498	9	ADZ83741	Adz83741 CD3 speci	384	45	70.3	637	5	AAU75370	Aau75370 Diptheri
312	45	70.3	498	9	ADZ83733	Adz83733 CD3 speci	385	45	70.3	638	5	AAU75382	Aau75382 Diptheri
313	45	70.3	498	9	ADZ83755	Adz83755 CD3 speci	386	45	70.3	642	5	AAU75382	Aau75382 Diptheri
314	45	70.3	498	9	ADZ83566	Adz83566 Vector pE	387	45	70.3	642	5	AAU75382	Aau75382 Diptheri
315	45	70.3	498	9	ADZ83568	Adz83568 Vector pE	388	45	70.3	642	5	AAU75382	Aau75382 Diptheri
316	45	70.3	498	9	ADZ83570	Adz83570 Vector pE	389	45	70.3	643	5	AAU75390	Aau75390 Diptheri

390	45	70.3	643	6	AA029670	Aa029670	Anti-T ce	463	44	68.8	114	7	ADJ80427	Adj80427	Hybrid hu
391	45	70.3	652	5	AAU75448	Aau75448	Immunotox	464	44	68.8	114	7	ADJ80433	Adj80433	Hybrid hu
392	45	70.3	656	5	AAU75383	Aau75383	Immunotox	465	44	68.8	114	7	AEA40020	Aea40020	TNF reia
393	45	70.3	657	5	AAU75389	Aau75389	Diphtheri	466	44	68.8	114	9	AEA40004	Aea40004	TNF reia
394	45	70.3	895	5	AAU75369	Aau75369	Diphtheri	467	44	68.8	115	9	AEA34944	Aea34944	Human ant
395	45	70.3	895	5	AAU75368	Aau75368	Diphtheri	468	44	68.8	115	9	AEBl17185	Aeb17185	EphA2-ep
396	45	70.3	895	5	AAU75374	Aau75374	Diphtheri	469	44	68.8	115	9	AEA42985	Aea42985	EphA2 ant
397	45	70.3	895	6	AAO29673	Aao29673	Anti-T ce	470	44	68.8	115	9	AEA89799	Aea89799	Antibody
398	45	70.3	896	5	AAU75367	Aau75367	Diphtheri	471	44	68.8	115	9	AEA44081	Aea44081	Anti-TPO
399	45	70.3	896	5	AAU75366	Aau75366	Diphtheri	472	44	68.8	117	2	AAK30014	Aak30014	Heavy cha
400	45	70.3	896	5	AAU75373	Aau75373	Diphtheri	473	44	68.8	117	2	AAK35032	Aak35032	GMP-140 M
401	45	70.3	896	6	AAO29672	Aao29672	Anti-T ce	474	44	68.8	117	5	AAE25526	Aae25526	S. aureus
402	45	70.3	896	6	AAO29671	Aao29671	Anti-T ce	475	44	68.8	117	6	ABO27168	Abt61902	Mouse ant
403	45	70.3	896	6	AAO29676	Aao29676	Anti-T ce	476	44	68.8	118	2	AAW27122	Adu39962	Anti-EphA
404	45	70.3	896	9	ADX01023	Adx01023	Amino aci	477	44	68.8	118	8	ADBE8701	Ady32219	Human Eph
405	45	70.3	899	5	AAU75375	Aau75375	Diphtheri	478	44	68.8	118	8	ADO32163	Adb17137	Mouse ant
406	44	70.3	899	6	AAO29674	Aao29674	Anti-T ce	479	44	68.8	118	8	ADRA6647	Ady32219	Human Eph
407	44	68.8	10	8	ADBE85702	Adbe85702	Abm softw	480	44	68.8	118	8	ADT61902	Ady32219	Human Eph
408	44	68.8	10	8	ADH17813	Adh17813	Abm softw	481	44	68.8	118	8	ADU39962	Ady32219	Human Eph
409	44	68.8	10	9	ADW11444	Adw11444	Murine an	482	44	68.8	118	9	AEBl17137	Ady32219	Human Eph
410	44	68.8	10	9	ADY32282	Ady32282	Human Eph	483	44	68.8	118	9	AEBl17137	Ady32219	Human Eph
411	44	68.8	10	9	ADY28841	Ady28841	Murine an	484	44	68.8	118	9	AEA42937	Ady32219	Human Eph
412	44	68.8	10	9	AEBl17138	Aebi17138	EphA2-ep	485	44	68.8	119	2	AAK39464	Ady32219	Human Eph
413	44	68.8	10	9	AEA42938	Aea42938	EphA2 ant	486	44	68.8	119	2	AAK79861	Ady32219	Human Eph
414	44	68.8	10	9	AEB23205	Aeb23205	Mouse ant	487	44	68.8	119	2	AAK79863	Ady32219	Human Eph
415	44	68.8	11	9	ADW95757	Adw95757	Anti-hil-	488	44	68.8	119	2	AAK94458	Ady32219	Human Eph
416	44	68.8	11	9	ADX15762	Adx15762	Mouse ant	489	44	68.8	119	2	AAW07436	Ady32219	Human Eph
417	44	68.8	13	7	AD157984	Ad157984	Anti-TNF-	490	44	68.8	119	2	AAW28532	Ady32219	Human Eph
418	44	68.8	13	7	AD157985	Ad157985	Anti-TNF-	491	44	68.8	119	2	AAW40821	Ady32219	Human Eph
419	44	68.8	15	7	AD157819	Ad157819	Monoclonal	492	44	68.8	119	2	AAW71240	Ady32219	Human Eph
420	44	68.8	15	7	AD157818	Ad157818	Monoclonal	493	44	68.8	119	2	AAV23244	Ady32219	Human Eph
421	44	68.8	83	4	AAU32978	Aau32978	Novel hum	494	44	68.8	119	4	AAV79126	Ady32219	Human Eph
422	44	68.8	96	8	ADO32145	Ado32145	Mouse ant	495	44	68.8	119	4	AAE10850	Ady32219	Human Eph
423	44	68.8	97	2	AAK89475	Aak89475	Salmonell	496	44	68.8	119	4	AAK67763	Ady32219	Human Eph
424	44	68.8	98	8	ADH17817	Adh17817	Antibody	497	44	68.8	119	5	ABG70573	Ady32219	Human-mur
425	44	68.8	98	8	ADO58517	Ado58517	GAMP gene	498	44	68.8	119	5	ABP54871	Ady32219	Human-mur
426	44	68.8	98	8	ADO58521	Ado58521	GAMP gene	499	44	68.8	119	5	AAK47942	Ady32219	Human-mur
427	44	68.8	98	8	ADO58506	Ado58506	GAMP gene	500	44	68.8	119	6	ABU09890	Ady32219	Human-mur
428	44	68.8	98	8	ADO58513	Ado58513	GAMP gene	501	44	68.8	119	6	ABG72949	Ady32219	Human-mur
429	44	68.8	98	8	ADO58520	Ado58520	GAMP gene	502	44	68.8	119	6	ABG75767	Ady32219	Human-mur
430	44	68.8	98	8	ADO58516	Ado58516	GAMP gene	503	44	68.8	119	6	ABG75774	Ady32219	Human-mur
431	44	68.8	98	8	ADO58518	Ado58518	GAMP gene	504	44	68.8	119	6	ABU63588	Ady32219	Human-mur
432	44	68.8	98	8	ADO58519	Ado58519	GAMP gene	505	44	68.8	119	7	ADC46572	Ady32219	Human-mur
433	44	68.8	98	8	ADO58507	Ado58507	GAMP gene	506	44	68.8	119	7	ADC61358	Ady32219	Human-mur
434	44	68.8	98	8	ADO58537	Ado58537	GAMP gene	507	44	68.8	119	7	ADD44658	Ady32219	Human-mur
435	44	68.8	98	8	ADO58542	Ado58542	GAMP gene	508	44	68.8	119	7	ABW02402	Ady32219	Human-mur
436	44	68.8	98	8	ADO58524	Ado58524	GAMP gene	509	44	68.8	119	7	ADK96352	Ady32219	Human-mur
437	44	68.8	98	8	ADO58549	Ado58549	GAMP gene	510	44	68.8	119	7	ABW02037	Ady32219	Human-mur
438	44	68.8	98	8	ADO58553	Ado58553	GAMP gene	511	44	68.8	119	7	ADK91150	Ady32219	Human-mur
439	44	68.8	98	8	ADO58515	Ado58515	GAMP gene	512	44	68.8	119	7	ADG27432	Ady32219	Human-mur
440	44	68.8	98	8	ADO58525	Ado58525	GAMP gene	513	44	68.8	119	7	ADJ63989	Ady32219	Human-mur
441	44	68.8	98	8	ADO58511	Ado58511	GAMP gene	514	44	68.8	119	7	ADM15646	Ady32219	Human-mur
442	44	68.8	98	8	ADO58512	Ado58512	GAMP gene	515	44	68.8	119	7	ADM83151	Ady32219	Human-mur
443	44	68.8	98	8	ADO58540	Ado58540	GAMP gene	516	44	68.8	119	8	ADK89618	Ady32219	Human-mur
444	44	68.8	98	8	ADW11448	Adw11448	House mou	517	44	68.8	119	8	ADH89385	Ady32219	Human-mur
445	44	68.8	110	8	ADL27404	Adl27404	Amino aci	518	44	68.8	119	8	ADJ29707	Ady32219	Human-mur
446	44	68.8	111	2	AAW04586	Aaw04586	Anti-DNA	519	44	68.8	119	8	ADL70772	Ady32219	Human-mur
447	44	68.8	111	2	AAW04589	Aaw04589	Anti-DNA	520	44	68.8	119	8	ADP47320	Ady32219	Human-mur
448	44	68.8	111	8	ADT74988	Adt74988	Heavy cha	521	44	68.8	119	8	ADP47320	Ady32219	Human-mur
449	44	68.8	111	8	ADT74986	Adt74986	Heavy cha	522	44	68.8	119	9	ADW10843	Ady32219	Human-mur
450	44	68.8	111	8	ADT74984	Adt74984	Heavy cha	523	44	68.8	119	9	ADK97599	Ady32219	Human-mur
451	44	68.8	111	8	ADT74974	Adt74974	Heavy cha	524	44	68.8	119	9	ADL19075	Ady32219	Human-mur
452	44	68.8	111	8	ADT74979	Adt74979	Heavy cha	525	44	68.8	119	9	ADZ45357	Ady32219	Human-mur
453	44	68.8	111	8	ADT74871	Adt74871	Heavy cha	526	44	68.8	120	2	AAK13721	Ady32219	Human-mur
454	44	68.8	111	8	ADT74875	Adt74875	Heavy cha	527	44	68.8	120	2	AAK59985	Ady32219	Human-mur
455	44	68.8	111	8	ADT74990	Adt74990	Heavy cha	528	44	68.8	120	2	AAK88752	Ady32219	Human-mur
456	44	68.8	113	2	AAW95483	Aaw95483	Mouse der	529	44	68.8	120	2	AAK88754	Ady32219	Human-mur
457	44	68.8	113	9	AEBl21715	Aebi21715	Anti-Nogo	530	44	68.8	120	2	AAW19915	Ady32219	Human-mur
458	44	68.8	113	9	AEBl08749	Aebi08749	Anti-NOCO	531	44	68.8	120	8	ADG25811	Ady32219	Human-mur
459	44	68.8	113	9	AEBl08796	Aebi08796	Humanized	532	44	68.8	120	8	ADH17831	Ady32219	Human-mur
460	44	68.8	114	2	AAK21279	Aak21279	Murine VH	533	44	68.8	120	8	ADH17832	Ady32219	Human-mur
461	44	68.8	114	2	AAK21276	Aak21276	Murine VH	534	44	68.8	120	9	ADW11463	Ady32219	Human-mur
462	44	68.8	114	2	AAK79244	Aak79244	Heavy cha	535	44	68.8	120	9	ADW11462	Ady32219	Human-mur

536	44	68.8	120	9	ADW86137	Novel Cyt	609	44	68.8	253	9	ADX69677	Adx69677 Protein b
537	44	68.8	121	8	ADG25809	Anti-CD30	610	44	68.8	256	2	AAR22587	Aar22587 ScFvB18 c
538	44	68.8	121	9	ADW95756	Mouse ant	611	44	68.8	256	2	AAR22568	Aar22568 ScFvB18 c
539	44	68.8	121	9	ADX15761	Mouse ant	612	44	68.8	256	2	AAR22582	Aar22582 ScFvB18 c
540	44	68.8	121	9	ADZ45353	Murine fa	613	44	68.8	256	2	AAR22585	Aar22585 ScFvB18 c
541	44	68.8	121	9	ABE21865	Murine DC-	614	44	68.8	256	2	AAR22586	Aar22586 ScFvB18 c
542	44	68.8	121	9	ABE21868	Human DC-	615	44	68.8	256	2	AAR22583	Aar22583 ScFvB18 c
543	44	68.8	121	9	ABE21864	Human DC-	616	44	68.8	256	2	AAR22584	Aar22584 ScFvB18 c
544	44	68.8	121	9	ABE21869	Human DC-	617	44	68.8	269	2	AAR56482	Aar56482 ScFv prAs
545	44	68.8	121	9	ABE21863	Human DC-	618	44	68.8	269	4	AAR54756	Aar54756 PRAS111 b
546	44	68.8	122	2	AAR84555	B-cell ly	619	44	68.8	309	4	AAR70841	Aar70841 SNV-env 1
547	44	68.8	122	8	ADH17833	Murine an	620	44	68.8	402	2	AAR56485	Aar56485 ScFv prAs
548	44	68.8	122	8	ADW11464	Murine an	621	44	68.8	428	2	AAW24027	AAw24027 Single ch
549	44	68.8	123	8	ADH17852	Murine an	622	44	68.8	435	2	AAR56483	Aar56483 Single ch
550	44	68.8	123	8	ADH17847	Murine an	623	44	68.8	443	2	AAW24025	AAw24025 Single ch
551	44	68.8	123	8	ADH17848	Murine an	624	44	68.8	462	9	ABE08800	ABe08800 Anti-NOGO
552	44	68.8	123	9	ADW11479	Humanized	625	44	68.8	462	9	ABE08804	ABe08804 Reference
553	44	68.8	123	9	ADW11483	Murine an	626	44	68.8	470	8	ADM72027	Adm72027 Chimeric
554	44	68.8	123	9	ADW11478	Murine an	627	44	68.8	488	2	AAW86004	AAw86004 Human B7-
555	44	68.8	123	9	ABE23214	Mouse ant	628	44	68.8	488	2	AAW86004	AAw86004 Human B7-
556	44	68.8	124	3	AAE87655	Murine PI	629	44	68.8	488	6	ABU07262	ABu07262 Human exp
557	44	68.8	124	3	ADH17830	Murine an	630	44	68.8	488	6	ABU07253	ABu07253 Human exp
558	44	68.8	124	8	ADH17773	Murine Ab	631	44	68.8	592	4	AAW83838	AAw83838 Amino aci
559	44	68.8	124	8	ADH17767	Murine an	632	44	68.8	595	2	AAW86003	AAw86003 Anti-5T4
560	44	68.8	124	8	ADU67061	Human lPS	633	44	68.8	615	7	ADG32341	ADg32341 Fusion pr
561	44	68.8	124	9	ADW11398	Murine an	634	44	68.8	622	5	AAU70794	AAu70794 Hepatitis
562	44	68.8	124	9	ADW11404	Humanized	635	44	68.8	622	5	ADC85048	Adc85048 HBV HBcAg
563	44	68.8	124	9	ADW11461	Murine an	636	44	68.8	635	20	ADK14605	ADk14605 Hepatitis
564	44	68.8	125	2	AAZ27074	Monoclonal	637	44	68.8	637	20	ABG78234	ABg78234 Human Fv
565	44	68.8	126	5	AAU81272	Murine tr	638	44	68.8	638	9	ABG78235	ABg78235 Human Fv
566	44	68.8	131	9	AEA88771	Murine SA	639	44	68.8	639	5	ABG78236	ABg78236 Human Fv
567	44	68.8	134	9	ADY28838	Murine an	640	44	68.8	640	5	ABG91926	ABg91926 Human ant
568	44	68.8	136	1	AAE70624	Sequence	641	44	68.8	641	5	ABG91925	ABg91925 Human ant
569	44	68.8	136	2	AAH10239	Chimeric	642	44	68.8	642	5	ABG91927	ABg91927 Human ant
570	44	68.8	136	2	AAW10584	Anti-hepa	643	44	68.8	643	5	ADP10054	ADp10054 VEGF anti
571	44	68.8	136	2	AAW16340	Mouse-hum	644	44	68.8	644	5	ADP10157	ADp10157 Antibody
572	44	68.8	136	2	AAW41054	Human ant	645	44	68.8	645	7	ADF09949	ADf09949 Antibody
573	44	68.8	136	2	AAW47510	Human ant	646	44	68.8	646	7	ADJ80329	ADj80329 VH gene 1
574	44	68.8	136	2	AAW47517	Human ant	647	44	68.8	647	7	ADY75334	ADy75334 Protein e
575	44	68.8	136	2	AAW89555	Chimeric	648	44	68.8	648	9	ABY13610	ABy13610 Human var
576	44	68.8	136	2	AAW898085	Chimeric	649	44	68.8	649	9	AAW04593	AAw04593 Anti-DNA
577	44	68.8	136	6	ABU08927	Mouse amy	650	44	68.8	650	11	AAW04593	AAw04593 Ig H chai
578	44	68.8	137	2	ADC65003	Human imm	651	44	68.8	651	9	AEA42027	AEa42027 Ig H chai
579	44	68.8	137	2	AAW53818	Protein s	652	44	68.8	652	11	ADG24021	ADg24021 Amino aci
580	44	68.8	140	2	AAW53815	Murine Ac	653	44	68.8	653	9	ADM33983	ADm33983 Anti-NOGO
581	44	68.8	140	2	AAU11177	Mouse ant	654	44	68.8	654	8	ADY34450	ADy34450 NOGO rece
582	44	68.8	141	3	AAW43873	Heavy cha	655	44	68.8	655	7	ADJ80425	ADj80425 Hybrid hu
583	44	68.8	143	2	AAW43873	Heavy cha	656	44	68.8	656	8	ADP77173	ADp77173 Anti-VAP-
584	44	68.8	143	2	AAW43873	Heavy cha	657	44	68.8	657	8	ADU39949	ADu39949 Antibody
585	44	68.8	143	8	ADJ26636	Human ant	658	44	68.8	658	9	ADY21935	ADy21935 Human ant
586	44	68.8	143	8	ADJ26636	Human ant	659	44	68.8	659	9	ADY21941	ADy21941 Human ant
587	44	68.8	144	2	AAW53816	Consensus	660	44	68.8	660	9	ADZ45469	ADz45469 Ig H chai
588	44	68.8	146	3	AAW53816	Heavy cha	661	44	68.8	661	9	ADZ45469	ADz45469 Murine fa
589	44	68.8	159	1	AAW53816	Heavy cha	662	44	68.8	662	11	AAW53816	AAw53816 Murine fa
590	44	68.8	180	5	AAW53813	Heavy cha	663	44	68.8	663	4	AAW53813	AAw53813 Human HIV
591	44	68.8	180	5	AAW53813	Heavy cha	664	44	68.8	664	4	ADZ55821	ADz55821 Anti-alpha
592	44	68.8	192	7	ABO62548	Mouse hum	665	44	68.8	665	8	ADZ55821	ADz55821 Anti-alpha
593	44	68.8	192	7	ABO62548	Mouse hum	666	44	68.8	666	8	ADG25806	ADg25806 Anti-CD30
594	44	68.8	219	9	ADC79230	Remicade	667	44	68.8	667	8	ADT75019	ADt75019 Heavy cha
595	44	68.8	226	6	ABR55861	Remicade	668	44	68.8	668	8	ADT75019	ADt75019 Heavy cha
596	44	68.8	226	8	ADN49714	Human ant	669	44	68.8	669	8	ADT75018	ADt75018 Heavy cha
597	44	68.8	226	8	ADU74390	Remicade-	670	44	68.8	670	8	ADT75032	ADt75032 Heavy cha
598	44	68.8	238	9	ADX69679	Protein b	671	44	68.8	671	8	ADT75032	ADt75032 Heavy cha
599	44	68.8	240	2	AAW11243	scFv comp	672	44	68.8	672	8	ADT75026	ADt75026 Heavy cha
600	44	68.8	240	8	ADH89383	Human tra	673	44	68.8	673	8	ADT75035	ADt75035 Heavy cha
601	44	68.8	243	2	AAW60781	Fv (GP-4)	674	44	68.8	674	8	ADT75027	ADt75027 Heavy cha
602	44	68.8	243	2	AAW60781	Fv (GP-4)	675	44	68.8	675	8	ADT75025	ADt75025 Heavy cha
603	44	68.8	243	2	AAW60781	Fv (GP-4)	676	44	68.8	676	8	ADT75025	ADt75025 Heavy cha
604	44	68.8	243	2	AAW60781	Fv (GP-4)	677	44	68.8	677	8	ADT75030	ADt75030 Heavy cha
605	44	68.8	244	4	AAW60780	Fv (GP-2)	678	44	68.8	678	8	ADT75034	ADt75034 Heavy cha
606	44	68.8	248	7	ADG32327	Mouse scF	679	44	68.8	679	8	ADT75024	ADt75024 Heavy cha
607	44	68.8	248	9	ADW95688	Anti-IL-6	680	44	68.8	680	8	ADT75021	ADt75021 Heavy cha
608	44	68.8	248	9	ADX15693	Mouse ant	681	44	68.8	681	8	ADT75021	ADt75021 Heavy cha

682	43	67.2	119	8	ADT75031	Adc75031 Heavy cha	755	43	67.2	469	8	ADX94577	Adx94577 Plant ful
683	43	67.2	119	9	ADZ42025	Adz42025 Ig H chai	756	43	67.2	470	2	AAW83036	AAw83036 Anti-Fas
684	43	67.2	119	9	ADZ42022	Adz42022 Ig H chai	757	43	67.2	470	2	AAW83037	AAw83037 Anti-Fas
685	43	67.2	119	9	ADZ42023	Adz42023 Ig H chai	758	43	67.2	470	3	AAW83037	AAw83037 Anti-Fas
686	43	67.2	119	9	ADZ42026	Adz42026 Ig H chai	759	43	67.2	470	3	AAW83037	AAw83037 Anti-Fas
687	43	67.2	119	9	ADZ42028	Adz42028 Ig H chai	760	43	67.2	470	3	AAW83037	AAw83037 Anti-Fas
688	43	67.2	119	9	ADZ45485	Adz45485 Murine fa	761	43	67.2	470	3	AAW90934	AAw90934 Humanised
689	43	67.2	119	9	AEA18679	Aea18679 Amino aci	762	43	67.2	470	3	AAW90935	AAw90935 Humanised
690	43	67.2	119	9	AEA18671	Aea18671 Amino aci	763	43	67.2	470	3	AAW90933	AAw90933 Humanised
691	43	67.2	120	3	AAW03721	AAw03721 Human sec	764	43	67.2	470	3	AAW90936	AAw90936 Humanised
692	43	67.2	120	8	ADG25810	Adg25810 Anti-CD30	765	43	67.2	470	3	AAW90929	AAw90929 Humanised
693	43	67.2	120	8	ADT75097	Adt75097 Heavy cha	766	43	67.2	470	5	ABB74941	Abb74941 Humanised
694	43	67.2	120	8	ADT75090	Adt75090 Heavy cha	767	43	67.2	470	5	ABB74944	Abb74944 Humanised
695	43	67.2	120	8	ADT75099	Adt75099 Heavy cha	768	43	67.2	470	5	ABB74945	Abb74945 Humanised
696	43	67.2	120	8	ADT75092	Adt75092 Heavy cha	769	43	67.2	470	5	ABB74898	Abb74898 Humanised
697	43	67.2	120	8	ADT75098	Adt75098 Heavy cha	770	43	67.2	470	5	ABB74904	Abb74904 Mouse hum
698	43	67.2	120	8	ADT75089	Adt75089 Heavy cha	771	43	67.2	470	5	ABB74902	Abb74902 Humanised
699	43	67.2	120	8	ADZ42029	Adz42029 Ig H chai	772	43	67.2	470	5	ABB74903	Abb74903 Mouse hum
700	43	67.2	121	2	AAW74943	AAw74943 Immunoglo	773	43	67.2	470	5	ABB74895	Abb74895 Humanised
701	43	67.2	121	2	AAW74964	AAw74964 Anti-Idio	774	43	67.2	493	9	ADY22001	Ady22001 Antibody
702	43	67.2	121	8	ADT79362	Adt79362 Thytrotop	775	43	67.2	493	9	ADY22003	Ady22003 Antibody
703	43	67.2	121	8	ADU87694	Adu87694 Mouse Luc	776	43	67.2	493	9	ADY21999	Ady21999 Antibody
704	43	67.2	123	9	ADZ45373	Adz45373 Murine fa	777	43	67.2	493	9	ADY21953	Ady21953 Antibody
705	43	67.2	123	9	ADZ45365	Adz45365 Murine fa	778	43	67.2	493	9	ADY21951	Ady21951 Antibody
706	43	67.2	123	9	ADZ45377	Adz45377 Murine fa	779	43	67.2	493	9	ADY21955	Ady21955 Antibody
707	43	67.2	123	9	ADZ45369	Adz45369 Murine fa	780	43	67.2	495	9	ADY21945	Ady21945 Antibody
708	43	67.2	130	5	AAU70768	AAu70768 Hepatitis	781	43	67.2	495	9	ADY21949	Ady21949 Antibody
709	43	67.2	130	7	ADU85022	Adu85022 HBV HBcAg	782	43	67.2	499	9	ADY21947	Ady21947 Antibody
710	43	67.2	130	8	ADP79366	Adp79366 Hepatitis	783	43	67.2	500	9	ADY22007	Ady22007 Antibody
711	43	67.2	131	8	ADP79366	Adp79366 Thytrotop	784	43	67.2	586	9	ADY22009	Ady22009 Antibody
712	43	67.2	143	2	AAW12233	AAw12233 Mouse Mab	785	43	67.2	592	9	ADY22005	Ady22005 Antibody
713	43	67.2	144	2	AAW12355	AAw12355 Heavy cha	786	43	67.2	594	9	ABB29087	Abb29087 Immunokln
714	43	67.2	145	2	AAW83038	AAw83038 Anti-Fas	787	43	67.2	597	2	ABB29089	Abb29089 Immunokln
715	43	67.2	145	3	AAW14775	AAw14775 Fragment	788	43	67.2	637	2	AAW26983	AAw26983 (FRP51)-E
716	43	67.2	145	3	AAW90925	AAw90925 Humanised	789	43	67.2	1033	9	ABB29091	Abb29091 Immunokln
717	43	67.2	145	5	ABB74940	Abb74940 Humanised	790	42.5	66.4	114	4	AAW50793	AAw50793 Murine an
718	43	67.2	145	5	ABB74940	Abb74940 Humanised	791	42.5	66.4	121	4	ABB21866	Abb21866 Human DC-
719	43	67.2	147	2	AAW54050	AAw54050 Sequence	792	42.5	66.4	121	8	ABB21867	Abb21867 Human DC-
720	43	67.2	147	2	AAW01528	AAw01528 Monoclonia	793	42.5	66.4	123	8	AAW75344	AAw75344 Antibody
721	43	67.2	147	2	AAW24987	AAw24987 Monoclonia	794	42.5	66.4	136	2	AAW06446	AAw06446 HuMc3 VH
722	43	67.2	152	8	ADU57084	Adu57084 3G4 anti-b	795	42.5	66.4	136	2	AAW06442	AAw06442 HuMc3 VH
723	43	67.2	159	8	ADU57088	Adu57088 3G4-2BVA-	796	42.5	66.4	137	8	ADU94531	ADu94531 TSH recep
724	43	67.2	176	8	ADU43522	Adu43522 Amino aci	797	42.5	66.4	214	6	ABP96763	ABp96763 TSH recep
725	43	67.2	222	2	AAW15934	AAw15934 Antibody	798	42.5	66.4	214	6	ABP96756	ABp96756 TSH recep
726	43	67.2	240	2	AAW85495	AAw85495 Scfv(FWPS	799	42.5	66.4	214	6	ABP96755	ABp96755 TSH recep
727	43	67.2	241	2	AAW26981	AAw26981 FWP51 fus	800	42.5	66.4	214	6	ABP96764	ABp96764 TSH recep
728	43	67.2	242	6	ABR62131	ABr62131 Single ch	801	42.5	66.4	241	5	ABP45937	ABp45937 Human Bly
729	43	67.2	242	8	ADT91207	Adt91207 Single ch	802	42.5	66.4	241	7	ADG96764	ADg96764 Single ch
730	43	67.2	248	5	ABP46077	ABp46077 Human Bly	803	42.5	66.4	245	5	ABP45889	ABp45889 Human Bly
731	43	67.2	248	7	ADG96904	ADg96904 Single ch	804	42.5	66.4	245	7	ADG96716	ADg96716 Single ch
732	43	67.2	259	5	ABG31023	ABg31023 Mouse 6in	805	42.5	66.4	248	5	ABP44939	ABp44939 Human Bly
733	43	67.2	259	7	ADD25452	Ad25452 Binding d	806	42.5	66.4	248	7	ADG95766	ADg95766 Single ch
734	43	67.2	259	7	ADW42727	Adw42727 Synthetic	807	42	65.6	10	7	ABR01558	ABr01558 Human ant
735	43	67.2	259	9	ABE94429	ABe94429 Mouse ant	808	42	65.6	10	7	ADW07744	ADw07744 Carline Im
736	43	67.2	259	9	ABE94429	ABe94429 Mouse ant	809	42	65.6	10	8	ADP47157	ADp47157 Human pho
737	43	67.2	261	9	ADY21943	Ady21943 Human ant	810	42	65.6	10	8	ADP47139	ADp47139 Human pho
738	43	67.2	261	9	ADY21939	Ady21939 Human 6in	811	42	65.6	10	8	ADP47135	ADp47135 Human pho
739	43	67.2	272	2	AAW00557	AAw00557 Nematode	812	42	65.6	10	8	ADP47213	ADp47213 Human pho
740	43	67.2	272	2	AAW43913	AAw43913 Mus muscu	813	42	65.6	10	8	ADP47213	ADp47213 Human pho
741	43	67.2	272	5	ABG31024	ABg31024 Synthetic	814	42	65.6	11	9	ADX15521	ADx15521 Human ant
742	43	67.2	272	7	ADW42728	Adw42728 Binding d	815	42	65.6	11	9	ADW95773	ADw95773 Anti-hlv-
743	43	67.2	272	7	ADW42728	Adw42728 Synthetic	816	42	65.6	11	9	ADX15778	ADx15778 Mouse ant
744	43	67.2	272	7	ABE95396	ABe95396 Mouse G28	817	42	65.6	20	3	AAV70799	AAv70799 Murine ant
745	43	67.2	272	9	ABE94430	ABe94430 Mouse ant	818	42	65.6	58	9	AEC20860	Aec20860 Human var
746	43	67.2	296	9	ADY22011	Ady22011 Antibody	819	42	65.6	84	2	AAW62797	AAw62797 Amino aci
747	43	67.2	441	9	AEC20771	Aec20771 M-CSF spe	820	42	65.6	98	2	AAW54800	AAw54800 SpA-react
748	43	67.2	464	2	AAW83041	AAw83041 Anti-Fas	821	42	65.6	98	2	AAW54800	AAw54800 SpA-react
749	43	67.2	464	3	AAW90897	AAw90897 Murine an	822	42	65.6	98	5	ABG78233	ABg78233 Human Fv
750	43	67.2	464	3	ABW74912	ABw74912 Humanised	823	42	65.6	98	5	ABG78232	ABg78232 Human Fv
751	43	67.2	464	5	ABW74866	ABw74866 Humanised	824	42	65.6	98	5	ABG91924	ABg91924 Human ant
752	43	67.2	465	2	AAW6758	AAw6758 Anti-toba	825	42	65.6	98	5	ABG91922	ABg91922 Human ant
753	43	67.2	467	6	AAE38408	AAe38408 Mouse vir	826	42	65.6	98	5	ABG91923	ABg91923 Human ant
754	43	67.2	467	6	AAE38408	AAe38408 Mouse vir	827	42	65.6	98	5	ABG91923	ABg91923 Human ant

828	42	65.6	98	6	ABU56609	Human	Imm	901	42	65.6	118	9	AEA44063	Anti-TPO	Aea44063
829	42	65.6	98	6	ABP56508	Human	ant	902	42	65.6	118	9	AEA44065	Anti-TPO	Aea44065
830	42	65.6	98	6	ABJ18687	Antibody		903	42	65.6	118	9	AEA44073	Anti-TPO	Aea44073
831	42	65.6	98	6	ABO27112	Human	ger	904	42	65.6	118	9	AEA44077	Anti-TPO	Aea44077
832	42	65.6	98	7	ADP69247	Human	hea	905	42	65.6	118	9	AEA44087	Anti-TPO	Aea44087
833	42	65.6	98	7	ADP10156	Antibody		906	42	65.6	118	9	AEA44061	Anti-TPO	Aea44061
834	42	65.6	98	7	ADP09948	Antibody		907	42	65.6	119	6	ABP57968	Murine Ig	Abp57968
835	42	65.6	98	7	ADP10053	VEGF anti		908	42	65.6	119	7	ADP69207	Human ant	Adp69207
836	42	65.6	98	7	ADK18943	Anti-huma		909	42	65.6	119	8	ADP79380	Human ant	Adp79380
837	42	65.6	98	7	ADK18888	Anti-huma		910	42	65.6	119	8	ADP42024	Ig H chai	Adt45385
838	42	65.6	98	7	ADK18877	Anti-huma		911	42	65.6	119	9	ADZ45385	Murine fa	Adt45385
839	42	65.6	98	7	ADK18878	Anti-huma		912	42	65.6	120	2	AAR47934	Humanised	Aar47934
840	42	65.6	98	7	ADK18912	Anti-huma		913	42	65.6	120	2	AAW04176	Variant v	Aaw04176
841	42	65.6	98	7	ADK18582	Anti-huma		914	42	65.6	120	2	AAW16619	Human Ab	Aaw16619
842	42	65.6	98	7	ADK18896	Anti-huma		915	42	65.6	120	2	AAW27555	Humanised	Aaw27555
843	42	65.6	98	7	ADK18894	Anti-huma		916	42	65.6	120	2	AAW893350	Humanised	Aaw893350
844	42	65.6	98	7	ADK18894	Anti-huma		917	42	65.6	120	6	ABJ18677	Antibody	Abj18677
845	42	65.6	98	7	ADJ80328	VR gene 1		918	42	65.6	120	6	ABJ18720	Antibody	Abj18720
846	42	65.6	98	7	ADJ80328	VR gene 1		919	42	65.6	120	6	ABJ18720	Antibody	Abj18720
847	42	65.6	98	8	ADP46847	Human VHS		920	42	65.6	120	7	ADG75664	Humanised	Adg75664
847	42	65.6	98	8	ADY75333	Protein e		921	42	65.6	120	8	ADQ76069	Heterotec	Adq76069
848	42	65.6	98	9	AEH13609	Human var		922	42	65.6	120	8	ADQ95772	Mouse ant	Adw95772
849	42	65.6	98	9	AEH01021	Human hea		923	42	65.6	120	9	ADX15434	Mouse ant	Adx15777
850	42	65.6	98	9	AEC20849	Human var		924	42	65.6	120	9	ADX15777	Mouse ant	Adx15777
851	42	65.6	104	2	AAW89170	Anti-p53		925	42	65.6	120	9	ADY31676	Anti-IL9	Ady31676
852	42	65.6	109	8	ADP22377	Human ant		926	42	65.6	120	9	ADZ51184	Amino aci	Adz51184
853	42	65.6	109	8	ADP22385	Human ant		927	42	65.6	120	9	ADZ42058	Human ant	Adz42058
854	42	65.6	109	8	ADP12513	Human Vhs		928	42	65.6	121	2	AAW00833	Variable	Aaw00833
855	42	65.6	109	8	ADP12515	Human Vhs		929	42	65.6	121	2	AAW62798	Amino aci	Aaw62798
856	42	65.6	109	8	ADP12514	Human Vhs		930	42	65.6	121	2	AAW62798	Amino aci	Aaw62798
857	42	65.6	110	8	ADP47302	Human pho		931	42	65.6	121	7	ABR63917	Murine CS	Abt63917
858	42	65.6	111	2	AAW04590	Anti-DNA		932	42	65.6	122	8	ADJ25647	Mouse act	Adj25647
859	42	65.6	113	2	AAW47932	Heavy cha		933	42	65.6	122	8	ADP03661	Human ant	Adp03661
860	42	65.6	113	2	AAW89348	Mouse 23P		934	42	65.6	122	8	AEA44059	Anti-TPO	Aea44059
861	42	65.6	113	6	ABU08149	Human Erb		935	42	65.6	123	6	ABU56810	Monkey Im	Abu56810
862	42	65.6	113	7	ADP69211	Human ant		936	42	65.6	123	6	ABU56810	Monkey Im	Abu56810
863	42	65.6	115	3	AAU76446	Mouse mon		937	42	65.6	124	2	AAW45409	Anti-CD4	Aaw45409
864	42	65.6	115	3	AAU76446	Mouse mon		938	42	65.6	124	8	ADP79384	Human ant	Adp79384
865	42	65.6	115	3	AAU76446	Mouse mon		939	42	65.6	125	2	AAW08510	C6 human	Abp56509
866	42	65.6	115	3	AAU76446	Mouse mon		940	42	65.6	125	6	ABP56509	Human ant	Abp56509
867	42	65.6	116	2	AAW00827	Variant v		941	42	65.6	126	7	ADK18876	Anti-huma	Adk18876
868	42	65.6	116	2	AAW19014	Anti-huma		942	42	65.6	126	7	ADK18599	Anti-huma	Adk18599
869	42	65.6	117	2	AAW66339	Human Imm		943	42	65.6	126	7	ADK18622	Anti-huma	Adk18622
870	42	65.6	117	2	AAW00837	Variable		944	42	65.6	126	7	ADK18824	Anti-huma	Adk18824
871	42	65.6	117	2	AAW00831	Variable		945	42	65.6	126	7	ADK18793	Anti-huma	Adk18793
872	42	65.6	117	2	AAW19017	Anti-huma		946	42	65.6	126	7	ADK18889	Anti-huma	Adk18889
873	42	65.6	117	4	AAW19017	Anti-huma		947	42	65.6	126	7	ADK18942	Anti-huma	Adk18942
874	42	65.6	117	4	ABG26889	Novel hum		948	42	65.6	126	8	ADL25416	Human mAb	Adl25416
875	42	65.6	117	5	ABG26889	Novel hum		949	42	65.6	126	8	ADL25416	Human mAb	Adl25416
876	42	65.6	117	5	ABG26889	Novel hum		950	42	65.6	127	6	ADA901022	Anti-Abec	Ada901022
877	42	65.6	117	8	ADP470771	Anti-TNFA		951	42	65.6	127	6	ADA901022	Anti-Abec	Ada901022
878	42	65.6	117	8	ADP47229	Human pho		952	42	65.6	127	7	ADK18828	Anti-huma	Adk18828
879	42	65.6	117	8	ADP47223	Human pho		953	42	65.6	128	4	AAW23996	Human EST	Aaw23996
880	42	65.6	117	8	ADP47223	Human pho		954	42	65.6	128	4	AAW23996	Human EST	Aaw23996
881	42	65.6	117	8	ADP47223	Human pho		955	42	65.6	129	3	ADK18605	Anti-huma	Adk18605
882	42	65.6	117	8	ADP47223	Human pho		956	42	65.6	129	3	ADK18605	Anti-huma	Adk18605
883	42	65.6	117	8	ADP47223	Human pho		957	42	65.6	129	7	ADK18791	Anti-huma	Adk18791
884	42	65.6	118	4	AAH85349	Antibody		958	42	65.6	129	7	ADK18895	Anti-huma	Adk18895
885	42	65.6	118	8	ADN49403	Human ant		959	42	65.6	129	7	ADK18826	Human mAb	Adk18826
886	42	65.6	118	8	ADN49403	Human ant		960	42	65.6	129	7	ADK18826	Human mAb	Adk18826
887	42	65.6	118	8	ADN49403	Human ant		961	42	65.6	130	7	ADL25428	Human mAb	Adl25428
888	42	65.6	118	8	ADP47100	Human pho		962	42	65.6	132	9	ADW04954	PAP-A im	Adw04954
889	42	65.6	118	8	ADP47115	Human pho		963	42	65.6	132	9	ADW04954	PAP-A im	Adw04954
890	42	65.6	118	8	ADP47230	Human pho		964	42	65.6	133	2	ADY28850	Murine ant	Ady28850
891	42	65.6	118	8	ADP47226	Human pho		965	42	65.6	134	2	AAW44177	Monoclonal	Aaw44177
892	42	65.6	118	8	ADP47219	Human pho		966	42	65.6	137	3	AAW32260	Mouse ant	Aay32260
893	42	65.6	118	8	ADP47219	Human pho		967	42	65.6	137	3	AAW32260	Mouse ant	Aay32260
894	42	65.6	118	8	ADP47228	Human pho		968	42	65.6	138	6	AAE37207	Human AB	Aae37207
895	42	65.6	118	8	ADP47220	Human pho		969	42	65.6	139	9	AAE16229	Anti-huma	Aae16229
896	42	65.6	118	8	ADP47224	Human pho		970	42	65.6	139	9	ADX98257	Human ant	Adx98257
897	42	65.6	118	9	ADP47224	Human ant		971	42	65.6	141	2	AAW01631	Ber-H2 he	Aaw01631
898	42	65.6	118	9	ADP47224	Human ant		972	42	65.6	144	2	AAW01631	Ber-H2 he	Aaw01631
899	42	65.6	118	9	ADP47224	Human ant		973	42	65.6	146	4	AAW01631	Ber-H2 he	Aaw01631
900	42	65.6	118	9	ADP47224	Human ant		974	42	65.6	146	4	AAW01631	Ber-H2 he	Aaw01631

974	42	65.6	151	4	AAG75997	Human	col
975	42	65.6	222	6	ABR01532	Human	ant
976	42	65.6	224	6	ABR01528	Human	ant
977	42	65.6	224	6	ABR01545	Human	ant
978	42	65.6	224	6	ABR01533	Human	ant
979	42	65.6	224	6	ABR01539	Human	ant
980	42	65.6	224	6	ABR01530	Human	ant
981	42	65.6	224	6	ABR01527	Human	ant
982	42	65.6	224	6	ABR01543	Human	ant
983	42	65.6	224	6	ABR01544	Human	ant
984	42	65.6	225	4	ABR75052	TR0005	Hu
985	42	65.6	225	4	AA875056	TR0005	Hu
986	42	65.6	225	4	AA875053	TR0005	Hu
987	42	65.6	225	6	ABR01525	Human	ant
988	42	65.6	225	6	ABR01536	Human	ant
989	42	65.6	225	6	ABR01541	Human	ant
990	42	65.6	225	6	ABR01529	Human	ant
991	42	65.6	225	6	ABR01520	Human	ant
992	42	65.6	225	6	ABR01521	Human	ant
993	42	65.6	226	6	ABR01522	Human	ant
994	42	65.6	226	6	ABR01542	Human	ant
995	42	65.6	239	6	ADA91408	Anti-Abec	
996	42	65.6	240	3	AA715128	Anti-mur1	
997	42	65.6	241	6	ABU08158	Human	B7b
998	42	65.6	242	2	AAW53881	Firefly	1
999	42	65.6	243	2	AAW09436	Anti-CD19	
1000	42	65.6	243	9	Adw95684	Anti-IL-6	

ALIGNMENTS

RESULT 1

AAW62010 standard; peptide; 10 AA.

AAW62010;

01-OCT-1998 (first entry)

XX Heavy chain variable region complementarity determining region 1.
 XX Complementarity determining region; heavy chain variable region;
 KW humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;
 KW human CD11a I domain; MHM24 epitope; alpha subunit;
 KW lymphocyte function-associated antigen 1; LFA-1; immunoassay;
 KW in vivo imaging; diagnosis; CD11a-associated disease.
 XX Mus sp.
 OS Homo sapiens.
 XX WO9823761-A1.
 XX 04-JUN-1998.
 XX 20-OCT-1997; 97WO-US019041.
 XX 27-NOV-1996; 96US-00757205.
 XX (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG;
 XX WPI; 1998-322737/28.
 XX New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
 PT also to treat conditions such as immunological or inflammatory disease.
 XX Claim 6; Page 2; 66pp; English.
 CC AAW62010-12 represent complementarity determining regions of the heavy
 CC chain variable region of humanised antibody MHM24F(ab)-8. The fragments
 CC were used to make a humanised anti-CD11a antibody that binds specifically

CC to the human CD11a I domain (MHM24 epitope). CD11a refers to the alpha
 CC subunit of lymphocyte function-associated antigen 1 (LFA-1) from any
 CC mammal. The humanised anti-CD11a antibodies are used to determine
 CC presence of CD11a in usual immunoassays or by in vivo imaging,
 CC particularly for diagnosis of CD11a-associated diseases (typically immune
 CC responses and inflammation such as psoriasis, Crohn's disease, rheumatoid
 CC arthritis, transplant rejection, leukaemia, etc
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 64; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0009;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTGHMMN 10

Db 1 GYSFTGHMMN 10

RESULT 2

AAW82337 standard; peptide; 10 AA.

AAW82337;

22-JUN-2000 (first entry)

Humanised anti-CD11a antibody heavy chain CDRI SEQ ID NO:10.

XX Humanised, anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 KW antitumour; antiviral; inflammation; immunological response; LFA-1;
 KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KW viral infection; transplant rejection; graft rejection.
 XX

OS Homo sapiens.

Mus sp.

US6037454-A.

14-MAR-2000.

20-NOV-1997; 97US-00974899.

27-NOV-1996; 96US-0031971P.

(GETH) GENENTECH INC.

Jardieu PM, Presta LG;

WPI; 2000-282241/24.

XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 PT inflammation and transplant rejection, contains human heavy variable
 PT region complementarity determining regions.
 XX Claim 1; Col 55-56; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that
 CC binds specifically to the human CD11a I-domain. The Ab has anti-
 CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
 CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 CC involved in leucocyte adhesion associated with inflammatory and
 CC immunological responses. The Ab are used: (i) optionally when coupled to
 CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
 CC rhinitis, leukaemia, viral infections and many others, also for
 CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine

CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MHM24) CDR-H1 peptide. This sequence is used in the exemplification of
 CC the invention.
 CC XX
 CC Sequence 10 AA:
 SQ
 Query Match 100.0%; Score 64; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0009;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GYSFTGHMNN 10
 Db 1 GYSFTGHMNN 10
 RESULT 5
 AAW62013
 ID AAW62013 standard; peptide; 121 AA.
 AC AAW62013;
 XX
 XX 01-OCT-1998 (first entry)
 DT
 XX Heavy chain variable region of humanised anti-CD11a antibody.
 DE
 XX Complementarity determining region; heavy chain variable region;
 KW humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;
 KW human CD11a I domain; MHM24 epitope; alpha subunit;
 KW lymphocyte function-associated antigen 1; LFA-1; immunoassay;
 KW in vivo imaging; diagnosis; CD11a-associated disease.
 KW XX
 XX Mus sp.
 OS Homo sapiens.
 OS XX
 XX WO9823761-A1.
 PN
 XX 04-JUN-1998.
 PD
 XX 20-OCT-1997; 97WO-US019041.
 PF
 XX 27-NOV-1996; 96US-00757205.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX (GETH) GENENTECH INC.
 PI
 XX Jardieu PM, Presta LG;
 XX WPI; 1998-322737/28.
 DR
 XX New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
 PT also to treat conditions such as immunological or inflammatory disease.
 XX
 XX Claim 7; Page 50; 66pp; English.
 PS
 CC The present sequence represents the heavy chain variable region of a
 CC humanised anti-CD11a antibody that binds specifically to the human CD11a
 CC I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte
 CC function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-
 CC CD11a antibodies are used to determine presence of CD11a in usual
 CC immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-
 CC associated diseases (typically immune responses and inflammation such as
 CC psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,

CC leukaemia, etc
 XX
 XX Sequence 121 AA;
 SQ
 Query Match 100.0%; Score 64; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GYSFTGHMNN 10
 Db 26 GYSFTGHMNN 35
 RESULT 6
 AAW62019
 ID AAW62019 standard; peptide; 121 AA.
 AC AAW62019;
 XX
 XX 01-OCT-1998 (first entry)
 DT
 XX Rhesusised heavy chain of humanised anti-CD11a antibody.
 DE
 XX Complementarity determining region; heavy chain variable region;
 KW humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;
 KW human CD11a I domain; MHM24 epitope; alpha subunit;
 KW lymphocyte function-associated antigen 1; LFA-1; immunoassay;
 KW in vivo imaging; diagnosis; CD11a-associated disease.
 KW XX
 XX Unidentified.
 OS
 OS WO9823761-A1.
 PN
 XX 04-JUN-1998.
 PD
 XX 20-OCT-1997; 97WO-US019041.
 PF
 XX 27-NOV-1996; 96US-00757205.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX (GETH) GENENTECH INC.
 PI
 XX Jardieu PM, Presta LG;
 XX WPI; 1998-322737/28.
 DR
 XX New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
 PT also to treat conditions such as immunological or inflammatory disease.
 XX
 XX Disclosure; Page 56; 66pp; English.
 PS
 CC The present sequence represents the heavy chain of a "rhesusised" (sic)
 CC humanised anti-CD11a antibody that binds specifically to the human CD11a
 CC I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte
 CC function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-
 CC CD11a antibodies are used to determine presence of CD11a in usual
 CC immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-
 CC associated diseases (typically immune responses and inflammation such as
 CC psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
 CC leukaemia, etc
 CC XX
 CC Sequence 121 AA;
 SQ
 Query Match 100.0%; Score 64; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GYSFTGHMNN 10
 Db 26 GYSFTGHMNN 35
 RESULT 7
 AAW63542

ID AAW63542 standard; protein; 121 AA.
 AC AAW63542;
 XX
 XX 06-OCT-1998 (first entry)
 DT
 DE Murine MHM24 heavy chain variable domain mutant.
 XX
 XX Antibody mutant production; species-dependent antibody; malignancy;
 KM infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KM intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 KM autoimmune disease; transplant rejection; tumour cell invasion;
 KM human immune deficiency virus infection; heavy chain.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 XX WO9823746-A1.
 XX
 XX 04-JUN-1998.
 XX
 XX 29-OCT-1997; 97WO-US020169.
 XX
 XX 27-NOV-1996; 96US-00756150.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 XX Jardieu PM, Presta LG;
 PI
 DR WPI; 1998-322726/28.
 XX
 XX Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD11a.
 XX
 XX
 PS Claim 13; Page 59-60; 71pp; English.
 XX
 XX This sequence represents the heavy chain variable domain of a mutant
 CC murine antibody MHM24 of the invention. The mutants are of a species-
 CC dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 XX
 SQ Sequence 121 AA;
 XX
 XX Query Match 100.0%; Score 64; DB 2; Length 121;
 XX Best Local Similarity 100.0%; Pred. No. 0.013;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 DE Murine MHM24 heavy chain.
 XX
 XX Antibody mutant production; species-dependent antibody; malignancy;
 KM infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KM intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 KM autoimmune disease; transplant rejection; tumour cell invasion;
 KM human immune deficiency virus infection; heavy chain.
 XX
 OS Mus sp.
 XX
 XX WO9823746-A1.
 XX
 XX 04-JUN-1998.
 XX
 XX 29-OCT-1997; 97WO-US020169.
 XX
 XX 27-NOV-1996; 96US-00756150.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 XX Jardieu PM, Presta LG;
 PI
 DR WPI; 1998-322726/28.
 XX
 XX Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD11a.
 XX
 XX
 PS Disclosure; Page 54; 71pp; English.
 XX
 XX This sequence represents the heavy chain of the murine antibody MHM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 XX
 SQ Sequence 121 AA;
 XX
 XX Query Match 100.0%; Score 64; DB 2; Length 121;
 XX Best Local Similarity 100.0%; Pred. No. 0.013;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 AAW63532
 ID AAW63532 standard; protein; 121 AA.
 AC AAW63532;
 XX
 XX 06-OCT-1998 (first entry)
 DT
 DE Humanised MHM24 heavy chain.
 XX
 XX Antibody mutant production; species-dependent antibody; malignancy;
 KM infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KM intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;


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PN    US6037454-A.
XX    14-MAR-2000.
XX    20-NOV-1997; 97US-00974899.
XX    27-NOV-1996; 96US-0031971P.
XX    (GENTH ) GENENTECH INC.
XX    Jardiou PM, Presta LG;
XX    MPI; 2000-282241/24.
XX    New humanized anti-CD11a antibody, useful for treating or preventing e.g.
XX    inflammation and transplant rejection, contains human heavy variable
XX    region complementarity determining regions.
XX    Claim 1; Fig 1; 38pp; English.
XX    The present invention describes a humanised anti-CD11a antibody (Ab) that
XX    binds specifically to the human CD11a I-domain. The Ab has anti-
XX    inflammatory, immunosuppressant, antitumour and antiviral activities. The
XX    Ab blocks lymphocyte function-associated antigen (LFA-1) which is
XX    involved in leucocyte adhesion associated with inflammatory and
XX    immunological responses. The Ab are used: (i) optionally when coupled to
XX    a cytotoxin, to treat or prevent disorders mediated by lymphocyte
XX    function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
XX    inflammatory bowel disease, eczema, systemic lupus erythematosus,
XX    rhinitis, leukaemia, viral infections and many others, also for
XX    inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
XX    tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
XX    to active anticancer agent; and (v) for affinity chromatography. The Ab
XX    retain about the same activity in adhesion and mixed lymphocyte response
XX    assays as the murine antibodies from which they are derived. The murine
XX    anti-CD11a antibody MEM24 has IC50 0.09 nM for preventing adhesion
XX    between Jurkat cells (expressing LFA-1) and normal epidermal
XX    keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
XX    The fully humanized version of MEM24 had IC50 0.13 nM. The present
XX    sequence represents the heavy chain variable region of the humanised anti
XX    -CD11a Ab
XX    SQ
XX    Sequence 121 AA;
XX    Query Match 100.0%; Score 64; DB 3; Length 121;
XX    Best Local Similarity 100.0%; Pred. No. 0.013;
XX    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY    1 GYSFTGHMNN 10
DB    26 GYSFTGHMNN 35

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PD    14-MAR-2000.
XX    20-NOV-1997; 97US-00974899.
XX    27-NOV-1996; 96US-0031971P.
XX    (GENTH ) GENENTECH INC.
XX    Jardiou PM, Presta LG;
XX    MPI; 2000-282241/24.
XX    New humanized anti-CD11a antibody, useful for treating or preventing e.g.
XX    inflammation and transplant rejection, contains human heavy variable
XX    region complementarity determining regions.
XX    Example; Fig 1; 38pp; English.
XX    The present invention describes a humanised anti-CD11a antibody (Ab) that
XX    binds specifically to the human CD11a I-domain. The Ab has anti-
XX    inflammatory, immunosuppressant, antitumour and antiviral activities. The
XX    Ab blocks lymphocyte function-associated antigen (LFA-1) which is
XX    involved in leucocyte adhesion associated with inflammatory and
XX    immunological responses. The Ab are used: (i) optionally when coupled to
XX    a cytotoxin, to treat or prevent disorders mediated by lymphocyte
XX    function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
XX    inflammatory bowel disease, eczema, systemic lupus erythematosus,
XX    rhinitis, leukaemia, viral infections and many others, also for
XX    inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
XX    tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
XX    to active anticancer agent; and (v) for affinity chromatography. The Ab
XX    retain about the same activity in adhesion and mixed lymphocyte response
XX    assays as the murine antibodies from which they are derived. The murine
XX    anti-CD11a antibody MEM24 has IC50 0.09 nM for preventing adhesion
XX    between Jurkat cells (expressing LFA-1) and normal epidermal
XX    keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
XX    The fully humanized version of MEM24 had IC50 0.13 nM. The present
XX    sequence represents the amino acid sequence of murine MEM24 heavy chain,
XX    which is used in the exemplification of the present invention
XX    SQ
XX    Sequence 121 AA;
XX    Query Match 100.0%; Score 64; DB 3; Length 121;
XX    Best Local Similarity 100.0%; Pred. No. 0.013;
XX    Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY    1 GYSFTGHMNN 10
DB    26 GYSFTGHMNN 35

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RESULT 12
ADG39012
ID    ADG39012 standard; protein; 121 AA.
XX
XX    AAY82346;
XX
XX    22-JUN-2000 (first entry)
XX
XX    Murine MEM24 heavy chain amino acid sequence SEQ ID NO:4.
XX
XX    Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
XX    antitumour; antiviral; inflammation; immunological response; LFA-1;
XX    lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
XX    inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
XX    viral infection; transplant rejection; graft rejection.
XX
XX    Mus sp.
XX
XX    US6037454-A.
XX

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RESULT 13
ADG39012
ID    ADG39012 standard; protein; 121 AA.
XX
XX    ADG39012;
XX
XX    26-FEB-2004 (first entry)
XX
XX    Rhesusised mouse anti-CD11a I-domain antibody VL.
XX
XX    Mouse; CD11a; I-domain; monoclonal antibody;
XX    cluster of differentiation 11a; mixed lymphocyte response assay;
XX    Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
XX    ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
XX    psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
XX    rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
XX    diabetes mellitus; prodrug activating enzyme.
XX
XX    Synthetic.
XX
XX    Mus sp.
XX
XX    US2003207336-A1.
XX

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XX 06-NOV-2003.
PD
XX
XX 28-FEB-2001; 2001US-00795798.
PR
XX 27-NOV-1996; 96US-0031971P.
PR 20-NOV-1997; 97US-00974899.
PR 20-OCT-1999; 99US-00420745.
XX
XX (GETH ) GENENTECH INC.
XX
XX Jardiou PM, Presta LG;
XX
XX WPI; 2004-051511/05.
XX
XX Humanized anti-CD11a antibody useful for treating lymphocyte function-
XX associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
XX ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
XX
XX Example; SEQ ID NO 24; 43bp; English.
XX
XX The invention relates to a Humanised anti-cluster of differentiation
XX (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
XX a Kd value of not more than 1x10-8 M, or concentration for 50 %
XX inhibition (IC50) (mM) value of not more than 1 nM in mixed lymphocyte
XX response assay or for preventing adhesion of Jurkat cells to normal human
XX epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
XX -1. Also included are a kit comprising the antibody and instructions for
XX use to detect the CD11a protein, an isolated nucleic acid encoding the
XX antibody, a vector comprising the nucleic acid, a host cell comprising
XX the vector and producing the antibody by culturing the cell so that the
XX antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The
XX antibody is useful for determining the presence of CD11a protein and for
XX treating lymphocyte function-associated antigen 1 mediated disorder such
XX as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
XX rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
XX and diabetes mellitus. The antibody is useful when conjugated to a
XX prodrug activating enzyme, or as an affinity purification agent. The
XX present sequence is the light chain of a rhesus ant-CD11a antibody of
XX the invention.
XX
XX Sequence 121 AA;
SQ
XX
XX Query Match 100.0%; Score 64; DB 8; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 0.013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GYSFTGHMMN 10
XX |||||
XX 26 GYSFTGHMMN 35
XX
XX
XX RESULT 14
XX ADG38992
XX ID ADG38992 standard; protein; 121 AA.
XX
XX AC ADG38992;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Mouse anti-CD11a antibody heavy chain variable region.
XX
XX Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
XX VH: cluster of differentiation 11a; mixed lymphocyte response assay;
XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; prodrug activating enzyme.
XX
XX Mus sp.
XX
XX US2003207336-A1.

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XX 06-NOV-2003.
PD
XX
XX 28-FEB-2001; 2001US-00795798.
PR
XX 27-NOV-1996; 96US-0031971P.
PR 20-NOV-1997; 97US-00974899.
PR 20-OCT-1999; 99US-00420745.
XX
XX (GETH ) GENENTECH INC.
XX
XX Jardiou PM, Presta LG;
XX
XX WPI; 2004-051511/05.
XX
XX Humanized anti-CD11a antibody useful for treating lymphocyte function-
XX associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
XX ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
XX
XX Example; SEQ ID NO 4; 43bp; English.
XX
XX The invention relates to a Humanised anti-cluster of differentiation
XX (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
XX a Kd value of not more than 1x10-8 M, or concentration for 50 %
XX inhibition (IC50) (mM) value of not more than 1 nM in mixed lymphocyte
XX response assay or for preventing adhesion of Jurkat cells to normal human
XX epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
XX -1. Also included are a kit comprising the antibody and instructions for
XX use to detect the CD11a protein, an isolated nucleic acid encoding the
XX antibody, a vector comprising the nucleic acid, a host cell comprising
XX the vector and producing the antibody by culturing the cell so that the
XX antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The
XX antibody is useful for determining the presence of CD11a protein and for
XX treating lymphocyte function-associated antigen 1 mediated disorder such
XX as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
XX rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
XX and diabetes mellitus. The antibody is useful when conjugated to a
XX prodrug activating enzyme, or as an affinity purification agent. The
XX present sequence is the heavy chain variable region (VH) of the wild-type
XX mouse anti-CD11a I domain monoclonal antibody MHM24.
XX
XX Sequence 121 AA;
SQ
XX
XX Query Match 100.0%; Score 64; DB 8; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 0.013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GYSFTGHMMN 10
XX |||||
XX 26 GYSFTGHMMN 35
XX
XX
XX RESULT 15
XX ADG38993
XX ID ADG38993 standard; protein; 121 AA.
XX
XX AC ADG38993;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE Humanised Mouse anti-CD11a antibody heavy chain variable region.
XX
XX Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
XX VH: cluster of differentiation 11a; mixed lymphocyte response assay;
XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; prodrug activating enzyme; humanised.
XX
XX Synthetic.
XX
XX Mus sp.

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PN US2003207336-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 28-FEB-2001; 2001US-00795798.
 XX
 PR 27-NOV-1996; 96US-0031971P.
 PR 20-NOV-1997; 97US-00974899.
 PR 20-OCT-1999; 99US-00420745.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-051511/05.
 XX
 PT Humanized anti-CD11a antibody useful for treating lymphocyte function-
 PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 XX
 PS Claim 7, SEQ ID NO 5; 43pp; English.
 XX
 CC The invention relates to a Humanised anti-cluster of differentiation
 CC (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 CC a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nm) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MEM24 on CD11a. The
 CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC product activating enzyme, or as an affinity purification agent. The
 CC present sequence is the heavy chain variable region (VH) of the humanised
 CC mouse anti-CD11a I domain monoclonal antibody MEM24.
 XX
 SQ Sequence 121 AA;
 QY
 Db 1 GYSFTGHMNN 10
 26 GYSFTGHMNN 35
 Query Match 100.0%; Score 64; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16
 ADR03368
 ID ADR03368 standard; protein; 121 AA.
 XX
 AC ADR03368;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MEM24 F(ab)-8 antibody variable heavy chain protein.
 KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;

KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain;
 KW VH; murine; human; fusion protein.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX
 PF 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 5; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MEM24) F(ab)-8 variable heavy chain protein. This sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 121 AA;
 QY
 Db 1 GYSFTGHMNN 10
 26 GYSFTGHMNN 35
 Query Match 100.0%; Score 64; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 17
 ADR03380
 ID ADR03380 standard; protein; 121 AA.
 XX
 AC ADR03380;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Rhesusised MEM24 antibody variable heavy chain mutant protein.
 KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;

KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculosis; sarcoidosis; polymyositis;
 KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KM skin hypersensitivity disorder; poison ivy; poison oak;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 KM VH; murine; rheus macaque; fusion protein; mutant; mutein.
 XX
 OS Mus sp.
 OS Macaca mulatta.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX
 PP 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GETH) GENENTECH INC.
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 17; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is rheus macaque anti-human CD11a monoclonal
 CC antibody (MHM24) variable heavy chain protein. This sequence is used in
 CC the exemplification of the invention.
 CC
 XX
 SQ Sequence 121 AA;
 QY
 Db 1 GYSFTGHMMN 10
 |||||
 26 GYSFTGHMMN 35
 RESULT 18
 ADR03367 100.0%; Score 64; DB 8; Length 121;
 ID ADR03367 standard; protein; 121 AA.
 XX
 AC ADR03367;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Murine MHM24 antibody variable heavy chain protein.
 XX

KM CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KM rhinovirus infection; inflammatory skin disease; psoriasis;
 KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculosis; sarcoidosis; polymyositis;
 KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KM skin hypersensitivity disorder; poison ivy; poison oak;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 KM VH; murine.
 XX
 OS Mus sp.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX
 PP 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GETH) GENENTECH INC.
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 4; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is murine anti-human CD11a monoclonal antibody (MHM24)
 CC variable heavy chain protein. This sequence is used in the
 CC exemplification of the invention.
 CC
 XX
 SQ Sequence 121 AA;
 QY
 Db 1 GYSFTGHMMN 10
 |||||
 26 GYSFTGHMMN 35
 RESULT 19
 ADM38458 100.0%; Score 64; DB 8; Length 121;
 ID ADM38458 standard; protein; 121 AA.
 XX
 AC ADM38458;
 XX
 DT 24-MAR-2005 (first entry)
 XX

XX CD11a heavy chain variable region #2.
DE
XX
XX monoclonal antibody; CD11a; light-chain variable region;
KM heavy-chain variable region.
XX
XX Homo sapiens.
OS
XX CN1439651-A.
PN
XX 03-SEP-2003.
PD
XX 20-FEB-2002; 2002CN-00110866.
PF
XX 20-FEB-2002; 2002CN-00110866.
PR
XX (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
PA
XX Wang H, Wang J;
PI
XX WPI; 2004-169719/17.
DR
XX Recombinant human CD11a monoclonal antibody and its preparation and
PT medicinal composition.
XX
XX Claim 1; Page 14-15; 16pp; Chinese.
PS
XX The present invention relates to a recombinant monoclonal antibody for
CC human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
CC No.5 in light-chain variable region and the amino acid sequence shown by
CC SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
CC bioactivity and the expression in host cell are greatly increased. The
CC DNA molecule for coding the antibody, its preparation process and the
CC medicinal composition containing it are also disclosed. The present
CC sequence represents a heavy chain variable region of human CD11a.
SQ
XX Sequence 121 AA;
SQ
XX
XX Query Match 100.0%; Score 64; DB 8; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 0.013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSFTGHMNN 10
DB 26 GYSFTGHMNN 35
XX
XX RESULT 20
XX ADX80646
XX ID ADX80646 standard; protein; 121 AA.
XX AC ADX80646;
XX
XX 05-MAY-2005 (first entry)
DT
XX
XX Humanized CD11a variable heavy chain amino acid sequence, seq id 6.
DE
XX Protein purification; leaching; protein A affinity chromatography; CD11a;
KM antibody.
XX
XX Synthetic.
OS
XX US2005038231-A1.
PN
XX
XX 17-FEB-2005.
PD
XX 24-JUN-2004; 2004US-00877532.
PF
XX 28-JUL-2003; 2003US-0490500P.
PR
XX (GETH) GENENTECH INC.
XX
XX Fahrner RL, Laverdiere A, McDonald PJ, O'leary RM;
PI

XX
XX WPI; 2005-172327/18.
DR
XX
XX Purifying a protein, e.g. antibody or immunoadhesin, comprises reducing
PT the temperature of a composition subjected to protein A affinity
PT chromatography to 3-20 degrees C, where protein A leaching is reduced.
XX
XX Disclosure; SEQ ID NO 6; 27pp; English.
PS
XX
XX The invention relates to a method of purifying a protein which comprises
CC a CH2/CH3 region by protein A affinity chromatography. The method
CC involves reducing the temperature of a composition comprising the protein
CC and one or more impurities subjected to protein A affinity chromatography
CC to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably
CC the protein is antibody. The antibody is selected from Trastuzumab,
CC humanized 2C4, humanized CD11a antibody, and humanized VEGF antibody.
CC Preferably, the antibody binds HER2 antigen, where the antibody is
CC Trastuzumab or humanized 2C4. The protein is an immunoadhesin,
CC specifically a TNP receptor immunoadhesin. The methods are useful for
CC purifying a protein, which comprises a CH2/CH3 region by protein A
CC affinity chromatography and for reducing leaching of protein A during
CC protein A affinity chromatography. The current sequence represents the
CC variable heavy chain amino acid sequence of CD11a.
SQ
XX
XX Sequence 121 AA;
SQ
XX
XX Query Match 100.0%; Score 64; DB 9; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 0.013;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSFTGHMNN 10
DB 26 GYSFTGHMNN 35
XX
XX RESULT 21
XX ADF11670
XX ID ADF11670 standard; protein; 451 AA.
XX AC ADF11670;
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX anti-CD11a rhumab heavy chain amino acid sequence #SEQ ID 4.
DE
XX
XX Purifying; target protein; non-affinity purification;
KM high-performance tangential flow filtration; HPRFF; pharmaceutical;
KM diagnostic; therapeutic; antibody.
XX
XX Synthetic.
OS
XX WO2003102132-A2.
PN
XX
XX 11-DEC-2003.
PD
XX
XX 25-APR-2003; 2003WO-US013054.
PF
XX 26-APR-2002; 2002US-0375953P.
PR
XX (GETH) GENENTECH INC.
XX
XX Fahrner RL, Pollman D, Lebreton B, Van Reis R;
PI
XX
XX WPI; 2004-043096/04.
DR
XX
XX Purifying target protein from mixture containing host cell protein
PT involves subjecting mixture to non-affinity purification, high-
PT performance tangential flow filtration and isolating purified protein.
XX
XX Disclosure; SEQ ID NO 4; 77pp; English.
PS
XX
XX The invention relates to a method for purifying a target protein from a
CC mixture containing a host cell protein. This method comprises subjecting
CC

CC the mixture to a non-affinity purification followed by high-performance
 CC tangential flow filtration (HPTF) and isolating the protein in a purity
 CC containing less than 100 parts/million (ppm) of the host cell protein,
 CC where the method of the invention includes no affinity purification
 CC process. The method of the invention is useful for purifying a target
 CC protein from a mixture containing a host cell protein, and is useful for
 CC incorporating the isolated protein into a pharmaceutical formulation.
 CC Proteins purified using the method of the invention are useful in a
 CC pharmaceutical respect, and are also useful in various diagnostic and
 CC therapeutic purposes. The method of the invention is efficient in
 CC purifying a target protein from a mixture containing a host cell protein,
 CC and may also be effectively performed at low cost. The current sequence
 CC represents the anti-CD14 rhumb heavy chain amino acid sequence. This
 CC particular protein was used to demonstrate the method of the invention.
 CC
 CC Sequence 451 AA;
 CC
 CC Query Match 100.0%; Score 64; DB 8; Length 451;
 CC Best Local Similarity 100.0%; Pred. No. 0.055;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 GYSFTGHMNN 10
 CC |||||
 CC Db 26 GYSFTGHMNN 35
 CC
 CC RESULT 22
 CC ADR03384 standard; peptide, 10 AA.
 CC
 CC ADR03384;
 CC
 CC DT 21-OCT-2004 (first entry)
 CC
 CC DE Humanised MEM24 CDR-H1 mutant peptide, SerH28A1a.
 CC
 CC CD14 antibody; human immunodeficiency virus infection; HIV infection;
 CC rhinovirus infection; inflammatory skin disease; psoriasis;
 CC inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 CC adult respiratory distress syndrome; allergic disease; eczema; asthma;
 CC autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 CC SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 CC tuberculosis; sarcoidosis; polymyositis;
 CC chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 CC skin hypersensitivity disorder; poison ivy; poison oak;
 CC B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 CC graft versus host disease; cancer; gene therapy;
 CC murine anti-human CD14 monoclonal antibody; MEM24; variable heavy chain;
 CC VH; murine; human; fusion protein; complementarity determining region;
 CC CDR; mutant; mutein.
 CC
 CC OS Mus sp.
 CC OS Homo sapiens.
 CC OS Chimeric.
 CC
 CC PN US2004146507-A1.
 CC PD 29-JUL-2004.
 CC
 CC PF 03-DEC-2003; 2003US-00727737.
 CC PR 27-NOV-1996; 96US-0031945P.
 CC PR 20-NOV-1997; 97US-00975329.
 CC
 CC PA (GETH) GENENTECH INC.
 CC PI Jardiou PM, Presta LG;
 CC DR WPI; 2004-552640/53.
 CC
 CC PT New antibody mutant of a species-dependent antibody, useful for treating
 CC PT and preventing infectious diseases, psoriasis, inflammatory bowel
 CC PT disease, allergic conditions, autoimmune diseases, or cancer.

XX Example; SEQ ID NO 21; 54pp; English.
 PS
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD14 monoclonal antibody
 CC (MEM24) CDR-H1 mutant peptide. This sequence is used in the
 CC exemplification of the invention.
 CC
 CC Sequence 10 AA;
 CC
 CC Query Match 95.3%; Score 61; DB 8; Length 10;
 CC Best Local Similarity 90.0%; Pred. No. 0.0028;
 CC Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 GYSFTGHMNN 10
 CC |||||
 CC Db 1 GYAFTHMNN 10
 CC
 CC RESULT 23
 CC AAY29452 standard; protein, 116 AA.
 CC
 CC AAY29452;
 CC
 CC DT 05-OCT-1999 (first entry)
 CC
 CC DE Human IgG1 subgroup III heavy chain variable domain.
 CC
 CC KW Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
 CC diagnosis; inflammatory disorder; conjugate; immunoglobulin;
 CC fusion protein.
 CC
 CC OS Homo sapiens.
 CC OS
 CC PN WO9937779-A1.
 CC PD 29-JUL-1999.
 CC
 CC PF 19-JAN-1999; 99WO-US001081.
 CC PR 22-JAN-1998; 98US-00012116.
 CC PR 20-FEB-1998; 98WO-US003337.
 CC PR 24-JUL-1998; 98US-00121952.
 CC PR 24-JUL-1998; 98US-00122513.
 CC
 CC PA (GETH) GENENTECH INC.
 CC PI Hseil V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z, Zapata GA;
 CC DR WPI; 1999-469134/39.
 CC
 CC PT New conjugates of nonproteinaceous polymers with antibody fragments, used
 CC PT for treating inflammatory disorders.
 CC
 CC PS Disclosure; Fig 29; 360pp; English.
 CC
 CC CC The present invention describes a novel conjugate having one or more
 CC CC antibody fragments covalently attached to one or more nonproteinaceous
 CC CC polymer molecules, where the apparent size of the conjugate is at least

about 500 kDa. Conjugates of antibody fragments which bind the human interleukin (IL) 8 with a nonproteinaceous polymer can be used for treating inflammatory disorders e.g. acute lung injury, ischemic reperfusion disorder, and autoimmune diseases. They can also be used for treating e.g. inflammatory skin diseases including psoriasis and atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases. The conjugates can also be used as reagents in an animal model system for in vivo study of the biological functions of the antigen recognised by the conjugate. The present sequence represents the human IgG1 subgroup III heavy chain variable domain form the present invention

SQ Sequence 116 AA;

Query Match 93.8%; Score 60; DB 2; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.057;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
|:|||||
Db 26 GFSFTGHMMN 35

RESULT 24

AA77755 ID AAY77755 standard; protein; 116 AA.

AC AAY77755;

DT 06-JUN-2000 (first entry)

DE Human IgG1 subgroup III heavy chain variable domain.

KW Interleukin-8; IL-8; monoclonal antibody; Mab; anti-IL-8; 6G4.2.SV1IN35A;
KM inflammatory disorder; adult respiratory distress syndrome; chimeric;
KW affinity purification; 6G4.2.5.

OS Homo sapiens.

FN US6025158-A.

PD 15-FEB-2000.

PF 20-FEB-1998; 98US-00027449.

PR 21-FEB-1997; 97US-0038664P.

PR 22-JAN-1998; 98US-0074330P.

PA (GETH) GENENTECH INC.

PI Presta LG, Leong SR, Gonzalez TN;

DR WPI; 2000-181809/16.

PT New nucleic acid molecule encodes a polypeptide which is an anti-interleukin-8 monoclonal antibody or antibody fragment useful for the production of anti-interleukin-8 monoclonal antibodies or fragments.

XX Example; Fig 29; 188pp; English.

XX The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody (Mab). The anti-IL-8 Mab comprises a sequence containing the CDRs (complementarity determining regions) of the humanized anti-IL-8 6G4.2.SV1IN35A light chain; and amino acids 24-253 of the humanized anti-IL-8 6G4.2.SV1IN35A heavy chain. The anti-IL-8 Mabs and fragments can be used in diagnosis, for affinity purification of IL-8 from recombinant cell culture or natural sources and for the treatment of inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic acids encoding the anti-IL-8 Mab can be associated in a vector with another gene encoding another protein or protein fragment to produce a fusion protein which can make isolation and/or purification of the protein an easier process

XX Sequence 116 AA;

Query Match 93.8%; Score 60; DB 3; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.057;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
|:|||||
Db 26 GFSFTGHMMN 35

RESULT 25

AAB30312 ID AAB30312 standard; protein; 116 AA.

AC AAB30312;

DT 12-FEB-2001 (first entry)

DE Human IgG1 subgroup III heavy chain V region SEQ ID NO: 50.

KW Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
KM adult respiratory distress syndrome; multiple organ failure;
KM bacterial pneumonia; inflammatory bowel disease.

OS Homo sapiens.

PN US6133426-A.

PD 17-OCT-2000.

PF 20-FEB-1998; 98US-00026985.

PR 21-FEB-1997; 97US-0038664P.

PR 22-JAN-1998; 98US-0074330P.

PA (GETH) GENENTECH INC.

PI Presta LG, Leong SR, Gonzalez TN;

DR WPI; 2000-686027/67.

PT Humanized anti-interleukin 8 monoclonal antibody variant useful for treating inflammatory disorders, such as adult respiratory distress syndrome, hypovolemic shock and ulcerative colitis.

PS Disclosure; Col 163-164; 240pp; English.

XX The present invention provides a number of humanised monoclonal anti-IL-8 antibodies which can be used in the diagnosis and treatment of inflammatory disorders, including adult respiratory distress syndrome, septic shock, multiple organ failure, bacterial pneumonia and inflammatory bowel disease. The present sequence comprises one of the antibodies of the invention

SQ Sequence 116 AA;

Query Match 93.8%; Score 60; DB 3; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.057;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
|:|||||
Db 26 GFSFTGHMMN 35

RESULT 26

ABU13789 ID ABU13789 standard; protein; 116 AA.

AC ABU13789;

DT 25-FEB-2003 (first entry)

DE Human IgG1 subgroup III heavy chain variable domain.
 XX
 KW Antibody; monoclonal antibody; 5.12.14; 6G4.2.5; interleukin-8; mAb;
 KW antiinflammatory; respiratory; acute lung injury; polyethylene glycol;
 KW PEG; lung injury; adult respiratory distress syndrome; ARDS; ashma;
 KW inflammatory disease; inflammatory bowel disease; psoriasis; sclerosis;
 KW ischaemic reperfusion disorder; stroke; multiple sclerosis; meningitis;
 KW osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis;
 KW alcoholic hepatitis; cystic fibrosis; human.
 XX
 OS Homo sapiens.
 XX
 PN US6468532-B1.
 XX
 PD 22-OCT-2002.
 XX
 PF 20-JAN-1999; 99US-00234340.
 XX
 PR 22-JAN-1998; 98US-0074330P.
 PR 20-FEB-1998; 98US-0075467P.
 PR 24-JUL-1998; 98US-0094003P.
 PR 24-JUL-1998; 98US-0094013P.
 XX
 PA (GETH) GENENTECH INC.
 PI Heel V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 XX WPI; 2003-138230/13.
 DR
 PT Treating acute lung injury in mammal by administering to mammal a 500 kD
 PT conjugate comprising F(ab')₂ antibody fragment that binds to human
 PT interleukin-8, covalently attached to one or two polyethylene glycol
 PT molecules.
 XX
 PS Example G; Fig 29; 2599P; English.
 XX
 CC The invention relates to treating acute lung injury in a mammal,
 CC comprising administering to the mammal an effective amount of a conjugate
 CC of a single antibody fragment covalently attached to 1 or 2 polyethylene
 CC glycol (PEG) molecules, where the antibody fragment is a F(ab')₂
 CC comprising: (a) first chain that is either a light chain or a heavy chain
 CC ; (b) a first opposite chain that is either a heavy chain opposite the
 CC first light chain or a light chain opposite the first heavy chain; (c) a
 CC second chain that is either a light chain or a heavy chain; and (d) a
 CC second opposite chain that is either a heavy chain opposite the second
 CC light chain or a light chain opposite the second heavy chain; where every
 CC PEG molecule is covalently attached to a first cysteine residue in the
 CC first or second chain that would ordinarily form a disulphide bridge with
 CC a second cysteine residue in the first or second opposite chain, where
 CC the disulphide bridge is avoided by substitution of another amino acid
 CC residue for the second cysteine residue in the first or second opposite
 CC chain, where the F(ab')₂ comprises an antigen binding site that binds to
 CC human interleukin-8 (IL-8), and where the apparent size of the conjugate
 CC is at least about 500 kD. The antigen binding sites may be derived from
 CC murine monoclonal antibodies 5.12.14 or 6G4.2.5. The method is useful for
 CC treating lung injury, including adult respiratory distress syndrome
 CC (ARDS) in a mammal and inflammatory diseases (such as ashma,
 CC inflammatory bowel disease, psoriasis and sclerostis), ischaemic
 CC reperfusion disorders, stroke, multiple sclerosis, meningitis,
 CC osteoarthritis, septic shock, autoimmune disease (e.g. rheumatoid
 CC arthritis), alcoholic hepatitis, cystic fibrosis and many other diseases
 CC and disorders listed in the specification. The present sequence
 CC represents a human antibody sequence included for comparison with the
 CC mouse humanised monoclonal antibody sequences
 XX
 XX Sequence 116 AA;
 SQ
 Query Match 93.8%; Score 60; DB 6; Length 116;
 Best Local Similarity 90.0%; Pred No. 0.057; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 1 GVSFTGHMMN 10
 |:|||||||

DB 26 GFSFTGHMMN 35
 RESULT 27
 ABUS9502
 ID ABUS9502 standard; protein; 116 AA.
 XX
 XX ABUS9502;
 AC
 AC 22-APR-2003 (first entry)
 XX
 XX
 XX Human IgG1 subgroup III heavy chain variable domain.
 DE
 DE
 XX Interleukin-8; IL-8; humanised antibody; antibody; 5.12.14; 6G4.2.5;
 KW inflammatory disorder; psoriasis; atopic dermatitis; sclerosis;
 KW systemic scleroderma; inflammatory bowel disease; Crohn's disease;
 KW ulcerative colitis; ischaemia; reperfusion; myocardial infarction;
 KW stroke; adult respiratory distress syndrome; rheumatoid arthritis;
 KW alcoholic hepatitis; acute lung injury; ashma; cerebral oedema;
 KW myocardial ischaemia; cranial trauma; asphyxia; Behcet's disease;
 KW dermatomyositis; polymyositis; multiple sclerosis; meningitis;
 KW encephalitis; uveitis; osteoarthritis; lupus nephritis; trauma;
 KW autoimmune disease; Sjogren's syndrome; vasculitis; septicemia;
 KW central nervous system inflammatory disorder; sepsis; sarcoidosis;
 KW multiple organ injury syndrome; bacterial pneumonia; glomerulonephritis;
 KW inflammation of the lung; human.
 XX
 XX
 OS Homo sapiens.
 XX
 PN US6458355-B1.
 XX
 PD 01-OCT-2002.
 XX
 PF 24-JUL-1998; 98US-00121952.
 XX
 PR 22-JAN-1998; 98US-0074330P.
 PR 20-FEB-1998; 98US-0075467P.
 XX
 PA (GETH) GENENTECH INC.
 PI Heel V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 XX WPI; 2003-208759/20.
 DR
 PT Treating inflammatory disorder in a mammal, involves administering a
 PT conjugate of polyethylene glycol and a single antibody fragment
 PT comprising antigen binding site that binds to human interleukin-8, to
 PT mammal.
 XX
 XX Example 3G; Fig 29; 2599P; English.
 PS
 CC The invention relates to treating an inflammatory disorder in a mammal,
 CC comprising administering to the mammal, an effective amount of a
 CC conjugate of a single antibody fragment (e.g. the heavy or light chains
 CC of the humanised mouse monoclonal antibodies 5.12.14 and 6G4.2.5, which
 CC also have their intramolecular disulphide bridges ablated by substitution
 CC mutations) covalently attached to one or two polyethylene glycol (PEG)
 CC molecules. The antibodies comprise an antigen binding site that binds to
 CC human interleukin-8 (IL-8), and the apparent size of the conjugate is at
 CC least 500 kDa. The method is useful for treating an inflammatory disorder
 CC e.g. ischaemic reperfusion disorder such as surgical tissue reperfusion
 CC injury, myocardial ischaemia or myocardial infarction, or hypovolemic
 CC shock, in a mammal e.g. human. The method is useful for treating
 CC inflammatory disorders including psoriasis, atopic dermatitis, systemic
 CC scleroderma and sclerosis, responses associated with inflammatory bowel
 CC disease, ischaemic reperfusion disorders, myocardial ischaemic
 CC conditions, cerebral oedema secondary to stroke, cranial trauma,
 CC asphyxia, adult respiratory distress syndrome, acute lung injury,
 CC Behcet's disease, dermatomyositis, polymyositis, multiple sclerosis,
 CC dermatitis, meningitis, encephalitis, uveitis, osteoarthritis, lupus
 CC nephritis, autoimmune diseases such as rheumatoid arthritis, Sjogren's
 CC syndrome, vasculitis, central nervous system inflammatory disorder,
 CC multiple organ injury syndrome secondary to septicemia or trauma,

CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
CC mediated diseases including glomerulonephritis, sepsis, sarcoidosis,
CC immunopathologic responses to tissue/organ transplantation, inflammations
CC of the lung, inflammatory bowel disease such as ulcerative colitis and
CC asthma. The present sequence represents the light or heavy chain of human
CC IgG, used to design the humanising mutations in the two mouse antibodies
XX
SQ Sequence 116 AA;

Query Match 93.8%; Score 60; DB 6; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.057;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSFTGHMWN 10
|:|||||
DB 26 GVSFTGHMWN 35

RESULT 28

AAE39085
ID AAE39085 standard; protein; 116 AA.

AC AAE39085;

DT 18-DEC-2003 (first entry)

DE Human IgG1 subgroup III heavy chain variable domain.

XX Interleukin-8 mediated disease; adult respiratory distress syndrome; II;
KW bacterial pneumonia; inflammatory bowel disease; hypovolemic shock; ARDS;
KW ulcerative colitis; ischaemic reperfusion injury; myocardial infarction;
KW acute lung injury; inflammatory disease; asthma; antibody; human; VH;
KW heavy chain variable domain.

XX Homo sapiens.

OS Location/Qualifiers

FT Region 26..35
/note="Complementarity determining region (CDR) #1"

FT Region 50..66
/note="Complementarity determining region (CDR) #2"

FT Region 100..111
/note="Complementarity determining region (CDR) #3"

FT US2003021790-A1.

PD 30-JAN-2003.

PF 29-NOV-2000; 2000US-00726258.

XX 22-JAN-1998; 98US-0074330P.

PR 20-FEB-1998; 98US-0075467P.

PR 24-JUL-1998; 98US-0094003P.

PR 24-JUL-1998; 98US-0094013P.

PR 20-JAN-1999; 99US-00234182.

XX (GERTH) GENENTECH INC.

PI Hseil V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;

DR WPI; 2003-605694/57.

XX Novel conjugates comprising antibody fragments covalently attached to
PT nonproteaceous polymer molecules, useful for treating inflammatory
PT diseases, acute lung injury, ischemic reperfusion injury, pneumonia and
PT asthma.

XX Example; Fig 29; 266pp; English.

XX The invention relates to novel conjugates comprising antibody fragments
CC covalently attached to nonproteaceous polymer molecules. The invention
CC is useful for treating interleukin (II)-8 mediated diseases or disorders
CC such as inflammatory diseases, acute lung injury e.g. adult respiratory

CC distress syndrome (ARDS), ischaemic reperfusion injury e.g. myocardial
CC infection, hypovolemic shock, inflammatory bowel disease e.g. ulcerative
CC colitis, bacterial pneumonia and asthma. The invention is also useful as
CC a reagent in an animal model system for in vivo study of the biological
CC functions of the antigen recognised by the conjugate. The present
CC sequence is human IgG1 subgroup III VH (heavy chain variable domain)
CC protein. This sequence is used in the exemplification of the invention
XX
SQ Sequence 116 AA;

Query Match 93.8%; Score 60; DB 7; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.057;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSFTGHMWN 10
|:|||||
DB 26 GVSFTGHMWN 35

RESULT 29

ADR03385
ID ADR03385 standard; peptide; 10 AA.

AC ADR03385;

DT 21-OCT-2004 (first entry)

DE Humanised MHM24 CDR-H1 mutant peptide, Thr301A.

XX CD14 antibody; human immunodeficiency virus infection; HIV infection;
XX rhinovirus infection; inflammatory skin disease; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
KW tuberculous; sarcoidosis; polymyositis;
KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KW skin hypersensitivity disorder; poison ivy; poison oak;
KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
KW graft versus host disease; cancer; gene therapy;
KW murine anti-human CD14 monoclonal antibody; MHM24; variable heavy chain;
KW VH; murine; human; fusion protein; complementarity determining region;
KW CDR; mutant; mutein.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

PN US2004146507-A1.

PD 29-JUL-2004.

PF 03-DEC-2003; 2003US-00727737.

XX 27-NOV-1996; 96US-0031945P.

PR 20-NOV-1997; 97US-00975329.

XX (GERTH) GENENTECH INC.

PI Jardieu PM, Presta LG;

DR WPI; 2004-552640/53.

XX New antibody mutant of a species-dependent antibody, useful for treating
PT and preventing infectious diseases, psoriasis, inflammatory bowel
PT disease, allergic conditions, autoimmune diseases, or cancer.

XX Example; SEQ ID NO 22; 54pp; English.

XX The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin

CC sequence represents a heavy chain variable region of human CD11a.
 XX Sequence 122 AA;

Query Match 85.9%; Score 55; DB 8; Length 122;
 Best Local Similarity 90.0%; Pred. No. 0.39;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 ||| |||||
 Db 26 GYSRTGHMNN 35

RESULT 32

ADRO3387 standard; peptide; 10 AA.

ADRO3387;

21-OCT-2004 (first entry)

Humanised MEM24 CDR-H1 mutant peptide, H1SH32A1a.

CD11a antibody; human immunodeficiency virus infection; HIV infection;
 rhinovirus infection; inflammatory skin disease; psoriasis;
 inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 adult respiratory distress syndrome; allergic disease; eczema; asthma;
 autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 tuberculosis; sarcoidosis; polymyositis;
 chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 skin hypersensitivity disorder; poison ivy; poison oak;
 B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 graft versus host disease; cancer; gene therapy;
 murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain;
 VH; murine; human; fusion protein; complementarity determining region;
 CDR; mutant; mutein.

Mus sp.
 Homo sapiens.
 Chimeric.

US2004146507-A1.

29-JUL-2004.

03-DEC-2003; 2003US-00727737.

27-NOV-1996; 96US-0031945P.

20-NOV-1997; 97US-00975329.

(GETH) GENENTECH INC.

Jardieu PM, Presta LG;

WPI, 2004-552640/53.

New antibody mutant of a species-dependent antibody, useful for treating
 and preventing infectious diseases, psoriasis, inflammatory bowel
 disease, allergic conditions, autoimmune diseases, or cancer.

Example; SEQ ID NO 24; 5app; English.

The present invention relates to an antibody mutant of a species-
 dependent antibody with beneficial properties. The invention is useful
 for treating and preventing infectious diseases such as human
 immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 disease and ulcerative colitis, adult respiratory distress syndrome,
 allergic diseases such as eczema and asthma, autoimmune diseases such as
 rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 mellitus, Reynaud's syndrome, immunological diseases such as
 tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary

CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MEM24) CDR-H1 mutant peptide. This sequence is used in the
 CC exemplification of the invention.

QY Sequence 10 AA;

Query Match 84.4%; Score 54; DB 8; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.038;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 ||| |||||
 Db 1 GYSFTGHMNN 10

RESULT 33

ABU56853 standard; protein; 66 AA.

ABU56853;

04-APR-2003 (first entry)

BONT/A Hc binding antibody scfv VH region from C1 #1.

Botulinum neurotoxin type A; BONT/A; mouse; heavy chain variable region;
 scfv; antibody; botulism; antibacterial; single chain antibody; VH;
 immunoglobulin.

Mus sp.

US2002155114-A1.

24-OCT-2002.

31-AUG-1998; 98US-00144886.

31-AUG-1998; 98US-00144886.

(MARK/) MARKS J D.

(AMER/) AMERSDORFER P.

Marks JD, Amersdorfer P;

WPI, 2003-182618/18.

Novel antibody that specifically binds and neutralizes botulinum
 neurotoxin type A useful for neutralizing botulinum neurotoxin and
 treating botulism.

Claim 6; Page 22; 31pp; English.

The invention relates to an isolated antibody that specifically binds to
 an epitope specifically bound by an antibody expressed by a clone such as
 CC clone S25, C25, C39, IC6 and clone 1f3, where the antibody binds to and
 CC neutralises botulinum neurotoxin type A (BONT/A). Also included are a
 CC polypeptide comprising BONT/A neutralising epitope comprising an epitope
 CC which is specifically bound by the antibody, where the polypeptide is not
 CC a full-length botulinum neurotoxin H c fragment and making an anti-BONT/A
 CC antibody that neutralises BONT/A (by contacting several antibodies with
 CC an epitope specifically bound by an antibody expressed by any of the
 CC novel clones and isolating an antibody that specifically binds to the
 CC epitope). The antibody is useful for neutralising a BONT/A, by contacting
 CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
 CC chain variable region complementarity determining region) and with a
 CC second anti-BONT/A antibody which comprises a VH CDR, where the second
 CC antibody binds to a different epitope than the first anti-BONT/A
 CC antibody. The antibody is useful in the treatment of pathologies
 CC associated with botulinum neurotoxin poisoning, for rapid

CC detection/diagnosis of botulism and in the detection and/or
CC quantification of BoNT/A in a biological sample obtained from an organism
CC which is indicative of a Clostridium botulinum infection of the organism.
CC The present sequence is a heavy chain variable region (VH) of a single
CC chain antibody (scFv) of the invention

XX Sequence 66 AA;

Query Match 81.2%; Score 52; DB 6; Length 66;
Best Local Similarity 80.0%; Pred. No. 0.61;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
|||:|
Db 26 GYSFTSYMMN 35

RESULT 34

ABUS6835
ID ABUS6835 standard; protein; 66 AA.

XX AC ABUS6835;

XX DT 04-APR-2003 (first entry)

XX DE BoNT/A Hc binding antibody scFv VH region from C15 #1.

XX KW Botulinum neurotoxin type A; BoNT/A; mouse; heavy chain variable region;
XX scFv; antibody; botulism; antibacterial; single chain antibody; VH;

XX KM immunoglobulin.

XX OS Mus sp.

XX PN US2002155114-A1.

XX PD 24-OCT-2002.

XX PF 31-AUG-1998; 98US-00144886.

XX PR 31-AUG-1998; 98US-00144886.

XX PA (MARK/) MARKS J D.

XX PA (AMER/) AMERSDORFER P.

XX PI Marks JD, Amersdorfer P;

XX DR WPI; 2003-182618/18.

XX PT Novel antibody that specifically binds and neutralizes botulinum
XX neurotoxin type A useful for neutralizing botulinum neurotoxin and
XX treating botulism.

XX PS Claim 6; Page 22; 31pp; English.

XX The invention relates to an isolated antibody that specifically binds to
CC an epitope specifically bound by an antibody expressed by a clone such as
CC clone S25, C25, C39, 1C6 and clone 1F3, where the antibody binds to and
CC neutralises botulinum neurotoxin type A (BoNT/A). Also included are a
CC polypeptide comprising BoNT/A neutralising epitope comprising an epitope
CC which is specifically bound by the antibody, where the polypeptide is not
CC a full-length botulinum neurotoxin H₂C fragment and making an anti-BoNT/A
CC antibody that neutralises BoNT/A (by contacting several antibodies with
CC an epitope specifically bound by an antibody expressed by any of the
CC novel clones and isolating an antibody that specifically binds to the
CC epitope). The antibody is useful for neutralising a BoNT/A, by contacting
CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
CC chain variable region complementarity determining region) and with a
CC second anti-BoNT/A antibody which comprises a VH CDR, where the second
CC antibody binds to a different epitope than the first anti-BoNT/A
CC antibody. The antibody is useful in the treatment of pathologies
CC associated with botulinum neurotoxin poisoning, for rapid
CC detection/diagnosis of botulism and in the detection and/or
CC quantification of BoNT/A in a biological sample obtained from an organism

CC which is indicative of a Clostridium botulinum infection of the organism.
CC The present sequence is a heavy chain variable region (VH) of a single
CC chain antibody (scFv) of the invention

XX Sequence 66 AA;

Query Match 81.2%; Score 52; DB 6; Length 66;
Best Local Similarity 80.0%; Pred. No. 0.61;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
|||:|
Db 26 GYSFTSYMMN 35

RESULT 35

ABUS6852
ID ABUS6852 standard; protein; 66 AA.

XX AC ABUS6852;

XX DT 04-APR-2003 (first entry)

XX DE BoNT/A Hc binding antibody scFv VH region from ID5 #1.

XX KW Botulinum neurotoxin type A; BoNT/A; mouse; heavy chain variable region;
XX scFv; antibody; botulism; antibacterial; single chain antibody; VH;

XX KM immunoglobulin.

XX OS Mus sp.

XX PN US2002155114-A1.

XX PD 24-OCT-2002.

XX PF 31-AUG-1998; 98US-00144886.

XX PR 31-AUG-1998; 98US-00144886.

XX PA (MARK/) MARKS J D.

XX PA (AMER/) AMERSDORFER P.

XX PI Marks JD, Amersdorfer P;

XX DR WPI; 2003-182618/18.

XX PT Novel antibody that specifically binds and neutralizes botulinum
XX neurotoxin type A useful for neutralizing botulinum neurotoxin and
XX treating botulism.

XX PS Claim 6; Page 22; 31pp; English.

XX The invention relates to an isolated antibody that specifically binds to
CC an epitope specifically bound by an antibody expressed by a clone such as
CC clone S25, C25, C39, 1C6 and clone 1F3, where the antibody binds to and
CC neutralises botulinum neurotoxin type A (BoNT/A). Also included are a
CC polypeptide comprising BoNT/A neutralising epitope comprising an epitope
CC which is specifically bound by the antibody, where the polypeptide is not
CC a full-length botulinum neurotoxin H₂C fragment and making an anti-BoNT/A
CC antibody that neutralises BoNT/A (by contacting several antibodies with
CC an epitope specifically bound by an antibody expressed by any of the
CC novel clones and isolating an antibody that specifically binds to the
CC epitope). The antibody is useful for neutralising a BoNT/A, by contacting
CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
CC chain variable region complementarity determining region) and with a
CC second anti-BoNT/A antibody which comprises a VH CDR, where the second
CC antibody binds to a different epitope than the first anti-BoNT/A
CC antibody. The antibody is useful in the treatment of pathologies
CC associated with botulinum neurotoxin poisoning, for rapid
CC detection/diagnosis of botulism and in the detection and/or
CC quantification of BoNT/A in a biological sample obtained from an organism
CC which is indicative of a Clostridium botulinum infection of the organism.
CC The present sequence is a heavy chain variable region (VH) of a single

CC chain antibody (scFv) of the invention
 XX Sequence 66 AA;
 SQ Query Match 81.2%; Score 52; DB 6; Length 66;
 Best Local Similarity 80.0%; Pred. No. 0.61;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
 |||||:
 Db 26 GYSFTSYMMN 35

RESULT 36
 ABUS6851
 ID ABUS6851 standard; protein; 66 AA.
 AC ABUS6851;
 XX
 XX 04-APR-2003 (first entry)
 DT
 XX BONT/A Hc binding antibody scFv VH region from C9 #1.
 DE
 XX Botulinum neurotoxin type A; BONT/A; mouse; heavy chain variable region;
 KW scFv; antibody; botulism; antibacterial; single chain antibody; VH;
 KM immunoglobulin.
 XX
 OS Mus sp.
 XX US2002155114-A1.
 XX
 XX 24-OCT-2002.
 PD
 XX 31-AUG-1998; 98US-00144886.
 PF
 XX 31-AUG-1998; 98US-00144886.
 PR
 XX (MARK/) MARKS J D.
 PA (AMER/) AMERSDORFER P.
 XX
 PI Marks JD, Amersdorfer P;
 DR WPI: 2003-182618/18.
 PT Novel antibody that specifically binds and neutralizes botulinum
 PT neurotoxin type A useful for neutralizing botulinum neurotoxin and
 XX treating botulism.
 PS Claim 6; Page 22; 31pp; English.

XX The invention relates to an isolated antibody that specifically binds to
 CC an epitope specifically bound by an antibody expressed by a clone such as
 CC clone S25, C25, C39, 1C6 and clone 1F3, where the antibody binds to and
 CC neutralises botulinum neurotoxin type A (BONT/A). Also included are a
 CC polypeptide comprising BONT/A neutralising epitope comprising an epitope
 CC which is specifically bound by the antibody, where the polypeptide is not
 CC a full-length botulinum neurotoxin Hc fragment and making an anti-BONT/A
 CC antibody that neutralises BONT/A (by contacting several antibodies with
 CC an epitope specifically bound by an antibody expressed by any of the
 CC novel clones and isolating an antibody that specifically binds to the
 CC epitope). The antibody is useful for neutralising a BONT/A, by contacting
 CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
 CC chain variable region complementarily determining region) and with a
 CC second anti-BONT/A antibody which comprises a VH CDR, where the second
 CC antibody binds to a different epitope than the first anti-BONT/A
 CC antibody. The antibody is useful in the treatment of pathologies
 CC associated with botulinum neurotoxin poisoning, for rapid
 CC detection/diagnosis of botulism and in the detection and/or
 CC quantification of BONT/A in a biological sample obtained from an organism
 CC which is indicative of a Clostridium botulinum infection of the organism.
 CC The present sequence is a heavy chain variable region (VH) of a single
 CC chain antibody (scFv) of the invention

SQ Sequence 66 AA;
 ~ Query Match 81.2%; Score 52; DB 6; Length 66;
 Best Local Similarity 80.0%; Pred. No. 0.61;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
 |||||:
 Db 26 GYSFTSYMMN 35

RESULT 37
 AAE22192
 ID AAE22192 standard; protein; 117 AA.
 XX
 XX AAE22192;
 AC
 XX
 XX 25-JUL-2002 (first entry)
 DT
 XX Murine MC-1 antibody heavy chain variable domain (VH) (1) #2.
 DE
 XX Chemokine construct; human immunodeficiency virus 1; allergic disease;
 KM skin disease; immunological disorder; autoimmune disease; psoriasis;
 KM multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
 KM diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
 KM inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine;
 KM MC-1 antibody; VH; heavy chain variable domain; chemokine receptor 5.
 XX
 OS Mus sp.
 XX WO200220615-A2.
 XX
 XX 14-MAR-2002.
 PD
 XX 10-SEP-2001; 2001WO-EP010433.
 PF
 XX 08-SEP-2000; 2000EP-00119694.
 PR
 XX 05-SEP-2001; 2001US-00948004.
 XX
 PA (MCCR-) MICROMET AG.
 XX
 PI Mack M, Schloendorff D, Spring M;
 DR WPI: 2002-362240/39.
 XX N-PSDB; AAD35251.
 DR
 XX Use of an antibody and/or chemokine construct that binds to a chemokine
 PT receptor, for eliminating cells latently infected with primate
 PT immunodeficiency virus, or treating, preventing and alleviating immune
 PT disorders.
 PS Claim 12; Page 50; 117pp; English.

XX The invention relates to the use of an antibody and/or chemokine
 CC construct that binds a chemokine receptor for preparing a pharmaceutical
 CC composition for eliminating cells latently infected with a primate
 CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They
 CC are used in gene therapy and as vaccines. The antibody and/or chemokine
 CC construct is also used for preparing a pharmaceutical composition for
 CC treating, preventing and/or alleviating immunological disorders including
 CC autoimmune diseases (e.g. multiple sclerosis, type 1 diabetes and
 CC rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
 CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases
 CC such as inflammatory joint diseases (chronic arthritis), inflammatory
 CC renal diseases and inflammatory bowel diseases and graft versus host and
 CC transplant rejections. The present sequence is murine MC-1 antibody heavy
 CC chain variable domain (VH) (1). This antibody is specific for human
 CC chemokine receptor 5 (CCR5)
 XX
 SQ Sequence 117 AA;
 Query Match 81.2%; Score 52; DB 5; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.1;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||:||||
 DB 36 GYSFTSYMMN 45

RESULT 38

AAW01579 standard; protein; 118 AA.

AAW01579;

22-AUG-1997 (first entry)

Lead binding MAb 10G5 heavy chain variable region.

Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
 pharmaceutical; health care; skin treatment; pesticide; herbicide;
 heavy metal.

Mus musculus.

WO9639518-A1.

12-DEC-1996.

05-JUN-1996; 96WO-US009258.

05-JUN-1995; 95US-00462798.

10-OCT-1995; 95US-00541373.

(BION-) BIONEBRASKA INC.

Wylie DE, Lopez O, Murray PJ;

WPI; 1997-043140/04.

N-PSDB; AAT58253.

DNA encoding heavy metal binding polypeptide sequences - used for
 detecting, removing, adding or neutralising heavy metals, such as lead
 cations.

Claim 12; Page 61; 125pp; English.

The present sequence represents the heavy chain variable region for
 monoclonal antibody (MAb) 10G5, which immunoreacts with a lead cation.

The sequence was derived from RNA isolated from mouse hybridoma cells.
 The protein can be used for binding heavy metals, such as lead cations.

It can be used for detecting, removing, adding or neutralising the heavy
 metals in biological and inanimate systems. It can be used in e.g.

aqueous liquid systems, in biological or environmental systems or in such
 compositions as perfumes, cosmetics, pharmaceuticals, health care

products, skin treatment products, pesticides, herbicides, solvents used
 in the production of semi-conductor and integrated circuit components and

production materials for electronic components. The products can provide
 for applications involving minute amounts of specific heavy metals

Sequence 118 AA;

Query Match 81.2%; Score 52; DB 2; Length 118;

Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||:||||

DB 26 GYSFTSYMMN 35

RESULT 39

AAW01576

AAW01576 standard; protein; 118 AA.

AAW01576;

22-AUG-1997 (first entry)

Lead binding MAb 6B11 heavy chain variable region.

Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
 pharmaceutical; health care; skin treatment; pesticide; herbicide;
 heavy metal.

Mus musculus.

WO9639518-A1.

12-DEC-1996.

05-JUN-1996; 96WO-US009258.

05-JUN-1995; 95US-00462798.

10-OCT-1995; 95US-00541373.

(BION-) BIONEBRASKA INC.

Wylie DE, Lopez O, Murray PJ;

WPI; 1997-043140/04.

N-PSDB; AAT58250.

DNA encoding heavy metal binding polypeptide sequences - used for
 detecting, removing, adding or neutralising heavy metals, such as lead
 cations.

Claim 12; Page 56; 125pp; English.

The present sequence represents the heavy chain variable region for
 monoclonal antibody (MAb) 6B11, which immunoreacts with a lead cation.

The sequence was derived from RNA isolated from mouse hybridoma cells.
 The protein can be used for binding heavy metals, such as lead cations.

It can be used for detecting, removing, adding or neutralising the heavy
 metals in biological and inanimate systems. It can be used in e.g.

aqueous liquid systems, in biological or environmental systems or in such
 compositions as perfumes, cosmetics, pharmaceuticals, health care

products, skin treatment products, pesticides, herbicides, solvents used
 in the production of semi-conductor and integrated circuit components and

production materials for electronic components. The products can provide
 for applications involving minute amounts of specific heavy metals

Sequence 118 AA;

Query Match 81.2%; Score 52; DB 2; Length 118;

Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||:||||

DB 26 GYSFTSYMMN 35

RESULT 40

ADZ21535 standard; protein; 118 AA.

ADZ21535;

30-JUN-2005 (first entry)

Anti-Muc-1 single chain antibody B9 VH polypeptide.

Single chain antibody; MUC-1; tumor-associated antigen;

heavy chain variable region; antibody therapy; cytostatic.

Mus sp.
 Synthetic.

XX MO2005032454-A2.
 PN 14-APR-2005.
 PD 07-MAY-2004; 2004WO-US014159.
 PF 09-MAY-2003; 2003US-00435614.
 PR (RESC) UNIV CALIFORNIA.
 PA Denardo SJ, Winthrop MD, Denardo GL, Xiong C;
 PI WPI; 2005-285319/29.
 DR
 XX New antibodies that specifically bind to cancer antigen MUC-1, useful for
 PT tumor targeting, for inhibiting the growth or proliferation of cancer
 PT cells or as diagnostic agents to identify tumors and monitor levels of
 PT circulating antigen.
 PS Claim 6; SEQ ID NO 13; 79pp; English.
 XX The invention provides novel antibodies that specifically bind to the MUC
 CC -1 cancer antigen. Preferred single chain antibodies were obtained from a
 CC phage display library and were designated as 12B, 3D, A5, C4, B5, B1 and
 CC B9 ADZ21537-ADZ21543. The heavy chain variable regions (VH) and light
 CC chain variable regions (VL) of these antibodies are also provided
 CC ADZ21533-ADZ21536. The VH and VL domains govern the specificity and
 CC binding affinity of the antibodies and permit the construction of a
 CC variety of antibodies that specifically target the MUC-1 antigen and
 CC cells bearing/displaying the antigen. The antibodies are useful targeting
 CC moieties for specifically directing imaging agents and various
 CC therapeutic moieties to a cancer. A claimed method of inhibiting the
 CC growth or proliferation of a cell bearing a MUC-1 antigen comprises
 CC contacting the cell with a chimeric molecule comprising an anti-MUC-1
 CC antibody attached to a cytotoxicin, a radionuclide, a liposome comprising
 CC an anti-cancer drug, a prodrug or an anti-cancer drug. The present
 CC sequence is that of the VH region of single chain antibody B9 ADZ21543.
 XX
 SQ Sequence 118 AA;
 Query Match 81.2%; Score 52; DB 9; Length 118;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYSFTGHMMN 10
 DB 26 GYSFTSYMMN 35
 RESULT 41
 ADE25819
 ID ADE25819 standard; protein; 121 AA.
 XX
 AC ADE25819;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Anti-alpha-v-beta-6 monoclonal Ab heavy chain variable domain SEQ:25.
 XX
 XX monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;
 KW cytostatic; dermatological; vulnery; hepatotropic; immunosuppressive;
 KW vaccine; fibrosis; scleroderma; scarring; liver fibrosis;
 KW kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.
 XX
 OS Synthetic.
 XX
 PN MO2003100033-A2.
 XX
 PD 04-DEC-2003.
 XX
 PF 13-MAR-2003; 2003WO-US008048.
 XX

PR 13-MAR-2002; 2002US-0364991P.
 PR 13-NOV-2002; 2002US-0426286P.
 XX
 XX (BIOJ) BIOGEN INC.
 PA (RESC) UNIV CALIFORNIA.
 XX
 PI Violette SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;
 DR WPI; 2004-035139/03.
 XX
 PT New monoclonal antibody that specifically binds to alpha-v-beta-6, and
 PT inhibits the binding of alpha v beta 6 to latency associated peptide
 PT (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's
 PT syndrome.
 PS Claim 18; SEQ ID NO 26; 83pp; English.
 XX
 CC The present invention describes a monoclonal antibody (1) that
 CC specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v
 CC -beta-6 to latency associated peptide (LAP) with an IC50 value lower than
 CC that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody
 CC comprising heavy chain complementarity determining regions (CDR) 1, 2,
 CC and 3, or a heavy and light chain variable domain sequence; (2) a
 CC monoclonal antibody that specifically binds to alpha-v-beta-6 but does
 CC not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for
 CC preventing or treating a disease mediated by alpha-v-beta-6 in a mammal
 CC subject having or at risk of having a disease mediated by alpha-v-beta-6
 CC by administering to the subject the composition described above, and so
 CC alleviating or postponing the onset of the disease; (5) a method of
 CC detecting alpha-v-beta-6 in a tissue sample by contacting the tissue
 CC sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6,
 CC 6.2B1, 7.1G10, 7.7G5, or 7.1Cr, which respectively comprises American
 CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-
 CC 3643, PTA-3646, PTA-3896, PTA-3899, or PTA-3900. (1) has cytostatic,
 CC dermatological, vulnery, hepatotropic, and immunosuppressive activities,
 CC and can be used in vaccines. The antibodies, compositions and methods of
 CC the present invention can be used for preventing or treating a disease
 CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,
 CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,
 CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,
 CC laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or
 CC Alport's syndrome. The present sequence is used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 121 AA;
 Query Match 81.2%; Score 52; DB 8; Length 121;
 Best Local Similarity 80.0%; Pred. No. 1.2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYSFTGHMMN 10
 DB 26 GYSFTSYMMN 35
 RESULT 42
 ADE25818
 ID ADE25818 standard; protein; 121 AA.
 XX
 AC ADE25818;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Anti-alpha-v-beta-6 monoclonal Ab heavy chain variable domain SEQ:25.
 XX
 XX monoclonal antibody; alpha-v-beta-6; latency associated peptide; LAP;
 KW cytostatic; dermatological; vulnery; hepatotropic; immunosuppressive;
 KW vaccine; fibrosis; scleroderma; scarring; liver fibrosis;
 KW kidney fibrosis; lung fibrosis; psoriasis; cancer; Alport's syndrome.
 XX
 OS Synthetic.
 XX

PN WO2003100033-A2.
 XX 04-DEC-2003.
 XX 13-MAR-2003; 2003WO-US008048.
 XX 13-MAR-2002; 2002US-0364991P.
 PR 13-NOV-2002; 2002US-0426286P.
 PA (BIOJ) BIOGEN INC.
 PA (REBC) UNIV CALIFORNIA.
 PI Violette SM, Weinreb PH, Simon KJ, Sheppard D, Leone DR;
 DR WPI, 2004-035139/03.
 XX
 PT New monoclonal antibody that specifically binds to alpha-v-beta-6, and
 PT inhibits the binding of alpha v beta 6 to latency associated peptide
 PT (LAP), useful for treating fibrosis, psoriasis, cancer, or Alport's
 PT syndrome.
 PS Claim 18; SEQ ID NO 25; 83pp; English.
 XX
 CC The present invention describes a monoclonal antibody (I) that
 CC specifically binds to alpha-v-beta-6, and inhibits the binding of alpha-v-
 CC beta-6 to latency associated peptide (LAP) with an IC50 value lower than
 CC that of 10D5. Also described: (1) an anti-alpha-v-beta-6 antibody
 CC comprising heavy chain complementarity determining regions (CDR) 1, 2,
 CC and 3, or a heavy and light chain variable domain sequence; (2) a
 CC monoclonal antibody that specifically binds to alpha-v-beta-6 but does
 CC not inhibit binding of alpha-v-beta-6 to LAP; (3) a composition for
 CC preventing or treating a disease mediated by alpha-v-beta-6 in a mammal
 CC comprising the antibody and a carrier; (4) a method for treating a
 CC subject having or at risk of having a disease mediated by alpha-v-beta-6
 CC by administering to the subject the composition described above, and so
 CC alleviating or postponing the onset of the disease; (5) a method of
 CC detecting alpha-v-beta-6 in a tissue sample by contacting the tissue
 CC sample with the antibody; and (6) a cell hybridoma 6.1A8, 6.3G9, 6.8G6,
 CC 6.2B1, 7.1G10, 7.7G5, or 7.1Cr, which respectively comprises American
 CC Type Culture Collection (ATCC) Accession number PTA-3647, PTA-3649, PTA-
 CC 3645, PTA-3646, PTA-3898, PTA-3899, or PTA-3900. (1) has cytostatic,
 CC dermatological, vulnerary, hepatotropic and immunosuppressive activities,
 CC and can be used in vaccines. The antibodies, compositions and methods of
 CC the present invention can be used for preventing or treating a disease
 CC mediated by alpha-v-beta-6, e.g. fibrosis such as scleroderma, scarring,
 CC liver fibrosis, kidney fibrosis or lung fibrosis; psoriasis; cancer,
 CC preferably epithelial cancer, oral, skin, cervical, pharyngeal,
 CC laryngeal, oesophageal, lung, breast, kidney or colorectal cancer; or
 CC Alport's syndrome. The present sequence is used in the exemplification of
 CC the present invention.
 CC
 SQ Sequence 121 AA;
 QY
 Db 1 GYSFTGHMMN 10
 26 GYSFTSYMMN 35
 Query Match 81.2%; Score 52; DB 8; Length 121;
 Best Local Similarity 80.0%; Pred. No. 1.2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KW heavy chain variable region; single chain antibody; scFv.
 OS Mus sp.
 XX US2004175385-A1.
 PN 09-SEP-2004.
 XX
 PD 01-AUG-2003; 2003US-00632706.
 PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 PA (REBC) UNIV CALIFORNIA.
 PI Marks JD, Amerdorter P;
 DR WPI, 2004-652009/63.
 XX
 PT New isolated antibody that neutralizes botulinum neurotoxin type A.
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 PS Example 1; SEQ ID NO 51; 110pp; English.
 XX
 CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (1) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, JG6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and 1N61, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin
 CC scFv.
 CC
 SQ Sequence 121 AA;
 QY
 Db 1 GYSFTGHMMN 10
 26 GYSFTSYMMN 35
 Query Match 81.2%; Score 52; DB 8; Length 121;
 Best Local Similarity 80.0%; Pred. No. 1.2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DE Mouse heavy chain variable region scFv seqid 50.
 XX anti-bacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KM heavy chain variable region; single chain antibody; scFv.
 XX Mus sp.
 XX US2004175385-A1.
 PN 09-SEP-2004.
 PD 01-AUG-2003; 2003US-00632706.
 PF 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX (REGC) UNIV CALIFORNIA.
 PA Marks JD, Amersdorfer P;
 PI WPI; 2004-652009/63.
 DR New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX Example 1; SEQ ID NO 50; 110pp; English.
 PS The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C39, C39, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin
 CC scFv.
 XX SQ Sequence 125 AA;
 XX
 XX Query Match 81.2%; Score 52; DB 8; Length 125;
 XX Best Local Similarity 80.0%; Pred. No. 1.2;
 XX Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYSFTGHMNN 10
 XX ||||| : |||
 Db 26 GYSFTSYMMN 35
 XX
 XX RESULT 45
 XX ADR38646
 XX ID ADR38646 standard; peptide; 125 AA.
 XX AC ADR38646;

XX 02-DEC-2004 (first entry)
 DT Mouse heavy chain variable region scFv seqid 48.
 XX anti-bacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 DE BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM BoNT/A neutralisation; botulinum neurotoxin poisoning; mouse;
 KM heavy chain variable region; single chain antibody; scFv.
 XX Mus sp.
 XX US2004175385-A1.
 PN 09-SEP-2004.
 PD 01-AUG-2003; 2003US-00632706.
 PF 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX (REGC) UNIV CALIFORNIA.
 PA Marks JD, Amersdorfer P;
 PI WPI; 2004-652009/63.
 DR New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX Example 1; SEQ ID NO 48; 110pp; English.
 PS The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C39, C39, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin
 CC scFv.
 XX SQ Sequence 125 AA;
 XX
 XX Query Match 81.2%; Score 52; DB 8; Length 125;
 XX Best Local Similarity 80.0%; Pred. No. 1.2;
 XX Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYSFTGHMNN 10
 XX ||||| : |||
 Db 26 GYSFTSYMMN 35
 XX
 XX RESULT 46
 XX ADR38647

ID ADR38647 standard; peptide; 125 AA.
 XX
 XX ADR38647;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 XX Mouse heavy chain variable region scfV seqid 49.
 DE
 XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KM heavy chain variable region; single chain antibody; scfV.
 XX
 OS Mus sp.
 XX
 XX US2004175385-A1.
 XX
 XX 09-SEP-2004.
 PD
 XX 01-AUG-2003; 2003US-00632706.
 PF
 XX 31-AUG-1998; 98US-0014886.
 PR 01-AUG-2002; 2002US-0400721P.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Marks JD, Amerdorfer P;
 PI
 XX WPI; 2004-652009/63.
 DR
 XX
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 PT
 XX
 XX Example 1; SEQ ID NO 49; 110pp; English.
 PS
 XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C39, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, W1(V), W1(F), 3-L,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin
 CC scfV.
 XX
 XX Sequence 125 AA;
 SQ

Query Match 81.2%; Score 52; DB 8; Length 125;
 Best Local Similarity 80.0%; Pred. No. 1.2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
 |||||:
 Db 26 GYSFTSYMMN 35

RESULT 47
 AAE22191
 ID AAE22191 standard; protein; 138 AA.
 XX
 XX AAE22191;
 AC
 XX 25-JUL-2002 (first entry)
 DT
 XX Murine MC-1 antibody heavy chain variable domain (VH) (1) #1.
 DE
 XX Chemokine construct; human immunodeficiency virus 1; allergic disease;
 XX skin disease; immunological disorder; autoimmune disease; psoriasis;
 KM multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
 KM diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
 KM inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine;
 KM MC-1 antibody; VH; heavy chain variable domain; chemokine receptor 5.
 XX
 XX Mus sp.
 XX
 OS
 XX
 XX WO200220615-A2.
 PN
 XX 14-MAR-2002.
 PD
 XX 10-SEP-2001; 2001WO-EP010433.
 PF
 XX 08-SEP-2000; 2000EP-00119694.
 PR 05-SEP-2001; 2001US-00948004.
 PR
 XX (MICR-) MICROMET AG.
 PA
 XX Mack M, Schloendorff D, Spring M;
 PI
 XX WPI; 2002-362240/39.
 DR
 XX N-PSDB; AAD35250.
 DR
 XX
 PT Use of an antibody and/or chemokine construct that binds to a chemokine
 PT receptor, for eliminating cells latently infected with primate
 PT immunodeficiency virus, or treating, preventing and alleviating immune
 PT disorders.
 PT
 XX
 XX Example 2; Page 50; 117pp; English.
 PS
 XX The invention relates to the use of an antibody and/or chemokine
 CC construct that binds a chemokine receptor for preparing a pharmaceutical
 CC composition for eliminating cells latently infected with a primate
 CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They
 CC are used in gene therapy and as vaccines. The antibody and/or chemokine
 CC construct is also used for preparing a pharmaceutical composition for
 CC treating, preventing and/or alleviating immunological disorders including
 CC autoimmune diseases (e.g. multiple sclerosis, type I diabetes and
 CC rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
 CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases
 CC such as inflammatory joint diseases (chronic arthritis), inflammatory
 CC renal diseases and inflammatory bowel diseases and graft versus host and
 CC transplant rejections. The present sequence is murine MC-1 antibody heavy
 CC chain variable domain (VH) (1). This antibody is specific for human
 CC chemokine receptor 5 (CCR5)
 CC
 XX
 XX Sequence 138 AA;
 SQ

Query Match 81.2%; Score 52; DB 5; Length 138;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
 |||||:
 Db 45 GYSFTSYMMN 54

RESULT 48
 ADZ21543
 ID ADZ21543 standard; protein; 177 AA.

XX AC ADZ21543;
 XX DT 30-JUN-2005 (first entry)
 XX DE Anti-Muc-1 single chain antibody B9.
 XX KW Single chain antibody; MUC-1; tumor-associated antigen; antibody therapy;
 XX KM cytostatic.
 XX OS Mus sp.
 XX OS Synthetic.
 XX FT Key Location/Qualifiers
 XX FT Domain 3..120
 XX FT Domain /label = VH
 XX FT Domain 136..177
 XX FT Domain /label = VL
 XX PN WO2005032454-A2.
 XX PD 14-APR-2005.
 XX PF 07-MAY-2004; 2004WO-US014159.
 XX PR 09-MAY-2003; 2003US-00435614.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Denardo SJ, Winthrop MD, Denardo GL, Xiong C;
 XX DR WPI; 2005-285319/29.
 XX PT New antibodies that specifically bind to cancer antigen MUC-1, useful for
 XX PT tumor targeting, for inhibiting the growth or proliferation of cancer
 XX PT cells or as diagnostic agents to identify tumors and monitor levels of
 XX PT circulating antigen.
 XX PS Claim 7; SEQ ID NO 21; 79pp; English.
 XX CC The invention provides novel antibodies that specifically bind to the MUC
 XX CC -1 cancer antigen. Preferred single chain antibodies were obtained from a
 XX CC phage display library and were designated as 12E, 3D, A5, C4, B5, B1 and
 XX CC B9 ADZ21537-ADZ21543. The heavy chain variable regions (VH) and light
 XX CC chain variable regions (VL) of these antibodies are also provided
 XX CC ADZ21533-ADZ21536. The VH and VL domains govern the specificity and
 XX CC binding affinity of the antibodies and permit the construction of a
 XX CC variety of antibodies that specifically target the MUC-1 antigen and
 XX CC cells bearing/displaying the antigen. The antibodies are useful targeting
 XX CC moieties for specifically directing imaging agents and various
 XX CC therapeutic moieties to a cancer. A claimed method of inhibiting the
 XX CC growth or proliferation of a cell bearing a MUC-1 antigen comprises
 XX CC contacting the cell with a chimeric molecule comprising an anti-MUC-1
 XX CC antibody attached to a cytotoxin, a radionuclide, a liposome comprising
 XX CC an anti-cancer drug, a prodrug or an anti-cancer drug. The present
 XX CC sequence is that of single chain antibody B9.
 XX SQ Sequence 177 AA;
 XX
 XX Query Match 81.2%; Score 52; DB 9; Length 177;
 XX Best Local Similarity 80.0%; Pred. No. 1.8;
 XX Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

XX DT 25-JUL-2002 (first entry)
 XX DE Murine CCR5xCD3 bispecific single chain antibody construct.
 XX KW Chemokine construct; human immunodeficiency virus 1; allergic disease;
 XX KW skin disease; immunological disorder; autoimmune disease; psoriasis;
 XX KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
 XX KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
 XX KW inflammatory renal disease; HIV-1; transplant rejection; CCR5xCD3;
 XX KW antibody; chemokine receptor 5; CD3 antigen; chimeric; murine.
 XX OS Mus sp.
 XX OS Unidentified.
 XX OS Chimeric.
 XX PN WO200220615-A2.
 XX PD 14-MAR-2002.
 XX PF 10-SEP-2001; 2001WO-EP010433.
 XX PR 08-SEP-2000; 2000EP-00119694.
 XX PR 05-SEP-2001; 2001US-00948004.
 XX PA (MICR-) MICROMET AG.
 XX PI Mack M, Schloendorff D, Spring M;
 XX DR WPI; 2002-362240/39.
 XX DR N-PSDB; AAD35252.
 XX PT Use of an antibody and/or chemokine construct that binds to a chemokine
 XX PT receptor, for eliminating cells latently infected with primate
 XX PT immunodeficiency virus, or treating, preventing and alleviating immune
 XX PT disorders.
 XX PS Claim 29; Page 52; 117pp; English.
 XX CC The invention relates to the use of an antibody and/or chemokine
 XX CC construct that binds a chemokine receptor for preparing a pharmaceutical
 XX CC composition for eliminating cells latently infected with a primate
 XX CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They
 XX CC are used in gene therapy and as vaccines. The antibody and/or chemokine
 XX CC construct is also used for preparing a pharmaceutical composition for
 XX CC treating, preventing and/or alleviating immunological disorders including
 XX CC autoimmune diseases (e.g. multiple sclerosis, type I diabetes and
 XX CC rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
 XX CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases
 XX CC such as inflammatory joint diseases (chronic arthritis), inflammatory
 XX CC renal diseases and inflammatory bowel diseases and graft versus host and
 XX CC transplant rejections. The present sequence is CCR5xCD3 bispecific single
 XX CC chain antibody construct. This antibody construct comprises light chain
 XX CC variable domain (VL) and heavy chain variable (VH) domains of murine MC-1
 XX CC antibody specific for human chemokine receptor 5 (CCR5) and VH and VL
 XX CC domains of an antibody specific for a CD3 antigen joined by a peptide
 XX CC linker
 XX SQ Sequence 495 AA;
 XX
 XX Query Match 81.2%; Score 52; DB 5; Length 495;
 XX Best Local Similarity 80.0%; Pred. No. 5.3;
 XX Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 49
 AAE22193
 ID AAE22193 standard; protein; 495 AA.
 XX
 AC AAE22193;

RESULT 50
 ADU66947
 ID ADU66947 standard; protein; 120 AA.
 XX

AC ADU66947;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human 3B10 heavy chain variable region (VH) protein.

XX PTN; pleiotrophin; cancer; carcinoma; sarcoma;
XX haematopoietic neoplastic disorder; Hodgkin's disease;
KW Non-hodgkin's lymphoma; multiple myeloma; leukaemia; neuroblastoma;
KW rhabdomyosarcoma; primary thrombocytosis; primary macroglobulinaemia;
KW small-cell lung tumour; malignant pancreatic insulinoma;
KW malignant carcinoid; melanoma; premalignant skin lesions; lymphomas;
KW malignant hypercalcaemia; cytostatic; human; heavy chain variable region;
VH.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 31..35 /note= "Complementarity determining region (CDRε) "

XX Region 50..66 /note= "Complementarity determining region (CDRε) "

XX Region 99..109 /note= "Complementarity determining region (CDRε) "

XX US2004234519-A1.

XX 25-NOV-2004.

XX 26-MAR-2004; 2004US-00812366.

XX 26-MAR-2003; 2003US-0458459P.

XX (TSOU/) TSO J Y.

XX (WELL/) WELLSTEIN A.

XX (CHAO/) CHAO D.

XX Tso JY, Wellstein A, Chao D;

XX WPI; 2004-821276/81.

XX N-PSDB; ADU66948.

XX New antibody that competitively inhibits binding of a pleiotrophin (PTV)
XX polypeptide to an antibody, useful for neutralizing at least one
XX biological activity of PTN in a subject thus treating or preventing
XX cancers e.g., leukemia.

XX Claim 16; SEQ ID NO 3; 38pp; English.

XX The present invention relates to an antibody that competitively inhibits
XX binding of a pleiotrophin (PTN) protein. The invention is useful for
XX neutralising at least one biological activity of PTN in a subject thus
XX preventing or treating cancers such as carcinomas, sarcomas, or
XX haematopoietic neoplastic disorders, Hodgkin's disease, Non-hodgkin's
XX lymphoma, multiple myeloma, leukaemia, neuroblastoma, breast cancer,
XX ovarian cancer, lung cancer, cancers of head and neck, cancer of
XX endothelium, cancers of bone, cancer of muscle, pancreatic cancer,
XX rhabdomyosarcoma, primary thrombocytosis, primary macroglobulinaemia,
XX small-cell lung tumours, stomach cancer, colon cancer, kidney cancer,
XX malignant pancreatic insulinoma, malignant carcinoid, urinary bladder
XX cancer, melanoma, premalignant skin lesions, testicular cancer,
XX lymphomas, thyroid cancer, oesophageal cancer, genitourinary tract
XX cancer, malignant hypercalcaemia, cervical cancer, endometrial cancer,
XX epidermal cancer, adrenal cortical cancer, prostate cancer, or uterine
XX cancer. The present sequence is the human 3B10 heavy chain variable
XX region (VH) protein.

XX Sequence 120 AA;

Query Match 79.7%; Score 51; DB 8; Length 120;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 GYSEFGHWN 10
||:|:||||
Db 26 GYATSSHMN 35

Search completed: January 17, 2006, 11:58:02
Job time : 82.5758 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:48:18 : Search time 9.39394 Seconds
(without alignments)
102.424 Million cell updates/sec

Title: US-10-665-658-10

Perfect score: 64

Sequence: 1 GYSFTGHMMN 10

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: pir80:*
2: pir1:*
3: pir2:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	78.1	40	2	S33404 Ig heavy chain V r
2	50	78.1	98	2	PH1145 Ig heavy chain V r
3	49	76.6	101	2	H37262 Ig heavy chain V r
4	49	76.6	103	2	PH0986 Ig heavy chain V r
5	49	76.6	106	2	S26315 Ig heavy chain V r
6	49	76.6	107	2	PH0987 Ig heavy chain V r
7	49	76.6	110	2	S26317 Ig heavy chain V r
8	49	76.6	114	2	A49060 Ig heavy chain V r
9	49	76.6	117	2	G45722 anti-glycoprotein
10	49	76.6	118	2	C30560 Ig heavy chain V r
11	48	75.0	98	2	S17604 Ig heavy chain V r
12	48	75.0	114	2	S26319 Ig heavy chain V r
13	48	75.0	135	2	PS0057 Ig heavy chain pre
14	47	73.4	101	2	S42183 Ig gamma chain V r
15	47	73.4	117	2	S55541 Ig heavy chain V r
16	47	73.4	119	2	JN0295 Ig heavy chain V-D
17	47	73.4	123	2	D33548 Ig heavy chain V-1
18	47	73.4	136	2	B47159 Ig heavy chain V r
19	47	73.4	66	2	S36384 Ig heavy chain V r
20	45	70.3	101	2	PH0983 Ig heavy chain V r
21	45	70.3	102	2	B37263 Ig heavy chain V r
22	45	70.3	104	2	PH0981 Ig heavy chain V r
23	45	70.3	106	2	PH1005 Ig heavy chain V r
24	45	70.3	107	2	PH0984 Ig heavy chain V r
25	45	70.3	111	2	S26463 Ig heavy chain V r
26	45	70.3	120	2	F45722 anti-glycoprotein
27	45	70.3	120	2	S09956 Ig heavy chain V-D
28	45	70.3	122	2	PH0887 Ig heavy chain V r
29	45	70.3	122	2	PH0887 Ig heavy chain V r

30	45	70.3	135	2	A30577 Ig heavy chain pre
31	45	70.3	137	2	E29380 Ig heavy chain pre
32	45	70.3	138	2	E32513 Ig heavy chain pre
33	44	68.8	69	2	D25150 Ig heavy chain V r
34	44	68.8	76	2	PH1153 Ig heavy chain V r
35	44	68.8	80	2	F28833 Ig kappa chain V r
36	44	68.8	86	2	A25150 Ig heavy chain V r
37	44	68.8	91	2	PH1004 Ig heavy chain V r
38	44	68.8	94	2	S42185 Ig gamma chain V r
39	44	68.8	94	2	PH1142 Ig heavy chain V r
40	44	68.8	94	2	JT0078 Ig heavy chain V r
41	44	68.8	96	2	S17613 Ig heavy chain V r
42	44	68.8	96	2	S17616 Ig heavy chain V r
43	44	68.8	97	2	PH1137 Ig heavy chain V r
44	44	68.8	97	2	PH1155 Ig heavy chain V r
45	44	68.8	98	2	PH1164 Ig heavy chain V r
46	44	68.8	98	2	PH1141 Ig heavy chain V r
47	44	68.8	98	2	PH1138 Ig heavy chain V r
48	44	68.8	98	2	PH1154 Ig heavy chain V r
49	44	68.8	98	2	PH1106 Ig heavy chain V r
50	44	68.8	98	2	PH1118 Ig heavy chain V r
51	44	68.8	98	2	PH1139 Ig heavy chain V r
52	44	68.8	98	2	PH1150 Ig heavy chain V r
53	44	68.8	98	2	PH1156 Ig heavy chain V r
54	44	68.8	98	2	PH1125 Ig heavy chain V r
55	44	68.8	98	2	PH1134 Ig heavy chain V r
56	44	68.8	98	2	PH1105 Ig heavy chain V r
57	44	68.8	98	2	PH1126 Ig heavy chain V r
58	44	68.8	98	2	PH1108 Ig heavy chain V r
59	44	68.8	98	2	PH1119 Ig heavy chain V r
60	44	68.8	98	2	PH1124 Ig heavy chain V r
61	44	68.8	98	2	PH1149 Ig heavy chain V r
62	44	68.8	98	2	PH1157 Ig heavy chain V r
63	44	68.8	98	2	PH1114 Ig heavy chain V r
64	44	68.8	98	2	I28833 Ig kappa chain V r
65	44	68.8	98	2	PH1144 Ig heavy chain V r
66	44	68.8	98	2	PH1151 Ig heavy chain V r
67	44	68.8	98	2	PH1131 Ig heavy chain V r
68	44	68.8	105	2	PH0978 Ig heavy chain V r
69	44	68.8	107	2	S26320 Ig heavy chain V r
70	44	68.8	108	2	PH0985 Ig heavy chain V r
71	44	68.8	109	2	S25038 Ig heavy chain V r
72	44	68.8	109	2	S26318 Ig heavy chain V r
73	44	68.8	110	2	S25028 Ig heavy chain V r
74	44	68.8	111	2	S25024 Ig heavy chain V r
75	44	68.8	111	2	S25032 Ig heavy chain V r
76	44	68.8	111	2	S25047 Ig heavy chain V r
77	44	68.8	111	2	S25055 Ig heavy chain V r
78	44	68.8	111	2	S25045 Ig heavy chain V r
79	44	68.8	111	2	S25054 Ig heavy chain V r
80	44	68.8	111	2	S25046 Ig heavy chain V r
81	44	68.8	111	2	S25052 Ig heavy chain V r
82	44	68.8	111	2	S25040 Ig heavy chain V r
83	44	68.8	111	2	S25051 Ig heavy chain V r
84	44	68.8	112	2	S25042 Ig heavy chain V r
85	44	68.8	113	2	S25044 Ig heavy chain V r
86	44	68.8	113	2	S25041 Ig heavy chain V r
87	44	68.8	113	2	C27563 Ig heavy chain V r
88	44	68.8	116	2	I84704 Ig heavy chain V r
89	44	68.8	116	2	S26309 Ig heavy chain pre
90	44	68.8	117	1	HVMS02 Ig heavy chain pre
91	44	68.8	117	1	HVMS23 Ig heavy chain pre
92	44	68.8	117	1	HVMS3 Ig heavy chain pre
93	44	68.8	117	1	HVMS45 Ig heavy chain pre
94	44	68.8	117	1	HVMS61 Ig heavy chain pre
95	44	68.8	117	1	MHMSB4 Ig heavy chain pre
96	44	68.8	118	2	JC2269 Ig heavy chain V r
97	44	68.8	118	2	PL0084 Ig heavy chain V a
98	44	68.8	119	2	B53285 Ig heavy chain V r
99	44	68.8	119	2	PL0089 Ig heavy chain V r
100	44	68.8	120	1	MHMS15 Ig heavy chain V r
101	44	68.8	120	2	S25175 Ig heavy chain V r
102	44	68.8	120	2	S41394 Ig heavy chain V r

103	44	68.8	120	2	A54256	Ig heavy chain V r
104	44	68.8	120	2	B22769	Ig heavy chain V r
105	44	68.8	131	2	A37472	Ig heavy chain pre
106	44	68.8	136	2	UJ0077	Ig heavy chain pre
107	44	68.8	136	2	PL0208	Ig heavy chain pre
108	44	68.8	139	1	MMMS18	Ig heavy chain pre
109	44	68.8	139	2	PS0024	Ig heavy chain pre
110	44	68.8	141	2	UJ0076	Ig heavy chain pre
111	44	68.8	287	4	PC4402	pe1b leader/Ig hea
112	44	68.8	327	2	G96833	hypothetical prote
113	43	67.2	63	2	S36383	Ig heavy chain V r
114	43	67.2	87	2	PH1162	Ig heavy chain V r
115	43	67.2	88	2	PH1161	Ig heavy chain V r
116	43	67.2	98	2	PH1429	Ig heavy chain V r
117	43	67.2	98	2	PH1160	Ig heavy chain V r
118	43	67.2	101	2	S12431	Ig heavy chain V r
119	43	67.2	102	2	PH1239	Ig heavy chain V r
120	43	67.2	107	2	PH0971	Ig heavy chain V r
121	43	67.2	108	2	PH0972	Ig heavy chain V r
122	43	67.2	108	2	S26316	Ig heavy chain V r
123	43	67.2	115	2	PH1560	Ig heavy chain V r
124	43	67.2	116	2	S53751	Ig heavy chain V r
125	43	67.2	118	2	PL0200	anti-body Fab Jc1.1
126	43	67.2	119	2	F30502	anti-DNA autoantib
127	43	67.2	137	2	PH1562	Ig heavy chain V r
128	43	67.2	137	2	H32513	Ig heavy chain pre
129	43	67.2	137	2	F29380	Ig heavy chain pre
130	43	67.2	138	2	PH1564	Ig heavy chain V r
131	43	67.2	138	2	PH1565	Ig heavy chain V r
132	43	67.2	141	2	S31685	Ig heavy chain V r
133	43	67.2	144	2	PH1563	Ig heavy chain V r
134	43	67.2	147	2	PH1561	Ig heavy chain V r
135	42.5	66.4	105	2	S67941	Ig heavy chain var
136	42.5	66.4	108	2	PH0977	Ig heavy chain V r
137	42.5	66.4	120	2	A49982	Ig heavy chain V r
138	42	65.6	98	2	PH1274	Ig heavy chain V r
139	42	65.6	98	2	S26907	Ig heavy chain V r
140	42	65.6	101	2	S12428	Ig heavy chain V r
141	42	65.6	101	2	S12424	Ig heavy chain V r
142	42	65.6	102	2	PH1266	Ig heavy chain V r
143	42	65.6	102	2	PH1279	Ig heavy chain V r
144	42	65.6	102	2	PH1281	Ig heavy chain V r
145	42	65.6	102	2	PH1244	Ig heavy chain V r
146	42	65.6	102	2	PH1247	Ig heavy chain V r
147	42	65.6	102	2	PH1282	Ig heavy chain V r
148	42	65.6	102	2	PH1268	Ig heavy chain V r
149	42	65.6	102	2	PH1275	Ig heavy chain V r
150	42	65.6	102	2	PH1259	Ig heavy chain V r
151	42	65.6	102	2	PH1243	Ig heavy chain V r
152	42	65.6	102	2	PH1273	Ig heavy chain V r
153	42	65.6	102	2	PH1265	Ig heavy chain V r
154	42	65.6	102	2	PH1249	Ig heavy chain V r
155	42	65.6	102	2	PH1254	Ig heavy chain V r
156	42	65.6	102	2	PH1252	Ig heavy chain V r
157	42	65.6	102	2	PH1271	Ig heavy chain V r
158	42	65.6	102	2	PH1278	Ig heavy chain V r
159	42	65.6	104	2	B36006	Ig heavy chain V r
160	42	65.6	109	2	PH1672	Ig heavy chain V r
161	42	65.6	109	2	PH1003	Ig heavy chain V r
162	42	65.6	109	2	PL0233	Ig heavy chain V r
163	42	65.6	112	2	PH0980	Ig heavy chain V r
164	42	65.6	113	2	PH1428	Ig heavy chain V r
165	42	65.6	115	2	PH1557	Ig heavy chain V r
166	42	65.6	115	2	PL0238	Ig heavy chain V r
167	42	65.6	116	2	S09962	Ig heavy chain V-D
168	42	65.6	117	2	PL0237	Ig heavy chain V r
169	42	65.6	117	2	PL0234	Ig heavy chain V r
170	42	65.6	117	2	PL0235	Ig heavy chain V r
171	42	65.6	118	2	PL0231	Ig heavy chain V r
172	42	65.6	119	2	A24672	Ig heavy chain pre
173	42	65.6	121	2	S26798	Ig heavy chain V r
174	42	65.6	122	2	S24287	Ig heavy chain V r
175	42	65.6	123	2	S38492	Ig heavy chain - h
176	42	65.6	123	2	C36006	Ig heavy chain V r
177	42	65.6	127	2	PH1414	Ig heavy chain V r
178	42	65.6	127	2	PH1420	Ig heavy chain V r
179	42	65.6	127	2	PH1415	Ig heavy chain V r
180	42	65.6	128	2	S16685	Ig heavy chain V r
181	42	65.6	128	2	A49047	Ig heavy chain V r
182	42	65.6	136	2	PH1558	Ig heavy chain V r
183	42	65.6	139	2	PH1558	Ig heavy chain V r
184	41	64.1	140	2	S09216	Ig heavy chain pre
185	41	64.1	40	2	S33400	Ig heavy chain V r
186	41	64.1	98	2	S26912	Ig heavy chain V r
187	41	64.1	98	2	S26938	Ig heavy chain V r
188	41	64.1	102	2	PH1276	Ig heavy chain V r
189	41	64.1	102	2	PH1235	Ig heavy chain V r
190	41	64.1	109	2	PH1668	Ig heavy chain V r
191	41	64.1	110	2	PH1669	Ig heavy chain V r
192	41	64.1	111	1	MMMS76	Ig heavy chain V-I
193	41	64.1	113	1	AVMS09	Ig heavy chain V-I
194	41	64.1	113	1	AVMS57	Ig heavy chain V-I
195	41	64.1	113	1	AVMS61	Ig heavy chain V-I
196	41	64.1	113	1	AVMSAB	Ig heavy chain V-I
197	41	64.1	113	1	AVMSB7	Ig heavy chain V-I
198	41	64.1	113	1	HYMSAM	Ig heavy chain V-I
199	41	64.1	115	1	AVMS06	Ig heavy chain V-I
200	41	64.1	115	1	AVMS82	Ig heavy chain V-I
201	41	64.1	115	2	A25803	Ig heavy chain V r
202	41	64.1	117	1	G2MSU1	Ig heavy chain pre
203	41	64.1	117	2	HVHU35	Ig heavy chain pre
204	41	64.1	117	2	A28846	Ig heavy chain pre
205	41	64.1	117	2	S18551	Ig heavy chain V r
206	41	64.1	118	2	S36265	Ig heavy chain V r
207	41	64.1	126	2	PH1412	Ig heavy chain V r
208	41	64.1	129	2	S46393	Ig heavy chain V r
209	41	64.1	135	2	S49530	Ig heavy chain pre
210	41	64.1	137	2	B34903	anti-sm antibody V
211	41	64.1	140	2	S22657	Ig heavy chain pre
212	40	62.5	36	2	D31485	Ig heavy chain V r
213	40	62.5	98	2	PH1111	Ig heavy chain V r
214	40	62.5	98	2	PH1147	Ig heavy chain V r
215	40	62.5	102	2	PH1272	Ig heavy chain V r
216	40	62.5	102	2	PH1260	Ig heavy chain V r
217	40	62.5	102	2	PH1237	Ig heavy chain V r
218	40	62.5	106	2	S25036	Ig heavy chain V r
219	40	62.5	111	2	S25034	Ig heavy chain V r
220	40	62.5	112	2	PL0232	Ig heavy chain V r
221	40	62.5	116	2	S22558	Ig heavy chain V r
222	40	62.5	116	2	H29380	Ig heavy chain pre
223	40	62.5	117	2	B27563	Ig heavy chain V r
224	40	62.5	118	2	A31485	Ig heavy chain V r
225	40	62.5	123	2	S20646	Ig heavy chain V r
226	40	62.5	123	2	S20646	Ig heavy chain V r
227	40	62.5	125	2	PH0100	Ig heavy chain V r
228	40	62.5	137	2	B34903	Ig heavy chain pre
229	40	62.5	137	2	A34903	Ig heavy chain pre
230	40	62.5	137	2	D34903	Ig heavy chain pre
231	40	62.5	137	2	PH1413	Ig heavy chain pre
232	40	62.5	549	2	S04845	Ig heavy chain pre
233	40	62.5	1034	2	JCS569	serine proteinase
234	39.5	61.7	104	2	S69899	Ig heavy chain V r
235	39.5	61.7	126	2	I44151	Ig heavy chain V r
236	39.5	61.7	137	1	G2MS43	Ig heavy chain pre
237	39	60.9	90	2	PH1159	Ig heavy chain V r
238	39	60.9	90	2	PH1152	Ig heavy chain V r
239	39	60.9	96	2	S17611	Ig heavy chain V r
240	39	60.9	96	2	S17602	Ig heavy chain V r
241	39	60.9	98	2	H47624	Ig heavy chain V-I
242	39	60.9	98	2	PH1143	Ig heavy chain V r
243	39	60.9	101	2	S13692	Ig heavy chain V r
244	39	60.9	109	2	PH0973	Ig heavy chain V r
245	39	60.9	111	2	S25031	Ig heavy chain V r
246	39	60.9	112	2	S09957	Ig heavy chain V-D
247	39	60.9	112	2	S13690	Ig heavy chain V r
248	39	60.9	112	2	PH0979	Ig heavy chain V r

249	39	60.9	113	2	PH0974	Ig heavy chain V r
250	39	60.9	116	2	S13691	Ig heavy chain V r
251	39	60.9	118	1	MHWS38	Ig heavy chain V r
252	39	60.9	119	2	PL0086	Ig heavy chain V r
253	39	60.9	119	2	AH0414	conserved hypotnet
254	39	60.9	120	2	E45722	anti-glycoprotein
255	39	60.9	121	1	GVMS11	Ig heavy chain V r
256	39	60.9	122	1	PH1426	Ig heavy chain V r
257	39	60.9	137	2	S03326	Ig heavy chain pre
258	39	60.9	137	2	AD2943	proline dipeptidase
259	39	60.9	410	2	F98339	hypothetical prote
260	39	60.9	493	2	S36488	B2 protein - human
261	39	60.9	494	1	ALBYAF	alpha-amylose (EC
262	39	60.9	507	2	S33921	alpha-amylose (EC
263	39	60.9	512	2	S23355	alpha-amylose (EC
264	39	60.9	512	2	S06115	alpha-amylose (EC
265	39	60.9	528	2	S26025	NADH2 dehydrogenas
266	39	60.9	624	1	UC4510	pullulanase (EC 3.
267	38	59.4	89	2	G28833	Ig kappa chain V r
268	38	59.4	98	2	PH1129	Ig heavy chain V r
269	38	59.4	98	2	PH1122	Ig heavy chain V r
270	38	59.4	98	2	PH1112	Ig heavy chain V r
271	38	59.4	102	2	PH1264	Ig heavy chain V r
272	38	59.4	102	2	S25025	Ig heavy chain - m
273	38	59.4	114	2	PL0247	Ig heavy chain V r
274	38	59.4	114	2	A27563	Ig heavy chain V r
275	38	59.4	117	2	S19670	Ig heavy chain V r
276	38	59.4	117	2	S03289	Ig heavy chain pre
277	38	59.4	120	2	AF0522	conserved hypotnet
278	38	59.4	122	2	A27635	Ig heavy chain pre
279	38	59.4	126	2	PH1416	Ig heavy chain V r
280	38	59.4	126	2	PH1417	Ig heavy chain V r
281	38	59.4	126	2	PH1418	Ig heavy chain V r
282	38	59.4	126	2	PH1419	Ig heavy chain V r
283	38	59.4	126	2	S31930	Ig gamma chain pre
284	38	59.4	127	2	PH1421	Ig heavy chain V r
285	38	59.4	131	2	PH1425	Ig heavy chain V r
286	38	59.4	136	2	C85495	hypothetical prote
287	38	59.4	136	2	G64734	YacI protein - Bac
288	38	59.4	136	2	C90644	hypothetical prote
289	38	59.4	137	2	F34903	Ig heavy chain pre
290	38	59.4	148	2	H71007	hypothetical prote
291	38	59.4	280	2	AE2026	hypothetical prote
292	38	59.4	437	2	AH2159	hypothetical prote
293	38	59.4	483	2	S36470	B2 protein - human
294	38	59.4	502	2	S36494	B2 protein - human
295	38	59.4	600	2	S48509	transcription regu
296	38	59.4	685	2	E85112	probable methyltra
297	38	59.4	747	2	T01901	transcription regu
298	38	59.4	1070	2	S19686	alpha-glucosidase
299	38	59.4	1266	2	AG2695	conserved hypotnet
300	38	59.4	1266	2	G97477	hypothetical prote
301	38	59.4	1867	2	S22775	MOTI protein - yea
302	37	57.8	40	2	S33403	Ig heavy chain V r
303	37	57.8	96	2	S17615	Ig heavy chain V r
304	37	57.8	98	2	S46460	Ig heavy chain V r
305	37	57.8	102	2	PH1263	Ig heavy chain V r
306	37	57.8	102	2	PH1241	Ig heavy chain V r
307	37	57.8	106	2	S24521	Ig heavy chain V r
308	37	57.8	113	2	S25573	Ig heavy chain V r
309	37	57.8	113	2	S25575	Ig heavy chain V r
310	37	57.8	119	2	S09955	Ig heavy chain V-D
311	37	57.8	120	2	S26789	Ig heavy chain V r
312	37	57.8	121	2	H36005	Ig heavy chain V r
313	37	57.8	123	2	S34009	Ig heavy chain V r
314	37	57.8	145	2	A82994	hypothetical prote
315	37	57.8	150	2	S76687	hypothetical prote
316	37	57.8	518	1	A27705	alpha-amylose (EC
317	37	57.8	518	2	AD1930	ammonium transport
318	36.5	57.0	576	2	S68119	laccase (EC 1.10.3
319	36.5	57.0	576	2	S68117	laccase (EC 1.10.3
320	36	56.2	79	2	F70085	conserved hypotnet
321	36	56.2	86	2	S12580	Ig heavy chain V r
322	36	56.2	93	2	C24672	Ig heavy chain V r
323	36	56.2	96	2	S17614	Ig heavy chain V r
324	36	56.2	98	2	PL0121	Ig heavy chain V-I
325	36	56.2	98	2	S29545	Ig heavy chain V r
326	36	56.2	98	2	PH0877	Ig heavy chain V r
327	36	56.2	98	2	PL0123	Ig heavy chain V-I
328	36	56.2	98	2	S26896	Ig heavy chain V r
329	36	56.2	99	2	S26326	Ig heavy chain V r
330	36	56.2	101	2	S26460	Ig heavy chain V r
331	36	56.2	101	2	D24672	Ig heavy chain V r
332	36	56.2	102	2	PH1248	Ig heavy chain V r
333	36	56.2	102	2	PH1280	Ig heavy chain V r
334	36	56.2	102	2	PH1238	Ig heavy chain V r
335	36	56.2	102	2	PH1258	Ig heavy chain V r
336	36	56.2	102	2	PH1234	Ig heavy chain V r
337	36	56.2	102	2	PH1232	Ig heavy chain V r
338	36	56.2	102	2	PH1262	Ig heavy chain V r
339	36	56.2	105	2	S24764	Ig heavy chain V r
340	36	56.2	105	2	S24765	Ig heavy chain V r
341	36	56.2	107	2	PL0241	Ig heavy chain V r
342	36	56.2	109	2	S26325	Ig heavy chain V r
343	36	56.2	110	2	PH1655	Ig heavy chain V r
344	36	56.2	114	2	S36280	Ig heavy chain V r
345	36	56.2	115	2	S38714	Ig heavy chain V r
346	36	56.2	115	2	S19968	Ig heavy chain V r
347	36	56.2	115	2	S19965	Ig heavy chain V r
348	36	56.2	117	2	S19669	Ig heavy chain V r
349	36	56.2	117	2	S17079	Ig heavy chain V-D
350	36	56.2	117	2	S01822	Ig heavy chain V r
351	36	56.2	117	2	S78486	Ig heavy chain V r
352	36	56.2	118	2	S00700	Ig heavy chain V r
353	36	56.2	118	2	S19967	Ig heavy chain V r
354	36	56.2	119	2	PH1521	Ig heavy chain V a
355	36	56.2	119	2	A53285	Ig heavy chain V r
356	36	56.2	119	2	PH1519	Ig heavy chain V r
357	36	56.2	120	2	B42848	Ig heavy chain V-1
358	36	56.2	122	2	A33989	Ig heavy chain V r
359	36	56.2	124	2	PH1404	Ig heavy chain V r
360	36	56.2	136	2	S31587	Ig heavy chain V r
361	36	56.2	136	2	PH1559	Ig heavy chain V r
362	36	56.2	139	2	137781	Ig variable region
363	36	56.2	140	2	PH1489	Ig heavy chain V r
364	36	56.2	141	2	A39276	Ig heavy chain pre
365	36	56.2	146	4	S33905	Ig heavy chain pre
366	36	56.2	147	2	137780	Ig variable region
367	36	56.2	152	2	D84436	hypothetical prote
368	36	56.2	214	2	T29758	hypothetical prote
369	36	56.2	239	2	AC3505	mannose-1-phosphat
370	36	56.2	248	2	T14314	aquaporin T1P7 - C
371	36	56.2	248	2	T14002	malg protein homol
372	36	56.2	289	2	D72241	hypothetical prote
373	36	56.2	289	2	PH1983	hypothetical prote
374	36	56.2	324	2	AH1983	hypothetical prote
375	36	56.2	336	2	AP2085	transcription regu
376	36	56.2	336	2	E82311	conserved hypotnet
377	36	56.2	361	2	JC6551	chitinase (EC 3.2.
378	36	56.2	457	2	H81986	probable peptidase
379	36	56.2	469	2	C81042	hypothetical prote
380	36	56.2	469	2	C81042	hypothetical prote
381	36	56.2	500	2	A71306	probable exported
382	36	56.2	578	2	AEO428	hypothetical prote
383	36	56.2	623	2	C86184	threonine-tRNA lig
384	36	56.2	643	2	H64119	metabotropic gluta
385	36	56.2	908	2	T49142	probable glutamate
386	36	56.2	1039	2	T45779	chitinase (EC 3.2.
387	36	56.2	1635	2	T14075	Ig heavy chain V r
388	35.5	55.5	122	2	A37267	Ig heavy chain V r
389	35.5	55.5	128	2	S33217	hypothetical prote
390	35.5	55.5	216	2	T29554	hypothetical prote
391	35.5	55.5	382	2	AC2207	L-cysteine/cysteine
392	35.5	55.5	401	2	AC2207	protein containing
393	35.5	55.5	511	2	A97212	Ig heavy chain V r
394	35	54.7	36	2	S33401	Ig heavy chain V r

395	35	54.7	86	2	T18324	icmt protein - leg
396	35	54.7	91	2	PL0242	Ig heavy chain v r
397	35	54.7	95	2	G37262	Ig heavy chain v r
398	35	54.7	96	2	PH1165	Ig heavy chain v r
399	35	54.7	98	2	S26920	Ig heavy chain v r
400	35	54.7	98	2	A49051	Ig heavy chain v r
401	35	54.7	98	2	PH1128	Ig heavy chain v r
402	35	54.7	105	2	S38488	Ig heavy chain - h
403	35	54.7	107	2	PL0240	Ig heavy chain v r
404	35	54.7	107	2	PH0999	Ig heavy chain v r
405	35	54.7	107	2	PL0243	Ig heavy chain v r
406	35	54.7	109	2	PH0997	Ig heavy chain v r
407	35	54.7	110	2	PL0244	Ig heavy chain v r
408	35	54.7	111	2	S25030	Ig heavy chain v r
409	35	54.7	111	2	PH0998	Ig heavy chain v r
410	35	54.7	111	2	S13693	Ig heavy chain v r
411	35	54.7	112	2	PL0245	Ig heavy chain v r
412	35	54.7	113	2	B36259	Ig heavy chain v r
413	35	54.7	114	2	PH1027	Ig heavy chain v r
414	35	54.7	115	2	S09382	Ig heavy chain - c
415	35	54.7	115	2	S13694	Ig heavy chain v r
416	35	54.7	116	2	S31667	Ig heavy chain v r
417	35	54.7	117	2	S31680	Ig heavy chain v r
418	35	54.7	117	2	S18554	Ig heavy chain v r
419	35	54.7	117	2	S03305	Ig heavy chain v r
420	35	54.7	119	2	D30562	Ig heavy chain v r
421	35	54.7	119	2	E30562	Ig heavy chain v r
422	35	54.7	119	2	C30562	Ig heavy chain v r
423	35	54.7	120	2	PD0008	Ig heavy chain v r
424	35	54.7	121	2	E30502	Ig heavy chain v r
425	35	54.7	122	2	S20642	Ig heavy chain v r
426	35	54.7	124	2	PT0388	Ig heavy chain v r
427	35	54.7	124	2	S06824	Ig heavy chain v r
428	35	54.7	131	2	S26792	Ig heavy chain v r
429	35	54.7	131	2	PH1427	Ig heavy chain v r
430	35	54.7	136	2	S35759	BHD9D10 protein -
431	35	54.7	138	1	HVMST7	Ig heavy chain pre
432	35	54.7	142	2	A32483	Ig heavy chain v r
433	35	54.7	142	2	S19245	Ig heavy chain pre
434	35	54.7	145	2	T06616	hypothetical prote
435	35	54.7	175	2	UN0680	gamma1-crystallin
436	35	54.7	248	2	T14001	aquaporin T1P18 -
437	35	54.7	312	2	C84608	hypothetical prote
438	35	54.7	370	2	A72403	glucose-1-phosphat
439	35	54.7	376	2	T40591	hypothetical prote
440	35	54.7	383	2	S53379	probable membrane
441	35	54.7	409	2	F70633	probable lpqk prot
442	35	54.7	447	2	S54631	HSr3 protein - yea
443	35	54.7	450	2	C70081	metabolite-sodium
444	35	54.7	469	2	S37483	Ig gamma-2a chain
445	35	54.7	495	2	A85441	cytochrome P450-1i
446	35	54.7	506	2	AB2064	hypothetical prote
447	35	54.7	527	2	T16909	hypothetical prote
448	35	54.7	530	2	B23351	serendipity (8ty)
449	35	54.7	531	2	T19232	hypothetical prote
450	35	54.7	568	2	A34891	Ig heavy chain pre
451	35	54.7	603	2	T11284	MAH2 dehydrogenas
452	35	54.7	604	2	F87936	protein M01G12.12
453	35	54.7	604	2	T23669	hypothetical prote
454	35	54.7	639	1	MMVQ70	70K protein - pota
455	35	54.7	639	1	S03547	hypothetical prote
456	35	54.7	779	2	T47756	phosphatidylinosit
457	35	54.7	779	2	T30201	Norch homolog prot
458	35	54.7	119	2	PH1290	Ig heavy chain pre
459	35	54.7	119	2	PH1292	Ig heavy chain pre
460	35	54.7	133	2	PH1286	Ig heavy chain pre
461	35	54.7	133	2	PH1287	Ig heavy chain pre
462	35	54.7	144	2	PH1285	Ig heavy chain pre
463	35	54.7	144	2	PH1284	Ig heavy chain pre
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594	35					

541	33.5	52.3	93	2	S42182	Ig gamma chain V r	614	33	51.6	136	2	S13791	Ig heavy chain V r
542	33.5	52.3	94	2	S42177	Ig gamma chain V r	615	33	51.6	137	2	A03865	hypothetical prote
543	33.5	52.3	94	2	PH0996	Ig heavy chain V r	616	33	51.6	138	2	PH0105	anti-digoxin trans
544	33.5	52.3	95	2	S42178	Ig gamma chain V r	617	33	51.6	138	2	I51265	XCRABP - African c
545	33.5	52.3	96	2	S17621	Ig heavy chain V r	618	33	51.6	139	2	A25912	Ig heavy chain pre
546	33.5	52.3	96	2	S17230	Ig heavy chain V r	619	33	51.6	140	2	T01407	Ig heavy chain (my
547	33.5	52.3	96	2	S17612	Ig heavy chain V r	620	33	51.6	140	2	T15738	hypothetical prote
548	33.5	52.3	96	2	S17606	Ig heavy chain V r	621	33	51.6	155	2	T29947	hypothetical prote
549	33.5	52.3	96	2	S17617	Ig heavy chain V r	622	33	51.6	157	2	B95263	Tm2011-2b transpo
550	33.5	52.3	96	2	S17620	Ig heavy chain V r	623	33	51.6	157	2	D95422	Tm2011-2b transpo
551	33.5	52.3	96	2	S17618	Ig heavy chain V r	624	33	51.6	157	2	P95401	Tm2011-2b transpo
552	33.5	52.3	96	2	S17609	Ig heavy chain V r	625	33	51.6	157	2	H95385	lincomycin resist
553	33.5	52.3	97	2	S42181	Ig gamma chain V r	626	33	51.6	161	2	A25633	hypothetical prote
554	33.5	52.3	97	2	S17603	Ig heavy chain V r	627	33	51.6	162	2	P96025	hypothetical prote
555	33.5	52.3	98	2	S26913	Ig heavy chain V r	628	33	51.6	164	2	T32627	hypothetical prote
556	33.5	52.3	98	2	S26913	Ig heavy chain V r	629	33	51.6	172	2	F69506	probable 2-oxoisov
557	33.5	52.3	98	2	S26311	Ig heavy chain V r	630	33	51.6	175	2	H86913	probable membrane
558	33.5	52.3	101	2	S42184	Ig gamma chain V r	631	33	51.6	190	2	G89581	protein C18A11.4 [
559	33.5	52.3	101	2	S42184	Ig gamma chain V r	632	33	51.6	201	2	F95878	probable ISKm2011-
560	33.5	52.3	101	2	S42179	Ig gamma chain V r	633	33	51.6	204	2	S27448	Sc7 protein - brac
561	33.5	52.3	101	2	S26310	Ig heavy chain V r	634	33	51.6	205	2	B87296	ribonuclease HII [
562	33.5	52.3	102	2	S26471	Ig heavy chain V r	635	33	51.6	217	2	G64680	transcription regu
563	33.5	52.3	102	2	S26471	Ig heavy chain V r	636	33	51.6	232	2	T09898	hypothetical prote
564	33.5	52.3	104	2	PH1665	Ig heavy chain V r	637	33	51.6	236	2	B86635	hypothetical prote
565	33.5	52.3	104	2	PH0991	Ig heavy chain V r	638	33	51.6	248	2	T12632	water channel prot
566	33.5	52.3	104	2	S24763	Ig heavy chain V r	639	33	51.6	251	2	AE1051	probable water cha
567	33.5	52.3	105	2	F32513	Ig heavy chain V r	640	33	51.6	251	2	G91274	probable transcript
568	33.5	52.3	106	2	PH0989	Ig heavy chain V r	641	33	51.6	251	2	G81274	probable DEOR-type
569	33.5	52.3	109	2	PH1094	Ig heavy chain V r	642	33	51.6	251	2	G86115	probable DEOR-type
570	33.5	52.3	109	2	PH1096	Ig heavy chain V r	643	33	51.6	253	2	AE0809	conserved hypotet
571	33.5	52.3	110	2	PH0995	Ig heavy chain V r	644	33	51.6	257	2	G82119	probable esterase/
572	33.5	52.3	110	2	PH0993	Ig heavy chain V r	645	33	51.6	257	2	T23332	hypothetical prote
573	33.5	52.3	111	2	PH0994	Ig heavy chain V r	646	33	51.6	265	2	S65054	movement protein -
574	33.5	52.3	111	2	PH0992	Ig heavy chain V r	647	33	51.6	265	2	JC6515	beta 2 toxin - Clo
575	33.5	52.3	111	2	PH1667	Ig heavy chain V r	648	33	51.6	276	2	AD1987	hypothetical prote
576	33.5	52.3	114	2	S18552	Ig heavy chain V r	649	33	51.6	291	2	S67672	hypothetical prote
577	33.5	52.3	117	2	S18553	Ig heavy chain V r	650	33	51.6	294	2	T36711	probable dioxygena
578	33.5	52.3	117	2	S18553	Ig heavy chain V r	651	33	51.6	301	2	T07401	conserved hypotet
579	33.5	52.3	117	2	S09960	Ig heavy chain V-D	652	33	51.6	329	2	C70071	peroxidase (EC 1.1
580	33.5	52.3	117	2	S09960	Ig heavy chain V-D	653	33	51.6	329	2	T07401	hypothetical prote
581	33.5	52.3	118	2	PH1666	Ig heavy chain V r	654	33	51.6	331	2	B86638	zinc-binding dehyd
582	33.5	52.3	118	2	S38717	Ig heavy chain V r	655	33	51.6	331	2	AE2922	hypothetical zinc-
583	33.5	52.3	119	2	S03077	Ig heavy chain V r	656	33	51.6	336	2	F97696	queuine tRNA-ribos
584	33.5	52.3	119	2	S45714	Ig heavy chain V r	657	33	51.6	339	2	AC2041	hypothetical prote
585	33.5	52.3	119	2	S20640	Ig heavy chain V r	658	33	51.6	345	1	JH0185	D-amino-acid oxida
586	33.5	52.3	125	2	S20639	Ig heavy chain V r	659	33	51.6	347	1	OXRGDA	D-amino-acid oxida
587	33.5	52.3	131	2	S66537	Ig heavy chain V r	660	33	51.6	347	1	S01340	D-amino-acid oxida
588	33.5	52.3	138	2	S21810	Ig heavy chain V r	661	33	51.6	347	1	JX0132	D-amino-acid oxida
589	33.5	52.3	144	2	B30502	Ig heavy chain V r	662	33	51.6	380	2	H95129	glucose-1-phosphat
590	33.5	52.3	171	2	S23523	Ig heavy chain V r	663	33	51.6	380	2	P98000	glucose-1-phosphat
591	33.5	52.3	196	2	AH2046	hypothetical prote	664	33	51.6	385	2	T20404	hypothetical prote
592	33.5	52.3	401	2	S77167	L-cysteine desulfh	665	33	51.6	403	2	B95347	conserved hypotet
593	33	51.6	83	2	JQ0329	colicin E5 immunit	666	33	51.6	413	1	W2WLEP	asparagine synthas
594	33	51.6	83	2	B32535	colicin E5 immunit	667	33	51.6	415	1	B81740	E2 protein - Europ
595	33	51.6	84	2	DB3423	hypothetical prote	668	33	51.6	424	2	AC3095	3,4-dihydroxy-2-pu
596	33	51.6	94	2	I67528	CD33 antigen homol	669	33	51.6	424	2	G98191	conserved hypotet
597	33	51.6	95	2	I67527	CD33 antigen homol	670	33	51.6	424	2	T15966	hypothetical prote
598	33	51.6	98	2	H34964	Ig heavy chain V-I	671	33	51.6	428	2	D90176	hypothetical prote
599	33	51.6	98	2	S26932	Ig heavy chain V r	672	33	51.6	438	2	B90601	hypothetical prote
600	33	51.6	102	2	S42176	Ig gamma chain V r	673	33	51.6	467	2	A49901	NBU1 and NBU2 mobi
601	33	51.6	102	2	S25572	Ig heavy chain V r	674	33	51.6	467	2	I40236	mobilitization prote
602	33	51.6	112	2	S25572	Ig heavy chain V r	675	33	51.6	467	2	I40601	hypothetical prote
603	33	51.6	116	1	HVM544	Ig heavy chain pre	676	33	51.6	496	2	T23565	hypothetical prote
604	33	51.6	117	1	G2M573	Ig heavy chain V r	677	33	51.6	508	2	B64089	probable membrane
605	33	51.6	117	1	MEMS4E	Ig heavy chain V r	678	33	51.6	526	2	AE0601	probable enzyme (i
606	33	51.6	117	1	MEMS4E	Ig heavy chain V r	679	33	51.6	527	2	B90740	probable enzyme (i
607	33	51.6	118	2	A47329	Ig heavy chain V r	680	33	51.6	527	2	G85590	probable membrane
608	33	51.6	119	1	AVMSJ5	Ig heavy chain V r	681	33	51.6	533	2	G64818	high-affinity pote
609	33	51.6	119	1	AVMSJ5	Ig heavy chain V r	682	33	51.6	533	2	T33772	hypothetical prote
610	33	51.6	119	1	AVMSJ5	Ig heavy chain V r	683	33	51.6	537	1	Q08E30	hypothetical prote
611	33	51.6	120	2	E49590	Ig heavy chain V r	684	33	51.6	557	2	S56292	BRP2 protein - hu
612	33	51.6	122	2	T28977	hypothetical prote	685	33	51.6	557	2	S56292	hypothetical prote
613	33	51.6	123	2	S31509	Ig heavy chain - h	686	33	51.6	562	2	S75651	hypothetical prote

687	33	51.6	585	2	A12786	arginyl-tRNA synth	750	32	50.0	117	1	HNCOE1	Ig heavy chain pre
688	33	51.6	585	2	C97566	arginyl-tRNA synth	761	32	50.0	117	2	S31109	Ig heavy chain - h
689	33	51.6	591	2	G90181	hypothetical prote	762	32	50.0	117	2	A28966	Ig heavy chain pre
690	33	51.6	597	2	A35928	hypothetical 86k p	763	32	50.0	118	2	S38565	Ig heavy chain v r
691	33	51.6	642	1	SYECTT	theonine-tRNA lig	764	32	50.0	118	2	A24754	Ig heavy chain v r
692	33	51.6	642	2	AC0706	theonine-tRNA lig	765	32	50.0	119	2	S36257	Ig heavy chain pre
693	33	51.6	642	2	B50932	theonine-tRNA syn	766	32	50.0	119	2	S00981	Ig heavy chain pre
694	33	51.6	642	2	F85780	theonine-tRNA syn	767	32	50.0	119	2	S31591	Ig heavy chain v r
695	33	51.6	705	2	T00975	hypothetical prote	768	32	50.0	119	2	PH1510	Ig heavy chain v r
696	33	51.6	707	2	D86565	oligopeptide bindi	769	32	50.0	119	2	PH1505	Ig heavy chain v r
697	33	51.6	707	2	E72059	peptide ABC transp	770	32	50.0	119	2	PH1518	Ig heavy chain v r
698	33	51.6	733	2	E73767	stringent response	771	32	50.0	119	2	PH1517	Ig heavy chain v r
699	33	51.6	737	2	T30795	hypothetical prote	772	32	50.0	119	2	PH1502	Ig heavy chain v r
700	33	51.6	737	2	T28481	hypothetical prote	773	32	50.0	119	2	PH1503	Ig heavy chain v r
701	33	51.6	737	2	A72156	C2L protein - vari	774	32	50.0	119	2	PH1503	Ig heavy chain v r
702	33	51.6	737	2	F42508	E2L protein - vari	775	32	50.0	119	2	PH1504	Ig heavy chain v r
703	33	51.6	737	2	B36841	E2L protein - vari	776	32	50.0	119	2	PH1520	Ig heavy chain v r
704	33	51.6	909	2	AG3419	phage host specif	777	32	50.0	121	2	S31106	Ig heavy chain - h
705	33	51.6	938	1	STECIT	isoleucine-tRNA li	778	32	50.0	121	2	A21854	Ig heavy chain v r
706	33	51.6	938	2	B56483	isoleucine-tRNA sy	779	32	50.0	121	2	A26405	Ig heavy chain v r
707	33	51.6	938	2	E90632	isoleucine-tRNA sy	780	32	50.0	122	2	S20643	Ig heavy chain v r
708	33	51.6	944	2	A10507	isoleucyl-tRNA syn	781	32	50.0	123	2	A36006	Ig heavy chain v r
709	33	51.6	979	2	D96574	hypothetical prote	782	32	50.0	123	2	G48677	Ig heavy chain V-D
710	33	51.6	1002	2	T43236	cardoxypeptidase C	783	32	50.0	123	2	F48677	Ig heavy chain V-D
711	33	51.6	1179	2	A53213	integrin alpha-E c	784	32	50.0	123	2	E48677	Ig heavy chain V-D
712	33	51.6	1487	2	S48719	phospholipase-A(2)	785	32	50.0	125	2	PH1410	Ig heavy chain v r
713	33	51.6	1718	1	JO1734	genome polyprotein	786	32	50.0	133	2	PC1155	Ig heavy chain pre
714	33	51.6	1782	2	S45289	vitellogenin precu	787	32	50.0	134	2	S21916	Ig heavy chain v r
715	33	51.6	1849	2	T14096	guanine nucleotide	788	32	50.0	135	2	PH1494	Ig heavy chain v r
716	33	51.6	1872	2	T24683	hypothetical prote	789	32	50.0	135	2	PH1492	Ig heavy chain v r
717	33	51.6	2034	2	T22147	hypothetical prote	790	32	50.0	137	2	S78054	Ig heavy chain pre
718	33	51.6	2508	2	S61441	surface-associated	791	32	50.0	138	2	C28035	Ig heavy chain V-I
719	32.5	50.8	93	2	A37263	Ig heavy chain v r	792	32	50.0	138	2	A28035	Ig heavy chain V-I
720	32.5	50.8	96	2	S17619	Ig heavy chain v r	793	32	50.0	138	2	D28035	Ig heavy chain V-I
721	32.5	50.8	101	2	T37262	Ig heavy chain v r	794	32	50.0	138	2	B28035	Ig heavy chain V-I
722	32.5	50.8	105	2	S24766	Ig heavy chain v r	795	32	50.0	138	2	A30561	Ig heavy chain pre
723	32.5	50.8	109	2	PH1001	Ig heavy chain v r	796	32	50.0	139	2	S31678	Ig heavy chain v r
724	32.5	50.8	112	2	S26473	Ig heavy chain v r	797	32	50.0	140	1	HVMSG7	Ig heavy chain pre
725	32.5	50.8	117	1	S26473	Ig heavy chain v r	798	32	50.0	140	2	A36194	Ig heavy chain v r
726	32.5	50.8	120	2	P28195	Ig heavy chain v r	799	32	50.0	140	2	PH1483	Ig heavy chain v r
727	32.5	50.8	120	2	G28195	Ig heavy chain v r	800	32	50.0	140	2	PH1482	Ig heavy chain v r
728	32.5	50.8	120	2	S19963	Ig heavy chain v r	801	32	50.0	140	2	S33805	Ig heavy chain pre
729	32.5	50.8	121	2	S33131	Ig heavy chain v r	802	32	50.0	144	1	S52140	protein-tyrosine-p-
730	32.5	50.8	130	2	JC7918	lyozyme (EC 3.2.1	803	32	50.0	144	2	E41287	Ig heavy chain pre
731	32.5	50.8	136	1	HVMSB1	Ig heavy chain pre	804	32	50.0	147	2	S42421	hypothetical prote
732	32.5	50.8	138	2	S45249	Ig heavy chain pre	805	32	50.0	148	2	C82674	conserved hypothet
733	32.5	50.8	139	2	PH1225	Ig heavy chain pre	806	32	50.0	159	2	F59428	hypothetical prote
734	32.5	50.8	151	2	A27609	Ig heavy chain pre	807	32	50.0	165	2	A12924	conserved hypothet
735	32.5	50.8	151	2	PL0011	Ig heavy chain pre	808	32	50.0	168	2	B65849	conserved hypothet
736	32.5	50.8	246	2	S38950	Ig gamma chain - m	809	32	50.0	173	2	S69468	hypothetical prote
737	32.5	50.8	446	2	S40295	Ig gamma-2a chain	810	32	50.0	181	2	H97698	probable involveme
738	32.5	50.8	544	2	JC6063	chaperonin groEL -	811	32	50.0	189	2	S71465	fibronectin - chid
739	32.5	50.8	544	2	UC5130	heat shock protein	812	32	50.0	190	1	A44593	endo-1,4-beta-xyla
740	32.5	50.8	544	2	B83720	class I heat-shock	813	32	50.0	204	2	T04423	probable alpha-gal
741	32.5	50.8	692	2	B64381	hypothetical prote	814	32	50.0	211	1	AB2212	dihydrofolate redu
742	32.5	50.8	755	2	B41836	amine oxidase (fla	815	32	50.0	212	2	AE2882	carbonate dehydrat
743	32.5	50.8	1038	2	JC6027	11k outer membran	816	32	50.0	213	2	D97658	carbonate dehydrat
744	32	50.0	76	2	B28572	Ig heavy chain v r	817	32	50.0	213	2	S54138	probable coat prot
745	32	50.0	82	2	B55846	hypothetical prote	818	32	50.0	217	2	AE5313	antrogen-regulatee
746	32	50.0	96	2	A75291	transcription regu	819	32	50.0	231	2	A54313	hypothetical prote
747	32	50.0	98	2	B24752	Ig heavy chain v r	820	32	50.0	239	2	T34305	probable outer mem
748	32	50.0	98	2	A28572	Ig heavy chain v r	821	32	50.0	248	2	AC0712	conserved hypothet
749	32	50.0	100	2	S26925	Ig heavy chain v r	822	32	50.0	255	2	AC0321	hypothetical prote
750	32	50.0	100	2	S26926	Ig heavy chain v r	823	32	50.0	257	2	G90061	hypothetical prote
751	32	50.0	102	2	PH1491	Ig heavy chain v r	824	32	50.0	257	2	H84713	hypothetical prote
752	32	50.0	102	2	PH1491	Ig heavy chain v r	825	32	50.0	262	2	UN0557	lens fiber membran
753	32	50.0	107	2	B60754	glycan 1,4-alpha-g	826	32	50.0	263	1	MMBOLM	lens fiber membran
754	32	50.0	110	2	A32189	Ig heavy chain v r	827	32	50.0	264	2	A55279	major intrinsic pr
755	32	50.0	112	2	A37203	lens fiber membran	828	32	50.0	264	2	AC2095	hypothetical prote
756	32	50.0	114	2	PH0181	Ig heavy chain v r	829	32	50.0	265	2	B84108	hypothetical prote
757	32	50.0	114	2	PH1523	Ig heavy chain v r	830	32	50.0	266	2	B87394	protein Y71A2C.2
758	32	50.0	114	2	PH1522	Ig heavy chain v r	831	32	50.0	266	2	T27362	hypothetical prote
759	32	50.0	116	2	S55542	Ig heavy chain v r	832	32	50.0	267	2	S48700	probable transport

833	32	50.0	273	2	A28512	fibronectin - chic	906	32	50.0	572	2	G84238	hypothetical prote
834	32	50.0	290	2	A80947	ribonuclease BN (B	907	32	50.0	574	2	C83359	probable oxidoredu
835	32	50.0	290	2	A98230	tRNA processing ex	908	32	50.0	585	2	T36060	probable oxidoredu
836	32	50.0	290	2	H86076	tRNA processing ex	909	32	50.0	589	2	T38738	major facilitator
837	32	50.0	290	2	S40830	Ribonuclease BN (B	910	32	50.0	623	2	D83838	asparagine synthet
838	32	50.0	294	2	T01307	alternative splic1	911	32	50.0	625	2	A13488	outer membrane pro
839	32	50.0	302	2	A72510	hypothetical prote	912	32	50.0	635	2	A81656	theonyl-tRNA synt
840	32	50.0	303	2	S71185	splicing factor SF	913	32	50.0	638	2	T20944	hypothetical prote
841	32	50.0	303	2	F86158	alternative splic1	914	32	50.0	652	2	T20046	hypothetical prote
842	32	50.0	305	2	T45062	hypothetical prote	915	32	50.0	658	1	F0LJ3A	gag polypeptide -
843	32	50.0	320	2	B84358	probable phosphate	916	32	50.0	660	2	G71497	threonine-tRNA lig
844	32	50.0	320	2	JC1311	cell protein precu	917	32	50.0	663	2	S67259	MEI protein - yea
845	32	50.0	332	2	C72310	conserved hypotet	918	32	50.0	689	2	S66006	conserved hypotet
846	32	50.0	335	2	A82354	ATP-binding protei	919	32	50.0	699	2	D70533	hypothetical prote
847	32	50.0	341	2	A83002	conserved hypotet	920	32	50.0	708	2	B72619	NADH2 dehydrogen
848	32	50.0	341	2	F98281	hypothetical prote	921	32	50.0	714	2	A81353	penicillin-binding
849	32	50.0	342	1	S64322	probable membrane	922	32	50.0	724	2	T71719	hypothetical prote
850	32	50.0	344	2	T32342	ABC transporter (A	923	32	50.0	741	2	B49555	enhancer of splic
851	32	50.0	345	2	F84136	chitinase (EC 3.2.	924	32	50.0	749	2	I39708	cryptophan 2-mono
852	32	50.0	347	2	JC7178	probable arginase	925	32	50.0	770	2	B56695	transducin-like en
853	32	50.0	351	2	T13422	ABC-type transport	926	32	50.0	771	2	D56695	transducin-like en
854	32	50.0	354	2	S74323	two-component sens	927	32	50.0	797	2	S28103	scalloid attachmen
855	32	50.0	356	2	E70032	transcription fact	928	32	50.0	849	1	S64732	aminopeptidase N V
856	32	50.0	362	2	T08813	conserved hypotet	929	32	50.0	868	2	G82193	transcription fact
857	32	50.0	366	2	D69951	41k fiber protein	930	32	50.0	869	2	A55384	probable membrane
858	32	50.0	387	1	ERADY4	phosphopentomutase	931	32	50.0	898	2	A10283	hypothetical prote
859	32	50.0	387	1	ERADY4	phosphopentomutase	932	32	50.0	899	2	S17546	hypothetical prote
860	32	50.0	390	2	E72411	lysine-tRNA ligase	933	32	50.0	934	2	S75633	hypothetical prote
861	32	50.0	396	2	B71414	lysine-tRNA ligase	934	32	50.0	942	2	C96574	transposase - Bsch
862	32	50.0	401	2	T41049	probable MFS trans	935	32	50.0	988	1	T0EC21	probable virulence
863	32	50.0	404	2	A83612	hypothetical prote	936	32	50.0	993	2	A10669	hacr protein - Kle
864	32	50.0	405	2	A83038	conserved hypotet	937	32	50.0	1013	2	T30818	ATP-binding protei
865	32	50.0	407	2	G81010	probable exported	938	32	50.0	1071	2	S38164	complement C3d/Eps
866	32	50.0	414	2	AD1027	hypothetical prote	939	32	50.0	1091	1	P40009	alpha-amylase (EC
867	32	50.0	418	2	AH0184	probable trehalase	940	32	50.0	1104	2	A60999	hypothetical prote
868	32	50.0	418	2	E90841	peptidase, M20/M25	941	32	50.0	1123	2	T19713	hypothetical prote
869	32	50.0	430	2	A87634	male permease -	942	32	50.0	1136	2	T26953	probable membrane
870	32	50.0	431	2	T41614	amino transferase B	943	32	50.0	1178	2	S54073	hypothetical prote
871	32	50.0	437	2	G83779	probable permease	944	32	50.0	1209	2	AH2052	hypothetical prote
872	32	50.0	437	2	G82032	probable aminotran	945	32	50.0	1216	2	H84629	phosphorylase kinase
873	32	50.0	438	2	H70844	hypothetical prote	946	32	50.0	1223	2	I38111	furin (EC 3.4.21.7
874	32	50.0	441	2	S76440	ammonium transport	947	32	50.0	1269	2	S35366	hypothetical prote
875	32	50.0	442	2	S74801	beta-alanine-pyruv	948	32	50.0	1581	2	T32963	fibronectin - bovi
876	32	50.0	444	2	A83556	probable pyridoxal	949	32	50.0	2265	1	FNNH	fibronectin precu
877	32	50.0	444	2	C82981	hypothetical prote	950	32	50.0	2386	1	S14428	fibronectin - Afri
878	32	50.0	444	2	AH2965	probable pyridoxal	951	32	50.0	2477	2	S14428	protein unc-22 [lm
879	32	50.0	446	2	D98317	aminopeptidase P X	952	32	50.0	2481	2	A43908	twitichin [similari
880	32	50.0	452	2	F82609	beta-alanine-pyruv	953	32	50.0	6831	2	A88852	hypothetical prote
881	32	50.0	452	2	AH3525	amino transferase -	954	32	50.0	6839	2	S57242	hypothetical prote
882	32	50.0	457	2	T35443	replicative DNA he	955	32	50.0	7160	2	T27935	Ig heavy chain V r
883	32	50.0	459	2	F84993	hypothetical prote	956	32	50.0	96	2	S17607	Ig heavy chain V r
884	32	50.0	467	2	AE3142	hypothetical prote	957	31.5	49.2	96	2	S17610	Ig heavy chain V r
885	32	50.0	469	2	B82500	hypothetical prote	958	31.5	49.2	100	2	P40122	Ig heavy chain V-I
886	32	50.0	473	2	T38350	threonine-tRNA lig	959	31.5	49.2	113	2	S55530	frataxin-like prot
887	32	50.0	476	2	AF0191	probable sugar tra	960	31.5	49.2	106	2	AC0468	probable ribosoma
888	32	50.0	485	2	D85699	trehalase, peripla	961	31.5	49.2	109	2	T38657	Ig heavy chain V r
889	32	50.0	486	2	T45763	hypothetical prote	962	31.5	49.2	111	2	PH0990	hypothetical prote
890	32	50.0	489	2	T41241	glucosyltransferas	963	31.5	49.2	112	2	B84345	Ig heavy chain V r
891	32	50.0	501	2	T11587	oxyesterol-binding	964	31.5	49.2	113	2	S55533	Ig heavy chain V r
892	32	50.0	510	2	B75399	probable ornithine	965	31.5	49.2	113	2	S55530	Ig heavy chain V r
893	32	50.0	516	2	S52839	dhlc protein - Xan	966	31.5	49.2	113	2	S55530	Ig heavy chain V r
894	32	50.0	520	2	G96815	probable aminotran	967	31.5	49.2	113	2	S55528	Ig heavy chain V r
895	32	50.0	524	1	S76810	probable NMDH2 deh	968	31.5	49.2	113	2	E33935	Ig heavy chain V r
896	32	50.0	530	2	T01030	hypothetical prote	969	31.5	49.2	113	2	S55531	Ig heavy chain V r
897	32	50.0	537	2	T05816	hypothetical prote	970	31.5	49.2	113	2	S55532	Ig heavy chain V r
898	32	50.0	540	2	B45665	adult-specific 61.	971	31.5	49.2	113	2	S55531	Ig heavy chain V r
899	32	50.0	550	2	T10393	chitinase (EC 3.2.	972	31.5	49.2	115	2	A54378	Ig heavy chain pre
900	32	50.0	551	2	G72865	chitinase - Autogr	973	31.5	49.2	119	2	PH1293	Ig heavy chain V r
901	32	50.0	552	2	T41863	chitinase chi-A or	974	31.5	49.2	121	2	H37266	Ig heavy chain V r
902	32	50.0	558	2	T48078	hypothetical prote	975	31.5	49.2	121	2	F37266	Ig heavy chain V r
903	32	50.0	565	2	S04782	alpha,alpha-trehal	976	31.5	49.2	126	2	S84107	Ig heavy chain V r
904	32	50.0	571	1	JN0858	chitinase (EC 3.2.	977	31.5	49.2	127	2	S58213	Ig heavy chain V r
905	32	50.0	571	2	T42071	probable chitinase	978	31.5	49.2	128	2	C37267	Ig heavy chain V r

```

979      31.5      49.2      128      2      137267      Ig heavy chain V r
980      31.5      49.2      132      2      PH1289      Ig heavy chain pre
981      31.5      49.2      133      2      PH1288      Ig heavy chain pre
982      31.5      49.2      141      2      S30832      hypothetical prote
983      31.5      49.2      206      2      T12743      hypothetical prote
984      31.5      49.2      230      2      S76965      hypothetical prote
985      31.5      49.2      375      2      A12041      hypothetical prote
986      31.5      49.2      505      2      AC1469      internalin like pr
987      31.5      49.2      541      2      D82302      iron(III) ABC tran
988      31.5      49.2      547      2      T39659      cell wall biogynth
989      31.5      49.2      548      2      AH1107      internalin H (limpo
990      31.5      49.2      596      2      AE1515      internalin like pr
991      31.5      49.2      653      2      T03319      gene 112 protei
992      31.5      49.2      655      2      E64752      probable dihydroxy
993      31.5      49.2      757      2      E64889      amine oxidase (cop
994      31.5      49.2      1076      2      P66831      hypothetical prote
995      31      48.4      90      2      PH1485      Ig heavy chain V r
996      31      48.4      96      2      S17608      Ig heavy chain V r
997      31      48.4      96      2      H28195      Ig heavy chain V r
998      31      48.4      98      2      S26910      Ig heavy chain V r
999      31      48.4      98      2      F47624      Ig heavy chain V-I
1000     31      48.4      99      2      A48223      Ig heavy chain V r

```

ALIGNMENTS

RESULT 1

```

S33404      Ig heavy chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998
C/Accession: S33404
R/Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Eur. J. Immunol. 23, 206-211, 1993
A/Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes usi
A/Reference number: S33391; MUID:93122092; PMID:8419173
A/Accession: S33404
A/Molecule type: mRNA
A/Residues: 1-40 <KET>
A/Cross-references: UNIPARC:UPI0000176E99; EMBL:X73024
A/Experimental source: strain BALB/c
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match      78.1%; Score 50; DB 2; Length 40;
Best Local Similarity 80.0%; Pred. No. 0.078; 0; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy      1      GYSFTGHMNN 10
Db      26      GYSFTGHMNN 35

RESULT 2
PH1145      Ig heavy chain V region (clone V2030.2A) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C/Accession: PH1145
R/Schlttek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A/Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A/Reference number: PH1105; MUID:92364545; PMID:1500855
A/Accession: PH1145
A/Molecule type: DNA
A/Residues: 1-98 <SCH>
A/Cross-references: UNIPROT:Q924R6; UNIPARC:UPI0000176BBB
A/Experimental source: B cell
C/Superfamily: immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```

```

Query Match      78.1%; Score 50; DB 2; Length 98;
Best Local Similarity 70.0%; Pred. No. 0.19; 1; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy      1      GYSFTGHMNN 10
Db      26      GYFTSYMNN 35

```

RESULT 3

```

H37262      Ig heavy chain V region (2F8) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C/Accession: H37262
R/Goshorn, S.C.; Retzel, E.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A/Title: Common structural features among monoclonal antibodies binding the same antigen
A/Reference number: A38601; MUID:91115823; PMID:1703527
A/Accession: H37262
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-101 <GOS>
A/Cross-references: UNIPARC:UPI0000115184; GB:M57994; NID:G195273; PID:AAA63332.1; PID:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

```

```

Query Match      76.6%; Score 49; DB 2; Length 101;
Best Local Similarity 70.0%; Pred. No. 0.29; 1; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy      1      GYSFTGHMNN 10
Db      18      GYFTSYMNN 27

```

RESULT 4

```

PH0986      Ig heavy chain V region (clone 178-c6) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH0986
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH0986
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-103 <TIL>
A/Cross-references: UNIPARC:UPI0000176D06
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

```

```

Query Match      76.6%; Score 49; DB 2; Length 103;
Best Local Similarity 70.0%; Pred. No. 0.3; 1; Indels 0; Gaps 0;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy      1      GYSFTGHMNN 10
Db      26      GYFTSYMNN 35

```

RESULT 5

```

S26315      Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26315

```


R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein
 A:Reference number: S26309; PMID:91341421; PMID:1908510
 A:Accession: S26315
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-106 <STA>
 A:Cross-references: UNIPARC:UPI0000115P8B; EMBL:X59208; NID:G52079; P1DN:CAA41918.1; P1D
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 49; DB 2; Length 106;
 Best Local Similarity 70.0%; Pred. No. 0.31; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
 |||:|:|
 Db 13 GYTFSTYMMN 22

RESULT 6
 PH0987
 Ig heavy chain V region (clone 163.47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH0987
 R:Tillman, D.M.; Joo, N.T.; Hill, R.J.; Marlon, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
 A:Reference number: PH0971; PMID:92381444; PMID:1512540
 A:Accession: PH0987
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-107 <TIL>
 A:Cross-references: UNIPARC:UPI0000176D07
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 49; DB 2; Length 107;
 Best Local Similarity 70.0%; Pred. No. 0.31; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
 |||:|:|
 Db 26 GYTFSTYMMN 35

RESULT 7
 S26317
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
 C:Accession: S26317
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein
 A:Reference number: S26309; PMID:91341421; PMID:1908510
 A:Accession: S26317
 A:Molecule type: mRNA
 A:Residues: 1-110 <STA>
 A:Cross-references: UNIPARC:UPI00001769A6; EMBL:X59186
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:4-87/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 49; DB 2; Length 110;
 Best Local Similarity 70.0%; Pred. No. 0.32; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
 |||:|:|
 Db 15 GYTFSTYMMN 24

RESULT 8
 A49060
 Ig heavy chain V region, phenyl phosphonate hapten-specific catalytic monoclonal antibod
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
 C:Accession: A49060
 R:Angles, T.S.; Smith, R.G.; Darley, M.J.; Sugawara, R.; Sanchez, R.I.; Kenten, J.;
 Biochemistry 32, 12128-12135, 1993
 A:Title: Isozymes: structurally and mechanistically similar catalytic antibodies from
 A:Reference number: A49060; PMID:94032348; PMID:8218291
 A:Accession: A49060
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-114 <ANG>
 A:Cross-references: UNIPARC:UPI0000176C1E
 A:Experimental source: hybridoma cell
 A:Note: sequence extracted from NCBI backbone (NCBI:140371)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 49; DB 2; Length 114;
 Best Local Similarity 80.0%; Pred. No. 0.33; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
 |||:|:|
 Db 26 GYSFTSFMMN 35

RESULT 9
 G45722
 anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 115) - mouse (F
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
 C:Accession: G45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vaegu
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
 A:Reference number: A45722; PMID:9310833; PMID:1677958
 A:Accession: G45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-117 <SIM>
 A:Cross-references: UNIPARC:UPI0000176D42
 A:Note: sequence extracted from NCBI backbone (NCBI:120595)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 49; DB 2; Length 117;
 Best Local Similarity 70.0%; Pred. No. 0.34; Indels 1; Gaps 0;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
 |||:|:|
 Db 26 GYTFSTYMMN 35

RESULT 10
 C30560
 Ig heavy chain V region (35.8.2H) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1989 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999
 C:Accession: C30560
 R:Matzuda, T.; Kabat, E.A.
 J. Immunol. 142, 863-870, 1989
 A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclon

A:Reference number: A30560; MUID:89110062; PMID:2464028
A:Accession: C30560
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <MAT>
A:Cross-references: UNIPARC:UPI0000114E21; GB:M24270; NID:9195615; PIDN:AAA38371.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 49; DB 2; Length 118;
Best Local Similarity 70.0%; Pred. No. 0.34;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GVSFTGHMNN 10
|||:||||
Db 26 GYFTSYMMN 35

RESULT 11
S17604
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17604
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17604
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-98 <CLA>
A:Cross-references: UNIPARC:UPI0000176D59
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 48; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.41;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GVSFTGHMNN 10
|||:||||
Db 19 GYSFTGYFMN 28

RESULT 12
S26319
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26319
R:Stark, S.E.; Caton, A.U.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26319
A:Molecule type: mRNA
A:Residues: 1-114 <STA>
A:Cross-references: UNIPARC:UPI00001769A8; EMBL:X59172
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 48; DB 2; Length 114;
Best Local Similarity 80.0%; Pred. No. 0.48;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GVSFTGHMNN 10
|||:||||
Db 22 GYSFTGYFMN 31

RESULT 13
PS0057
Ig heavy chain precursor V region (PAR) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C:Accession: PS0057
R:Yacita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A:Title: Biased expression of variable region gene families of the immunoglobulin heavy
A:Reference number: PS0057; MUID:89197817; PMID:2467902
A:Accession: PS0057
A:Molecule type: DNA
A:Residues: 1-135 <YAO>
A:Cross-references: UNIPARC:UPI000011B257; GB:D00307; NID:9220448; PIDN:BA00213.1; PID:
A>Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly
C:Comment: The gene encoding this protein was isolated from a hybridoma that produces an
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-115/Product: Ig heavy chain V region PAR #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 48; DB 2; Length 135;
Best Local Similarity 80.0%; Pred. No. 0.57;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GVSFTGHMNN 10
|||:||||
Db 45 GYSFTGYFMN 54

RESULT 14
S42183
Ig gamma chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C:Accession: S42183
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:9409207; PMID:7691608
A:Accession: S42183
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <MO>
A:Cross-references: UNIPARC:UPI0000116565; EMBL:Z25455; NID:9407824; PIDN:CAA80942.1; PI:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.4%; Score 47; DB 2; Length 101;
Best Local Similarity 70.0%; Pred. No. 0.62;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GVSFTGHMNN 10
|||:||||
Db 26 GYFTTYMMN 35

RESULT 15
S55541
Ig heavy chain V region pel - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55541
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 933-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-preenkephalin antibodies usin
utations in the variable region genes.
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55541

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <BOB>
A:Cross-references: UNIPARC:UPI00001161F8; EMBL:X82580; NID:g854286; PIDN:CA57916.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 73.4%; Score 47; DB 2; Length 117;
Best Local Similarity 70.0%; Pred. No. 0.72;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||:|:|:
DB 25 GYFTGHMNN 34

RESULT 16

JN0295

Ig heavy chain V-D-J region (anti-thyroid peroxidase) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996

C:Accession: JN0295

R:Portolano, S.; Seto, P.; Chazenbalk, G.D.; Nagayama, Y.; McLachlan, S.M.; Rapoport, B.

Biochem. Biophys. Res. Commun. 179, 372-377, 1991

A>Title: A human Fab fragment specific for thyroid peroxidase generated by cloning thymo

A:Reference number: JN0295; MUID:91354278; PMID:1831977

A:Accession: JN0295

A:Molecule type: mRNA

A:Residues: 1-119 <FOR>

A:Cross-references: UNIPARC:UPI0000176C25

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-97/Domain: V segment <VSE>

F:15-98/Domain: immunoglobulin homology <IMM>

F:98-107/Domain: D segment <DSE>

F:108-119/Domain: J segment <JSE>

Query Match 73.4%; Score 47; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 0.74;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:|:
DB 26 GYFTGHMNN 35

RESULT 17

D33548

Ig heavy chain V-1 region (W1L2) - human

C:Species: Homo sapiens (man)

C>Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996

C:Accession: D33548

R:Klips, T.J.; Tomhave, E.; Prater, L.F.; Duffly, S.; Chen, P.P.; Carson, D.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989

A>Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr

A:Reference number: A33548; MUID:89345575; PMID:2503826

A:Accession: D33548

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-123 <KIP>

A:Cross-references: UNIPARC:UPI0000176909

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.4%; Score 47; DB 2; Length 123;
Best Local Similarity 70.0%; Pred. No. 0.76;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:|:
DB 26 GYFTGHMNN 35

RESULT 18

B47159

Ig heavy chain V region, anti-carcinoembryonic maid T84.66 antigen monoclonal anti-idiot

C:Species: Mus musculus (house mouse)

C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

C:Accession: B47159

R:Gaida, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.

J. Biol. Chem. 268, 14138-14145, 1993

A>Title: Molecular characterization of a cloned idiotype cascade containing a network a

A:Reference number: A47159; MUID:93300804; PMID:7686150

A:Accession: B47159

A:Molecule type: DNA

A>Status: preliminary

A:Residues: 1-136 <GAI>

A:Cross-references: UNIPARC:UPI0000176C84

A:Experimental source: hybridoma 666.C4

A>Note: sequence inconsistent with the nucleotide translation

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.4%; Score 47; DB 2; Length 136;
Best Local Similarity 70.0%; Pred. No. 0.84;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:|:
DB 45 GYFTGHMNN 54

RESULT 19

S36384

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999

C:Accession: S36384; S33399

R:Ansell, K.H.

submitted to the EMBL Data Library, April 1993

A:Reference number: S36376

A:Accession: S36384

A:Molecule type: mRNA

A:Residues: 1-66 <ANS>

A:Cross-references: UNIPARC:UPI0000116629; EMBL:X73020; NID:g295888; PIDN:CA51504.1; PI

R:Ketleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.W.

Eur. J. Immunol. 23, 206-211, 1993

A>Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes usi

A:Reference number: S33391; MUID:93122092; PMID:8419173

A:Accession: S33399

A:Molecule type: mRNA

A:Residues: 1-39 <KET>

A:Cross-references: UNIPARC:UPI0000176EA5; EMBL:X73020

A:Experimental source: strain BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-66/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 70.3%; Score 45; DB 2; Length 66;
Best Local Similarity 60.0%; Pred. No. 0.87;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:|:
DB 25 GYAFSNMNN 34

RESULT 20

PH0983

Ig heavy chain V region (clone 165.49) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

```

C:Accession: PH0983
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
C:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0983
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-101 <TIL>
A:Cross-references: UNIPARC:UPI0000176D03
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match          70.3%; Score 45; DB 2; Length 101;
Best Local Similarity 60.0%; Pred. No. 1.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
    |||:|:|
Db 19 GYTFSTYWIN 28

RESULT 21
PH0982
Ig heavy chain V region (clone 165.27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0982
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0982
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-101 <TIL>
A:Cross-references: UNIPARC:UPI0000176D02
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:12-95/Domain: immunoglobulin homology <IMM>

Query Match          70.3%; Score 45; DB 2; Length 101;
Best Local Similarity 60.0%; Pred. No. 1.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
    |||:|:|
Db 23 GYTFSTYWIN 32

RESULT 22
B37263
Ig heavy chain V region (IG3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C:Accession: B37263
R:Goshorn, S.C.; Retzel, B.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:91115823; PMID:1703527
A:Accession: B37263
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-102 <GOS>
A:Cross-references: UNIPARC:UPI0000115187; GB:M57997; NID:G195426; PIDN:AAA63335.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match          70.3%; Score 45; DB 2; Length 102;

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Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
    |||:|:|
Db 18 GYSFTGYTMN 27

RESULT 23
PH0981
Ig heavy chain V region (clone 111.185) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0981
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH0981
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-104 <TIL>
A:Cross-references: UNIPARC:UPI0000176D01
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          70.3%; Score 45; DB 2; Length 104;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
    |||:|:|
Db 26 GYTFSTYWIN 35

RESULT 24
PH1005
Ig heavy chain V region (clone 202.54) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1005
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1005
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-106 <TIL>
A:Cross-references: UNIPARC:UPI0000176D15
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          70.3%; Score 45; DB 2; Length 106;
Best Local Similarity 70.0%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
    |||:|:|
Db 26 GYSFTRYMMH 35

RESULT 25
PH0984
Ig heavy chain V region (clone 178.83) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH0984
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

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J. Exp. Med. 176, 761-779, 1992
 A>Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c
 A:Reference number: PH0971; MUID:92581444; PMID:1512540
 A:Accession: PH0984
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-107 <TIL>
 A:Cross-references: UNIPARC:UPI0000176D04
 A:Experimental source: B cell, strain [NZB x NZW] F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 70.3%; Score 45; DB 2; Length 107;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||:
 Db 26 GYFTSYWIN 35

RESULT 26
 S26463
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26463
 R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26463
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-111 <KAV>
 A:Cross-references: UNIPARC:UPI0000115F67; EMBL:X59113; NID:951922; PIDN:CAA1839.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-90/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 70.3%; Score 45; DB 2; Length 111;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||:
 Db 18 GYFTSYWIN 27

RESULT 27
 F45722
 anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 33) - mouse (fr
 C:Species: Mus musculus (house mouse)
 C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: F45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
 J. Vitrol. 67, 489-496, 1993
 A>Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
 A:Reference number: A45722; MUID:93100833; PMID:7677958
 A:Accession: F45722
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-120 <SIM>
 A:Cross-references: UNIPARC:UPI0000176D4D
 A>Note: sequence extracted from NCBI backbone (NCBIP:120594)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein
 F:15-99/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 70.3%; Score 45; DB 2; Length 120;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||:
 Db 26 GYSFTGYTMN 35

RESULT 28
 S09956
 Ig heavy chain V-D-J region (105-2H) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
 C:Accession: S09956
 R:Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
 Eur. J. Immunol. 20, 771-777, 1990
 A>Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
 A:Reference number: S09955; MUID:90269328; PMID:2347362
 A:Accession: S09956
 A:Molecule type: mRNA
 A:Residues: 1-120 <REI>
 A:Cross-references: UNIPARC:UPI0000115E5B; EMBL:X51844; NID:955243; PIDN:CAA36137.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 70.3%; Score 45; DB 2; Length 120;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||:
 Db 26 GYFTSYWIN 35

RESULT 29
 PH0887
 Ig heavy chain V region (anti-CD3) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
 C:Accession: PH0887
 R:Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodrigues, M.L.; Beverley, P.C.L.; Feldmann,
 J. Exp. Med. 175, 217-225, 1992
 A>Title: Development of humanized bispecific antibodies reactive with cytotoxic lymphocy
 A:Reference number: PH0885; MUID:92113462; PMID:1346155
 A:Accession: PH0887
 A:Molecule type: mRNA
 A:Residues: 1-122 <SHA>
 A:Cross-references: UNIPARC:UPI0000176B39
 A>Note: The authors translated the codon TTC for residue 70 as Leu
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match
 Best Local Similarity 70.3%; Score 45; DB 2; Length 122;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||:
 Db 26 GYSFTGYTMN 35

RESULT 30
 A30577
 Ig heavy chain precursor V region (WRL10) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 16-Aug-1996
 C:Accession: A30577
 R:Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theoc
 J. Exp. Med. 161, 805-815, 1985
 A>Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rela
 A:Reference number: A30577; MUID:85159423; PMID:3920343
 A:Accession: A30577
 A>Status: preliminary
 A:Molecule type: mRNA

Query Match
 Best Local Similarity 70.3%; Score 45; DB 2; Length 120;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

A:Residues: 1-135 <KOF>
A:Cross-references: UNIPARC:UPI0000176CAF; GB:M37621
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.3%; Score 45; DB 2; Length 135;
Best Local Similarity 60.0%; Pred. No. 1.8;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
||:|:|:|:
DB 45 GYFTSYWIN 54

RESULT 31
E29380

Ig heavy chain precursor V region (AC-1001) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999

C:Accession: E29380
R:Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
J. Biol. Chem. 262, 13579-13583, 1987

A:Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable
A:Reference number: A92612; MUID:88007582; PMID:3115981

A:Accession: E29380
A:Molecule type: mRNA

A:Residues: 1-137 <CHS>
A:Cross-references: UNIPARC:UPI0000114CB1; GB:M17164; GB:U02815; NID:G195411; PIDN:AAA38

C:Superfamily: immunoglobulin V region; immunoglobulin homology
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855

A:Accession: PH1105
A:Molecule type: DNA

A:Residues: 1-76 <SCH>
A:Cross-references: UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924Q5; UNIPROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924Q8; UNIPROT:Q924R2; UNIPROT:Q8K

PROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924Q8; UNIPROT:Q924R2; UNIPROT:Q8K
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F/34-117/Domain: immunoglobulin homology <IMM>

QY 1 GYSFTGHMMN 10
||:|:|:|:
DB 45 GYFTSYWIN 54

RESULT 32
E32513

Ig heavy chain precursor V region (MRL22) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999

C:Accession: E32513
R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization and
A:Reference number: A94683; MUID:88331594; PMID:3138286

A:Accession: E32513
A:Molecule type: DNA

A:Residues: 1-138 <KOF>
A:Cross-references: UNIPARC:UPI0000114D9D; GB:M20835; NID:G196945; PIDN:AAA3847.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.3%; Score 45; DB 2; Length 138;
Best Local Similarity 60.0%; Pred. No. 1.8;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
||:|:|:|:
DB 45 GYFTSYWIN 54

RESULT 33
D25150

Ig heavy chain V region (AC38 260.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)

QY 1 GYSFTGHMMN 10
||:|:|:|:
DB 45 GYFTSYWIN 54

C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Aug-1996

C:Accession: D25150
R:Didrop, R.; Boyens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.
EMBO J. 3, 517-523, 1984

A:Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes
A:Reference number: A91000; MUID:84182519; PMID:6201362

A:Accession: D25150
A:Molecule type: Protein

A:Residues: 1-69 <DLI>

A:Cross-references: UNIPARC:UPI00001769E1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 68.8%; Score 44; DB 2; Length 69;
Best Local Similarity 60.0%; Pred. No. 1.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
||:|:|:|:
DB 14 GYFTSYWMH 23

RESULT 34
PH1153

Ig heavy chain V region (clone 43F.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004

C:Accession: PH1153
R:Schlitz, B.; Rajewsky, K.
J. Exp. Med. 176, 427-436, 1992

A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855

A:Accession: PH1153
A:Molecule type: DNA

A:Residues: 1-76 <SCH>
A:Cross-references: UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924Q5; UNIPROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924Q8; UNIPROT:Q924R2; UNIPROT:Q8K

PROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924Q8; UNIPROT:Q924R2; UNIPROT:Q8K
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 76;
Best Local Similarity 60.0%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
||:|:|:|:
DB 4 GYFTSYWMH 13

RESULT 35
F28833

Ig kappa chain V region (HP20.119.25) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1983 #sequence_revision 30-Sep-1989 #text_change 31-Dec-2004

C:Accession: F28833
R:Corbett, S.; Hirt, M.; Roth, C.; Theze, J.; Fougereau, M.; Schiff, C.
J. Immunol. 141, 779-784, 1988

A:Title: Allelic manipulation of the GAT idiotype cascade. Immunization of C57BL/6 m
A:Reference number: A92827; MUID:88285674; PMID:3135311

A:Accession: F28833
A:Molecule type: mRNA

A:Residues: 1-80 <COR>

A:Cross-references: UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924Q5; UNIPROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924R2; UNIPARC:UPI0000176AD5

C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 68.8%; Score 44; DB 2; Length 80;
Best Local Similarity 60.0%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
||:|:|:|:
DB 1 GYFTSYWMH 13

Db 8 GYTFSTYMMH 17
||:|:|:

RESULT 36

A25150

Ig heavy chain V region (AC38 251.5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Aug-1996

C:Accession: A25150

R:Didrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.

EMBO J. 3, 517-523, 1984

A>Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes

A:Reference number: A51000; MUID:84182519; PMID:6201362

A:Accession: A25150

A:Molecule type: protein

A:Residues: 1-86 <DIL>

A:Cross-references: UNIPARC:UPI0000176A1D

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 68.8%; Score 44; DB 2; Length 86;
Best Local Similarity 60.0%; Pred. No. 1.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTHMMN 10
||:|:|:

Db 8 GYTFSTYMMH 17
||:|:|:

RESULT 37

PH1004

Ig heavy chain V region (clone 165.5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1004

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A>Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1004

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-91 <TIL>

A:Cross-references: UNIPARC:UPI0000176ACD

A:Experimental source: B cell, strain [NZB x NZW] F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 68.8%; Score 44; DB 2; Length 91;
Best Local Similarity 60.0%; Pred. No. 1.8;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTHMMN 10
||:|:|:

Db 8 GYTFSTYMMH 17
||:|:|:

RESULT 38

S42185

Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42185

R:Mo, J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A>Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42185

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-94 <MOJ>

A:Cross-references: UNIPARC:UPI0000116568; EMBL:Z25459; NID:9407828; PIDN:CAA80946.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 94;
Best Local Similarity 60.0%; Pred. No. 1.8;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTHMMN 10
||:|:|:

Db 19 GYTFSTYMMH 28
||:|:|:

RESULT 39

PH1142

Ig heavy chain V region (clone V2078.2A) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004

C:Accession: PH1142

R:Schlitz, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A>Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A:Reference number: PH1105; MUID:92364545; PMID:1500855

A:Accession: PH1142

A:Molecule type: DNA

A:Residues: 1-94 <SCH>

A:Cross-references: UNIPROT:Q91VA2; UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924P7; UNIPROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924Q8; UNIPROT:Q92

A:Experimental source: B cell

C:Superfamily: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 94;
Best Local Similarity 60.0%; Pred. No. 1.8;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTHMMN 10
||:|:|:

Db 22 GYTFSTYMMH 31
||:|:|:

RESULT 40

JL0078

Ig heavy chain V region (anti-glutamylalanylycrosine, F17.59.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 31-Dec-2004

C:Accession: JL0078

R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.

Mol. Immunol. 25, 859-865, 1988

A>Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reac

A:Reference number: JL0076; MUID:89096573; PMID:3211160

A:Accession: JL0078

A:Molecule type: mRNA

A:Residues: 1-94 <KAA>

A:Cross-references: UNIPROT:Q924R3; UNIPARC:UPI0000176AD7

A>Note: the authors translated the codon ACG for residue 90 as Ser

C:Superfamily: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-12/Region: complementarity-determining 1

F:27-43/Region: complementarity-determining 2

F:81-94/Region: J2 segment

Query Match 68.8%; Score 44; DB 2; Length 94;
Best Local Similarity 60.0%; Pred. No. 1.8;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTHMMN 10
||:|:|:

Db 3 GYTFSTYMMH 12
||:|:|:

RESULT 41

S17613

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S17613

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17613

A:Status: Preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <CLA>

A:Cross-references: UNIPARC:UPI0000176E7A

C:Superfamily: immunoglobulin V region; immunoglobulin

C:Keywords: heterotetramer; immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 96;

Best Local Similarity 60.0%; Pred. No. 1.9;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10

DB 19 GYFTFTYMMH 28

RESULT 42

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S17616

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17616

A:Status: Preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <CLA>

A:Cross-references: UNIPARC:UPI0000176E75

C:Superfamily: immunoglobulin V region; immunoglobulin

C:Keywords: heterotetramer; immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 96;

Best Local Similarity 60.0%; Pred. No. 1.9;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10

DB 19 GYFTFTYMMH 28

RESULT 43

Ig heavy chain V region (clone V2028.2B) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004

C:Accession: PH1137

R:Schlitz, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A:Reference number: PH1105; MUID:92364545; PMID:1500855

A:Accession: PH1137

A:Molecule type: DNA

A:Residues: 1-97 <SCH>

A:Cross-references: UNIPROT:Q91VA2; UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924R6; UNIPROT:Q924R7; UNIPROT:Q924R7; UNIPROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R5

C:Superfamily: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-96/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 97;

Best Local Similarity 60.0%; Pred. No. 1.9;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10

DB 26 GYFTFTYMMH 35

RESULT 44

Ig heavy chain V region (clone 3D.2A) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004

C:Accession: PH1155

R:Schlitz, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A:Reference number: PH1105; MUID:92364545; PMID:1500855

A:Accession: PH1155

A:Molecule type: DNA

A:Residues: 1-97 <SCH>

A:Cross-references: UNIPROT:Q924Q1; UNIPARC:UPI0000176BC1

A:Experimental source: B cell

C:Superfamily: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 97;

Best Local Similarity 60.0%; Pred. No. 1.9;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10

DB 25 GYFTFTYMMH 34

RESULT 45

Ig heavy chain V region (clone 37F.2A) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1164

R:Schlitz, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A:Reference number: PH1105; MUID:92364545; PMID:1500855

A:Accession: PH1164

A:Molecule type: DNA

A:Residues: 1-98 <SCH>

A:Cross-references: UNIPARC:UPI0000176BC6

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 98;

Best Local Similarity 60.0%; Pred. No. 1.9;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10

DB 26 GYFTFTYMMH 35

RESULT 46

Ig heavy chain V region (clone V2076.2A) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1141

R:Schltrek, B.; Rajewsky, K.
J.Exp. Med. 176, 427-438, 1992
A>Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1141
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPARC:UPI0000176BB7
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:|:
DB 26 GYFTFTSYMMH 35

RESULT 47

PH1138
Ig heavy chain V region (clones V29.1, V11.2B, V3.2A, V15.2B, V31.2B, V2001.2B, V2067.2B)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1138
R:Schltrek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A>Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1138
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPARC:UPI000011A9DA
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:|:
DB 26 GYFTFTSYMMH 35

RESULT 48

PH1154
Ig heavy chain V region (clone 45F.2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1154
R:Schltrek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A>Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1154
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPARC:UPI0000115596
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:|:
DB 26 GYFTFTSYMMH 35

RESULT 49

PH1106
Ig heavy chain V region (clones V4.2B, V17.2B, V33.2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1106
R:Schltrek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A>Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1106
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPARC:UPI0000176BBF
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:~|:|:
DB 26 GYFTFTSYMMH 35

RESULT 50

PH1118
Ig heavy chain V region (clone V32.2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1118
R:Schltrek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A>Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1118
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPROT:Q91VA2; UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIPROT:Q924P7; UNIPROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924Q8; UNIPROT:Q924Q3
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 44; DB 2; Length 98;
Best Local Similarity 60.0%; Pred. No. 1.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:|:
DB 26 GYFTFTSYMMH 35

Search completed: January 17, 2006, 12:05:31
Job time : 22.3939 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:47:28 ; Search time 56.3636 Seconds
(without alignments)
125.174 Million cell updates/sec

```

Title:      US-10-665-658-10
Perfect score: 64
Sequence:   1 GYSFTGHWNN 10

```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 1000 summaries
```

```
Database : .Uniprot_05.80:*
          1: uniprot_sprot:*
          2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	76.6	486	2	Q5HW3_MOUSE	Q5hw3 mus musculi
2	49	75.0	481	2	Q91WT3_MOUSE	Q91wt3 mus musculi
3	47	73.4	114	2	Q9J181_MOUSE	Q9j181 mus musculi
4	47	73.4	117	2	Q9Z1C6_MOUSE	Q9z1c6 mus musculi
5	47	73.4	483	2	Q5Z151_MOUSE	Q5z151 mus musculi
6	46	71.9	119	2	Q6GY22_MOUSE	Q6gy22 mus musculi
7	46	71.9	585	2	O6GPX4_XENLA	O6gpx4 xenopus laevis
8	44	68.8	117	1	HV04_MOUSE	P01748 mus musculi
9	44	68.8	117	1	HV05_MOUSE	P01749 mus musculi
10	44	68.8	117	1	HV06_MOUSE	P01750 mus musculi
11	44	68.8	117	1	HV07_MOUSE	P01753 mus musculi
12	44	68.8	117	1	HV10_MOUSE	P01754 mus musculi
13	44	68.8	117	1	HV49_MOUSE	P63328 mus musculi
14	44	68.8	118	2	O5R3X0_MOUSE	O5r3x0 mus musculi
15	44	68.8	120	1	HV50_MOUSE	P63329 mus musculi
16	44	68.8	137	2	Q924R6_MOUSE	Q924r6 mus musculi
17	44	68.8	139	1	HV07_MOUSE	P01751 mus musculi
18	44	68.8	139	2	Q924R5_MOUSE	Q924r5 mus musculi
19	44	68.8	140	2	Q924P8_MOUSE	Q924p8 mus musculi
20	44	68.8	140	2	Q924R2_MOUSE	Q924r2 mus musculi
21	44	68.8	141	2	Q924R0_MOUSE	Q924r0 mus musculi
22	44	68.8	142	2	Q924O1_MOUSE	Q924o1 mus musculi
23	44	68.8	143	2	Q91V67_MOUSE	Q91v67 mus musculi
24	44	68.8	143	2	Q91VA2_MOUSE	Q91va2 mus musculi
25	44	68.8	143	2	Q924R7_MOUSE	Q924r7 mus musculi
26	44	68.8	143	2	Q924P6_MOUSE	Q924p6 mus musculi
27	44	68.8	143	2	Q924O5_MOUSE	Q924o5 mus musculi
28	44	68.8	143	2	Q924R0_MOUSE	Q924r0 mus musculi
29	44	68.8	144	2	Q924P5_MOUSE	Q924p5 mus musculi
30	44	68.8	145	2	Q924P7_MOUSE	Q924p7 mus musculi
31	44	68.8	145	2	Q924O6_MOUSE	Q924o6 mus musculi

32	44	68.8	1.5	2	Q92407_MOUSE	Q92447 mus musculus
33	44	68.8	1.5	2	Q92409_MOUSE	Q92449 mus musculus
34	44	68.8	1.5	2	Q924R1_MOUSE	Q92451 mus musculus
35	44	68.8	1.5	2	Q924R3_MOUSE	Q92453 mus musculus
36	44	68.8	1.5	2	Q924R4_MOUSE	Q92454 mus musculus
37	44	68.8	1.46	2	Q924Q3_MOUSE	Q92448 mus musculus
38	44	68.8	1.6	2	Q924R8_MOUSE	Q92443 mus musculus
39	44	68.8	3.27	2	Q9S5B9_AARAT	Q9a5b9 arabidopsis
40	44	68.8	4.22	2	Q8K172_MOUSE	Q8k172 mus musculus
41	44	68.8	4.88	2	Q8K0F2_MOUSE	Q8k0f2 mus musculus
42	44	68.8	6.17	2	Q4KML5_MOUSE	Q4kml5 mus musculus
43	44	68.8	7.66	2	Q6F792_CANGA	Q6f792 candida glabrata
44	43	67.2	1.20	2	Q920B8_MOUSE	Q920b8 mus musculus
45	43	67.2	1.23	2	Q920Y1_MOUSE	Q920y1 mus musculus
46	43	67.2	1.32	2	Q8VJL1_MOUSE	Q8vj11 mus musculus
47	43	67.2	1.33	2	Q924P9_MOUSE	Q924p9 mus musculus
48	43	67.2	1.46	2	Q924Q8_MOUSE	Q924q8 mus musculus
49	43	67.2	3.39	2	Q8RDG7_TRETN	Q8rdg7 thermooanaeae
50	43	67.2	6.16	2	Q504M7_MOUSE	Q504m7 mus musculus
51	42	65.6	1.10	2	Q4UNQ4_XANCP	Q4unq4 xanthomanaa
52	42	65.6	1.10	2	Q8P3B3_XANCP	Q8p3b3 xanthomanaa
53	42	65.6	1.10	2	Q8PELP9_XANAC	Q8pel9 xanthomanaa
54	42	65.6	1.10	2	Q9J1B3_MOUSE	Q9j1b3 mus musculus
55	42	65.6	1.11	2	Q9D9B8_MOUSE	Q9d9b8 mus musculus
56	42	65.6	2.37	2	Q7X3K2_PSRPU	Q7x3k2 pseudomnaea
57	42	65.6	2.43	2	Q7T0M2_MOUSE	Q7t0m2 mus musculi
58	42	65.6	6.14	2	Q7TWT6_MOUSE	Q7twt6 mus musculi
59	41	64.1	1.10	2	Q9J177_MOUSE	Q9j177 mus musculi
60	41	64.1	1.11	1	HVJ5_MOUSE	P01797 mus musculi
61	41	64.1	1.13	1	HV27_MOUSE	P01799 mus musculi
62	41	64.1	1.13	1	HV28_MOUSE	P01799 mus musculi
63	41	64.1	1.13	1	HV29_MOUSE	P01799 mus musculi
64	41	64.1	1.13	1	HV30_MOUSE	P01800 mus musculi
65	41	64.1	1.13	1	HV31_MOUSE	P01801 mus musculi
66	41	64.1	1.13	1	HV34_MOUSE	P01803 mus musculi
67	41	64.1	1.15	1	HV32_MOUSE	P01801 mus musculi
68	41	64.1	1.15	1	HV33_MOUSE	P01802 mus musculi
69	41	64.1	1.17	1	HV1C_HUMAN	P23083 homo sapien
70	41	64.1	1.17	1	HV41_MOUSE	P01811 mus musculi
71	41	64.1	1.19	2	Q9J194_HUMAN	Q9j194 homo sapien
72	41	64.1	1.25	2	Q9ULP9_HUMAN	Q9ul99 homo sapien
73	41	64.1	1.36	2	Q7TPE3_MOUSE	Q7tpe3 mus musculi
74	41	64.1	1.36	2	Q67Y03_ORSEA	Q67y03 oryza sativa
75	41	64.1	3.63	2	Q514Z9_ENTHI	Q514z9 entamoeba
76	41	64.1	4.25	2	Q6H454_ORSEA	Q6h454 entamoeba
77	41	64.1	4.70	2	Q7TWK1_MOUSE	Q7twk1 mus musculi
78	41	64.1	4.83	2	Q80Z17_MOUSE	Q80z17 mus musculi
79	41	64.1	5.07	2	Q8MS75_DRMB	Q8ms75 drosophila
80	41	64.1	5.79	2	Q51D76_ENTHI	Q51d76 entamoeba
81	41	64.1	6.02	2	Q6C6Y8_YAKLI	Q6c6y8 yarrowia
82	41	64.1	6.81	2	Q41B33_GIIZE	Q41b33 gibberella
83	41	64.1	7.43	2	Q8A552_BACNT	Q8a552 bacterioides
84	41	64.1	1.43	2	Q8RR73_BACNT	Q8rr73 bacterioides
85	40	62.5	2.24	2	Q61BY4_BACCCZ	Q61by4 bacillus cereus
86	40	62.5	4.36	2	Q6BRX3_DEBNA	Q6brx3 debaryomyces
87	40	62.5	4.44	2	Q5T1M9_MALZE	Q5tim9 zea mays
88	40	62.5	4.58	2	Q6UVZ0_HUMAN	Q6uvz0 homo sapien
89	40	62.5	4.74	2	Q8RH36_MOUSE	Q8rh36 mus musculi
90	40	62.5	4.95	2	Q5MY95_HUMAN	Q5my95 homo sapien
91	40	62.5	7.15	2	Q5KYT5_GEOXA	Q5kyl5 geobacillus
92	40	62.5	10.34	2	Q54484_SERNA	Q54484 serattia m
93	40	62.5	1.36	1	Q54483_SERNA	Q54483 serattia m
94	39.5	61.7	1.37	1	HV11_MOUSE	P01755 mus musculus
95	39.5	61.7	6.29	2	Q41GY2_9BUPK	Q41gy2 burkholder
96	39.5	61.7	7.78	2	Q63RW7_BURPS	Q63rw7 burkholder
97	39.5	61.7	1.18	2	Q62LY6_BURMA	Q62ly6 burkholder
98	39	60.9	1.18	1	HV51_MOUSE	P06330 mus musculus
99	39	60.9	1.19	1	Y3414_YERPE	Q8abj5 yersinia p
100	39	60.9	1.19	1	Q66HE6_YERPS	Q66he6 yersinia p
101	39	60.9	1.21	2	HV01_MOUSE	P01745 mus musculus
102	39	60.9	1.43	2	Q924Q0_MOUSE	Q924q0 mus musculus
103	39	60.9	2.34	2	Q72N12_LEPFC	Q72n12 leptospi
104	39	60.9	2.34	2	Q8F817_LEPFLN	Q8f817 leptospi

105	39	60.9	269	1	MODE_HERSE	Q6f4k4	herbaepitri1	178	38	59.4	566	2	Q54N10	DICD1	Q54N10	dictyostei1
106	39	60.9	317	2	Q6S16_HYDMA	Q6s16x	hydra magni	179	38	59.4	573	2	Q6NUC3	XENLA	Q6NUC3	xenopus lae
107	39	60.9	323	2	Q4WEM3_ASPFU	Q4wem3	aspergillus	180	38	59.4	580	1	MTA70	HUMAN	Q6U44	homo sapien
108	39	60.9	351	2	Q4IF65_GIBZE	Q4if65	glibbrella	181	38	59.4	580	1	MTA70	MOUSE	Q6C3P	mus musculu
109	39	60.9	387	2	Q7MFV3_VIBVY	Q7mfvs	vibrio vuln	182	38	59.4	580	2	Q4V8G6	RAT	Q4V8G6	ratius notv
110	39	60.9	406	2	Q69DJO_MOUSE	Q69dj0	mus musculu	183	38	59.4	584	2	Q6NX36	BRARE	Q6NX36	brachydanio
111	39	60.9	410	2	Q8UB71_AGRTS	Q8ub71	agrobacteri	184	38	59.4	587	2	Q6CFV0	YARLI	Q6CFV0	yarivora li
112	39	60.9	420	2	Q6BFL2_PARTE	Q6bfl2	paramecium	185	38	59.4	600	1	IME4	YEAST	Q6F183	saccharomyc
113	39	60.9	430	2	Q8A5CO_BACTN	Q8a5co	bacteroides	186	38	59.4	602	1	Q73YN0	MYCPA	Q73YN0	mycobacteri
114	39	60.9	437	2	Q57WFS_grryp	Q57wfs	trypanosoma	187	38	59.4	608	1	MT70	DROME	Q5V65	drosophila
115	39	60.9	493	1	VE2_HPV19	P36786	human papil	188	38	59.4	616	2	Q7QD05	ANOGA	Q7QD05	anopheles g
116	39	60.9	494	1	AMV1_SACPI	P21567	saccharomyc	189	38	59.4	633	1	COO52	METAC	Q6E73	methanosarc
117	39	60.9	507	1	AMV2_DEBOC	Q08806	debrayomyc	190	38	59.4	634	1	COO52	METMA	Q6PUN3	methanosarc
118	39	60.9	512	1	AMV1_DEBOC	P19269	debrayomyc	191	38	59.4	680	2	Q5VRG4	ORYSA	Q5VRG4	oryza sativ
119	39	60.9	518	2	Q6N030_HUMAN	Q6n030	homo sapien	192	38	59.4	685	1	MTA70	ARATH	Q8A486	arabidopsis
120	39	60.9	547	1	NUSM_ASCSU	P24884	ascaris suu	193	38	59.4	705	2	Q6EUN0	ORYSA	Q6EUN0	oryza sativ
121	39	60.9	553	2	Q94U22_ORYSA	Q94j22	oryza sativ	194	38	59.4	760	2	Q816Z2	PLAF7	Q816Z2	plasmodium
122	39	60.9	558	2	Q568Y0_RAT	Q568y0	ratius notv	195	38	59.4	774	2	Q4Z3Z7	PLAFB	Q4Z3Z7	plasmodium
123	39	60.9	624	1	AMV1_LIPRO	Q01117	lipomyces k	196	38	59.4	811	2	Q7RP17	PLAYO	Q7RP17	plasmodium
124	39	60.9	628	1	JPH4_HUMAN	Q96j16	homo sapien	197	38	59.4	819	2	Q9VWH9	DROME	Q9VWH9	drosophila
125	39	60.9	628	1	JPH4_MOUSE	Q86wt0	mus musculu	198	38	59.4	895	2	Q8NN05	CORGL	Q8NN05	corynebacte
126	39	60.9	628	2	Q69FE2_MOUSE	Q69fb2	mus musculu	199	38	59.4	1070	1	AGLU	CAMTS	Q28064	candida tsu
127	39	60.9	630	2	Q69F33_HUMAN	Q69f33	homo sapien	200	38	59.4	1266	2	Q8UGR8	AGRTS	Q8UGR8	agrobacteri
128	39	60.9	630	2	Q69FB3_RAT	Q69fb3	ratius notv	201	38	59.4	1867	1	MOT1	YEAST	Q6F123	saccharomyc
129	39	60.9	635	2	Q689C0_PLAFA	Q689c0	plasmodium	202	38	59.4	1904	2	Q6FRV8	CANCA	P22333	candida gla
130	39	60.9	635	2	Q697258_PLAF7	Q697258	plasmodium	203	38	58.6	1922	2	Q6NGB7	CORDI	Q6NGB7	corynebacte
131	39	60.9	647	2	Q6YF33_LIPST	Q6yfc33	lipomyces s	204	37	57.8	90	2	Q6A4G1	BACTN	Q6A4G1	bacteroides
132	39	60.9	742	2	Q6FNV6_CANCA	Q6fnv6	candida gla	205	37	57.8	125	2	Q6PIL0	HUMAN	Q6PIL0	homo sapien
133	39	60.9	782	2	Q5K3X6_LBQPA	Q5K3x6	legionella	206	37	57.8	193	2	Q6EX97	SUBDO	Q6EX97	subdites d
134	39	60.9	1042	2	Q8PUP0_METMA	Q8pup0	methanosarc	207	37	57.8	202	2	Q4KES3	PSEFS	Q4KES3	pseudomonas
135	38	59.4	110	2	Q5GUA5_XANOR	Q5gua5	xanthomonas	208	37	57.8	215	2	Q8F575	LEPIN	Q8F575	leptosira
136	38	59.4	118	2	Q9Z1C4_MOUSE	Q9z1c4	mus musculu	209	37	57.8	232	2	Q5FLF7	IACAC	Q5FLF7	lactobacilla
137	38	59.4	120	1	YACL_ECOS7	P08865	escherichia	210	37	57.8	243	2	Q63064	BURPS	Q63064	burkholderi
138	38	59.4	120	1	YACL_ECOL6	Q8f140	escherichia	211	37	57.8	243	2	Q6ZGB6	BURPS	Q6ZGB6	burkholderi
139	38	59.4	120	1	YACL_ECOL1	P08865	escherichia	212	37	57.8	281	2	Q54M55	DICD1	Q54M55	dictyosteli
140	38	59.4	120	1	YACL_SALTI	Q84985	salmonella	213	37	57.8	288	2	Q7RH52	PLAYO	Q7RH52	plasmodium
141	38	59.4	120	1	YACL_SALTY	Q84986	salmonella	214	37	57.8	312	2	Q5D806	SCHUA	Q5D806	schistosoma
142	38	59.4	120	1	YACL_SHIFL	P53936	shigella fl	215	37	57.8	316	2	Q4Q137	LEIMA	Q4Q137	leishmania
143	38	59.4	120	2	QSPD96_SALPA	Q5QD96	salmonella	216	37	57.8	393	1	PIGM	RHOER	Q69349	rhodococcus
144	38	59.4	137	2	Q82TW3_NITTEU	Q82tw3	nitrosomona	217	37	57.8	393	2	Q887N5	PSESM	Q887N5	pseudomonas
145	38	59.4	140	2	Q94Y45_ORYSA	Q94y45	oryza sativ	218	37	57.8	416	2	Q45154	BACPR	Q45154	bacteroides
146	38	59.4	140	2	Q7XC33_ORYSA	Q7xc33	oryza sativ	219	37	57.8	447	2	Q8CV97	OCEIR	Q8CV97	oceanobacil
147	38	59.4	148	2	Q59083_PYROH	Q59083	pyrococcus	220	37	57.8	451	2	Q7UT79	RHOBA	Q7UT79	rhodospirill
148	38	59.4	151	2	Q57795_SALCH	Q57795	salmonella	221	37	57.8	454	2	Q4IVU6	AZOVI	Q4IVU6	azotobacter
149	38	59.4	152	2	Q8U3L8_PYRPH	Q8u3l8	pyrococcus	222	37	57.8	454	2	Q9HTY1	PSEAE	Q9HTY1	pseudomonas
150	38	59.4	229	2	Q83R58_SHIFL	Q83r58	shigella fl	223	37	57.8	455	2	Q4K432	PSEFS	Q4K432	pseudomonas
151	38	59.4	280	2	Q8TW53_ANASP	Q8tw53	anabaena sp	224	37	57.8	464	2	Q6PP95	MOUSE	Q6PP95	mus musculu
152	38	59.4	296	2	Q4R799_MACFA	Q4r799	macaca fasc	225	37	57.8	470	2	Q5LWB7	STLPO	Q5LWB7	stictobacte
153	38	59.4	299	2	Q8KZ09_PPROT	Q8kz09	uncultured	226	37	57.8	471	2	Q8BAR4	PSESM	Q8BAR4	pseudomonas
154	38	59.4	352	2	Q4L5D2_STRAHJ	Q4l5d2	staphylococ	227	37	57.8	479	2	Q7TMR4	MOUSE	Q7TMR4	mus musculu
155	38	59.4	358	2	Q4YMX7_PLABE	Q4ymx7	plasmodium	228	37	57.8	479	2	Q5POK9	RAT	Q5POK9	ratius notv
156	38	59.4	370	2	Q66F86_SCHUA	Q66fb6	schistosoma	229	37	57.8	480	1	SYC_THET2		SYC_THET2	thermus the
157	38	59.4	373	2	Q4I3J5_GIBZE	Q4i3j5	glibbrella	230	37	57.8	480	1	SYC_THET8		SYC_THET8	thermus the
158	38	59.4	389	2	Q8A9R8_BACTN	Q8a9r8	bacteroides	231	37	57.8	481	2	Q8DHR4	STNEL	Q8DHR4	stnecloccc
159	38	59.4	406	2	Q55RZ7_CRYNE	Q55rz7	cryptococcu	232	37	57.8	484	2	Q6UB08	PSESY	Q6UB08	pseudomonas
160	38	59.4	406	2	Q5KGB9_CRYNE	Q5kge9	cryptococcu	233	37	57.8	484	2	Q4ZU77	PSESY	Q4ZU77	pseudomonas
161	38	59.4	437	2	Q4RKY3_TETNG	Q4rky3	tetradodon n	234	37	57.8	491	2	Q4IP51	GIBZE	Q4IP51	glibbrella
162	38	59.4	437	2	Q8Y793_ANASP	Q8y793	anabaena sp	235	37	57.8	501	2	Q67RB0	SYMT8	Q67RB0	synthobacte
163	38	59.4	440	2	Q7PTM3_ANOGA	Q7ptm3	anopheles g	236	37	57.8	507	1	Y108	STNY3	Y108	stneclocybt
164	38	59.4	457	2	Q4T1D1_TETNG	Q4t1d1	tetradodon n	237	37	57.8	518	1	Q8DMD2	STNEL	Q8DMD2	stnecloccc
165	38	59.4	464	2	Q6P1P8_MOUSE	Q6p1p8	mus musculu	238	37	57.8	518	2	Q8Y761	ANASP	Q8Y761	anabaena sp
166	38	59.4	475	2	Q5REI17_PONPY	Q5rei17	pongo pygma	239	37	57.8	524	2	Q75J87	DICD1	Q75J87	dictyosteli
167	38	59.4	483	1	VE2_HPV14	P36783	human papil	240	37	57.8	524	2	Q5H6R0	XANOR	Q5H6R0	xanthomonas
168	38	59.4	484	2	Q6R5T8_SYNP2	Q6r5t8	synecloccc	241	37	57.8	562	2	Q5H4I8	XANOR	Q5H4I8	xanthomonas
169	38	59.4	488	2	Q6FY82_CANCA	Q6fy82	candida gla	242	37	57.8	564	2	Q8E9B1	SHEON	Q8E9B1	shearellia
170	38	59.4	502	1	VE2_HPV25	P36787	human papil	243	37	57.8	594	2	Q5H4I6	XANOR	Q5H4I6	xanthomonas
171	38	59.4	524	1	VE2_HPV21	P50767	human papil	244	37	57.8	599	2	Q5H4I6	XANOR	Q5H4I6	xanthomonas
172	38	59.4	524	2	Q5XKP5_KLUTA	Q5xkp5	kluyveromyc	245	37	57.8	600	2	Q8A957	BACTN	Q8A957	bacteroides
173	38	59.4	524	2	Q4S439_TETNG	Q4s439	arabidopsis	246	37	57.8	613	2	Q7M930	WOLSTU	Q7M930	wolinnella s
174	38	59.4	530	2	Q6BXAT_DEBHA	Q6bxat	debrayomyc	247	37	57.8	664	2	Q7M839	WOLSTU	Q7M839	wolinnella s
175	38	59.4	536	2	Q5ALV0_CANAL	Q5alv0	candida alb	248	37	57.8	664	2	Q6LKD3	PROPR	Q6LKD3	photobacter
176	38	59.4	543	2	Q753Z9_ASHGO	Q753z9	asbhyia goss	249	37	57.8	762	2	Q55B06	DICD1	Q55B06	dictyosteli
177	38	59.4	559	2	Q753Z9_ASHGO	Q753z9	asbhyia goss	250	37	57.8	762	2	Q55B06	DICD1	Q55B06	dictyosteli

251	37	57.8	770	2	054SW3	DICDI	054SW3	dictyosteli	324	36	56.2	324	2	08YX00	ANASP	08YX00	anabaena sp
252	37	57.8	783	2	05LAK0	BACFN	05LAK0	bacteroides	325	36	56.2	330	2	08A4G5	BACTN	08A4G5	bacteroides
253	37	57.8	783	2	064QZ4	BACFN	064QZ4	bacteroides	326	36	56.2	330	2	08YUX1	ANASP	08YUX1	anabaena sp
254	37	57.8	790	2	080YT5	MOUSE	080YT5	mus musculus	327	36	56.2	334	2	042111	BRARE	042111	brachydanio
255	37	57.8	807	2	04UIN6	9BACT	04UIN6	uncultured	328	36	56.2	336	2	08YU14	ANASP	08YU14	anabaena sp
256	37	57.8	880	2	05PB68	ANAMM	05PB68	anaplasm m	329	36	56.2	348	2	08C728	MOUSE	08C728	mouse musculus
257	37	57.8	892	2	08A0E5	BACTN	08A0E5	bacteroides	330	36	56.2	361	1	TRUD	VIBCH	TRUD	vibrio chol
258	37	57.8	1047	2	06AMJ9	DESPS	06AMJ9	desulfotale	331	36	56.2	362	1	SERC	HAEDU	SERC	haemophilus
259	37	57.8	1056	2	05LHX3	BACFN	05LHX3	bacteroides	332	36	56.2	367	2	05M8X4	XENTR	05M8X4	xenopus tro
260	37	57.8	1056	2	064YX4	BACFN	064YX4	bacteroides	333	36	56.2	370	2	07OC98	STRETR	07OC98	streptococ
261	37	57.8	1061	2	05LHX3	BACFN	05LHX3	bacteroides	334	36	56.2	370	2	09LAC7	STRETR	09LAC7	streptococ
262	37	57.8	1061	2	064XZ2	BACFN	064XZ2	bacteroides	335	36	56.2	389	2	09LAC7	STRETR	09LAC7	streptococ
263	37	57.8	1261	2	06GQZ3	XENLA	06GQZ3	xenopus lae	336	36	56.2	404	2	082KX6	STRAW	082KX6	strepomyce
264	37	57.8	1748	2	0989R4	RHTLO	0989R4	rhizobium l	337	36	56.2	413	2	05QTS6	IDILLO	05QTS6	idionema s
265	37	57.8	1798	2	08KYG8	RHTLO	08KYG8	rhizobium l	338	36	56.2	416	2	07Q4F2	ANOGA	07Q4F2	anopheles g
266	37	57.8	204	2	059ND4	CANAL	059ND4	candida alb	339	36	56.2	418	2	06UBR3	TRYCR	06UBR3	trypanosoma
267	36.5	57.0	213	2	04MTY6	BACCE	04MTY6	bacillus ce	340	36	56.2	421	2	08BFB1	PARTS	08BFB1	paramycium
268	36.5	57.0	213	2	081DU3	BACCN	081DU3	bacillus ce	341	36	56.2	421	2	06J6D8	ADDAE	06J6D8	aedes aegypt
269	36.5	57.0	213	2	0738Q2	BACCN	0738Q2	bacillus ce	342	36	56.2	421	2	07MRX6	WOLSU	07MRX6	wolinnella s
270	36.5	57.0	213	2	081OV6	BACCN	081OV6	bacillus an	343	36	56.2	437	2	059P04	CANAL	059P04	candida alb
271	36.5	57.0	213	2	06H157	BACCH	06H157	bacillus th	344	36	56.2	442	2	05ATZ8	EMENI	05ATZ8	aspergillus
272	36.5	57.0	213	2	063BN8	BACCN	063BN8	bacillus th	345	36	56.2	445	2	04WEN9	ASPFU	04WEN9	aspergillus
273	36.5	57.0	455	2	05AXF3	EMENI	05AXF3	aspergillus	346	36	56.2	452	2	06CP71	KUTLA	06CP71	kluyveromyc
274	36.5	57.0	469	2	05R1D9	BRARE	05R1D9	brachydanio	347	36	56.2	456	2	06MNA0	BDEBA	06MNA0	bdellovibri
275	36.5	57.0	469	2	04W9P1	ASPFU	04W9P1	aspergillus	348	36	56.2	457	2	06SEJ6	LEIMO	06SEJ6	leishmania
276	36.5	57.0	487	2	07S2U8	NEUCR	07S2U8	neurospora	349	36	56.2	457	2	0609J4	LEIMO	0609J4	leishmania
277	36.5	57.0	572	1	LAC3	THACU	002079	thanaetophor	350	36	56.2	457	2	0609J4	LEIMO	0609J4	leishmania
278	36.5	57.0	576	1	LAC1	THACU	P56193	thanaetophor	351	36	56.2	458	1	07S1S1	NEUCR	07S1S1	neurospora
279	36.5	57.0	596	2	09ANQ9	BRARA	09ANQ9	bradyrhizob	352	36	56.2	465	2	08GZV4	LYCBS	08GZV4	lycopersico
280	36	56.2	16	2	08QCA1	BRARA	08QCA1	brachydanio	353	36	56.2	465	2	06GZV4	LYCBS	06GZV4	lycopersico
281	36	56.2	47	2	07VH34	HELHP	07VH34	helicobacte	354	36	56.2	468	2	0569W9	MOUSE	0569W9	mus musculu
282	36	56.2	75	2	085KH4	GHYMB	085KH4	schletereer	355	36	56.2	469	2	09JVV4	NEIMA	09JVV4	neisseria m
283	36	56.2	78	2	04SDS1	TERNG	04SDS1	tetrarodon n	356	36	56.2	470	2	09JY10	NEIMB	09JY10	neisseria m
284	36	56.2	79	1	YVAO	BACSU	P37509	bacillus su	357	36	56.2	473	2	09NDP5	CIOIN	09NDP5	ciona intes
285	36	56.2	79	1	087DU5	XYLFT	087DU5	xyella fas	358	36	56.2	473	2	09NDP5	CIOIN	09NDP5	ciona intes
286	36	56.2	80	2	06A6H9	PROAC	06A6H9	propionibac	359	36	56.2	478	2	06T1B1	HUMAN	06T1B1	homo sapien
287	36	56.2	81	2	07SGR3	NEUCR	07SGR3	neurospora	360	36	56.2	485	2	09N314	CABEL	09N314	caenorhabdi
288	36	56.2	95	2	09ULB6	HUMAN	09ULB6	homo sapien	361	36	56.2	486	2	062XU5	BACLD	062XU5	bacillus l
289	36	56.2	95	2	082MY1	NITEPU	082MY1	nitrosomona	362	36	56.2	489	2	057M51	TRYRP	057M51	trypanosoma
290	36	56.2	97	2	06DOM1	ERRCT	06DOM1	erwinia car	363	36	56.2	489	2	09B965	GHYME	09B965	geratocolen
291	36	56.2	119	2	0836U9	ENTFA	0836U9	enterococcu	364	36	56.2	489	2	065M56	BACLD	065M56	bacillus l
292	36	56.2	122	2	05HXV6	GLUOX	05HXV6	gluconobact	365	36	56.2	495	2	06LS05	PHOPR	06LS05	photobacter
293	36	56.2	148	2	05HXV6	GLUOX	05HXV6	gluconobact	366	36	56.2	500	2	0836U1	TREPA	0836U1	treponema p
294	36	56.2	152	2	09ZVQ1	ARATH	09ZVQ1	arabidopsia	367	36	56.2	505	2	094KCB	MEBRANT	094KCB	meembryant
295	36	56.2	159	2	096GSO	HUMAN	096GSO	homo sapien	368	36	56.2	511	2	0522H3	MAGGR	0522H3	magnaporthe
296	36	56.2	161	1	IGRIA	CYPCA	090325	cyprinus ca	369	36	56.2	521	2	080QX5	YVIRU	080QX5	yuvirio rose
297	36	56.2	161	1	IGRIA	CYPCA	090325	cyprinus ca	370	36	56.2	522	2	08BDI3	SHEON	08BDI3	shewanella
298	36	56.2	161	1	IGRIA	CYPCA	090325	cyprinus ca	371	36	56.2	533	2	0869V1	DICDI	0869V1	dictyosteli
299	36	56.2	161	1	IGRIA	CYPCA	090325	cyprinus ca	372	36	56.2	543	2	09T5V9	PIG	09T5V9	pig scrofa
300	36	56.2	161	1	IGRIA	CYPCA	090325	cyprinus ca	373	36	56.2	558	2	07QXB8	ANOGA	07QXB8	anopheles g
301	36	56.2	161	1	IGRIA	CYPCA	090325	cyprinus ca	374	36	56.2	569	2	07L9B9	HUMAN	07L9B9	homo sapien
302	36	56.2	168	2	08VDC9	MOUSE	08VDC9	mouse musculu	375	36	56.2	569	2	09D7J3	MOUSE	09D7J3	mouse musculu
303	36	56.2	178	2	05BQH3	9TBLE	05BQH3	gymnocypria	376	36	56.2	569	2	08K3B5	MOUSE	08K3B5	mouse musculu
304	36	56.2	222	2	07P3X6	FUSNV	07P3X6	fusobacteri	377	36	56.2	569	2	05X174	RAT	05X174	rat mus musculu
305	36	56.2	238	2	05PPV3	XENLA	05PPV3	xenopus lae	378	36	56.2	573	2	09C0F7	HUMAN	09C0F7	homo sapien
306	36	56.2	239	2	05TAF9	BRUAB	05TAF9	bruceella ab	379	36	56.2	578	2	082B95	YERPE	082B95	yersinia pe
307	36	56.2	239	2	08FXZ3	BRUSU	08FXZ3	bruceella su	380	36	56.2	593	2	06SGW6	9BACT	06SGW6	uncultured
308	36	56.2	243	2	08YB53	BRUKE	08YB53	bruceella me	381	36	56.2	607	2	069ZC7	MOUSE	069ZC7	mouse musculu
309	36	56.2	244	2	04LM20	9BURK	04LM20	burholderi	382	36	56.2	620	2	059YK8	TRITH	059YK8	trichoderma
310	36	56.2	248	2	065ZC8	HUMAN	065ZC8	homo sapien	383	36	56.2	623	2	092VW7	ARATH	092VW7	arabidopsia
311	36	56.2	248	2	093706	DAUCUS	093706	daucus caro	384	36	56.2	624	2	05FYV9	TRICA	05FYV9	trypanosoma
312	36	56.2	248	2	042Z57	PSBSY	042Z57	pseudomona	385	36	56.2	643	1	SYT	HAEDU	SYT	haemophilus
313	36	56.2	249	2	0741G2	MYCPA	0741G2	mycobacteri	386	36	56.2	643	1	SYT	HAEDU	SYT	haemophilus
314	36	56.2	263	2	091PA6	RMV	091PA6	ribdriabs mo	387	36	56.2	643	1	SYT	MANSM	SYT	manheimia
315	36	56.2	264	1	MOVV	RMV	09qcl8	ribdriabs mo	388	36	56.2	643	1	SYT	PASMU	SYT	pasnm
316	36	56.2	265	1	MOVV	RMV	09qcl8	ribdriabs mo	389	36	56.2	643	1	SYT	PASMU	SYT	pasnm
317	36	56.2	271	2	08PYC8	METWA	08PYC8	methanosa	390	36	56.2	663	2	04QK77	HAETB	04QK77	haemophilus
318	36	56.2	277	2	048397	KLEBOX	048397	klebsiella	391	36	56.2	663	2	05LOA7	SILPO	05LOA7	silicibacte
319	36	56.2	289	2	09X114	THEMA	09X114	thermocoga	392	36	56.2	675	2	0461B5	DROSU	0461B5	drosophila
320	36	56.2	294	2	072DC5	DESYH	072DC5	desulfovibr	393	36	56.2	676	2	07N1F7	PHOLU	07N1F7	photorhabd
321	36	56.2	297	2	07VDS4	PROWA	07VDS4	prochloroco	394	36	56.2	681	2	05KEW5	CRAYNE	05KEW5	cryptococci
322	36	56.2	308	2	08GZ36	ARATH	08GZ36	arabidopsia	395	36	56.2	683	2	05B806	AZOSE	05B806	azotarcus sp
323	36	56.2	312	2	04XZN4	PLACH	04XZN4	plasmodium	396	36	56.2	684	2	05A658	CANAL	05A658	candida alb

397	36	56.2	686	2	OS5RA5	CRYNE	055ra5	cryptococcu	470	35	54.7	85	2	Q7X4L7	LEGN	Q7x4l7	legionella
398	36	56.2	688	2	OSMS85	DROME	08ms85	drosophila	471	35	54.7	85	2	Q7X4L8	LEGN	Q7x4l8	legionella
399	36	56.2	693	2	OSAI10	BACTN	08ai10	bacteroides	472	35	54.7	85	2	Q7X4L9	LEGN	Q7x4l9	legionella
400	36	56.2	704	2	OS3IO8	BURPS	063io8	burkholderi	473	35	54.7	86	2	Q6QF17	LEGN	Q6qf17	legionella
401	36	56.2	712	2	Q4LW7	9BURK	04lw7	burkholderi	474	35	54.7	86	2	Q6QF17	LEGN	Q6qf17	legionella
402	36	56.2	739	2	Q8XOP0	RALSO	08xop0	raistonia s	475	35	54.7	86	2	OS4658	LEGN	OS4658	legionella
403	36	56.2	769	2	Q8RGPI	FUSBN	08rgpi	fusobacteri	476	35	54.7	86	2	OSW299	LEGN	OSw299	legionella
404	36	56.2	781	2	Q6OYDK	CAE8R	06oydk	caenorhabdi	477	35	54.7	86	2	OSX7U8	LEGN	OSx7u8	legionella
405	36	56.2	781	2	Q4YT13	PIABE	04yt13	plasmidum	478	35	54.7	86	2	OSZYD1	LEGN	OSzyd1	legionella
406	36	56.2	786	2	Q7RQC3	PIAYO	07rqc3	plasmidum	479	35	54.7	91	2	OSDLJ1	9CALI	OSdlj1	norovirus h
407	36	56.2	798	2	Q6LXG0	PHOFR	06lxx0	photobacter	480	35	54.7	92	2	Q53IK1	3HEPC	Q53ik1	hepatitis c
408	36	56.2	857	2	Q6C116	YARLI	06c116	yarrowia li	481	35	54.7	96	2	Q4T5S4	TETNG	Q4t5s4	tetradon n
409	36	56.2	859	2	Q7XWB9	ORYSA	07xwb9	oryza sativ	482	35	54.7	105	2	Q4T1Z2	TETNG	Q4t1z2	tetradon n
410	36	56.2	870	2	Q8NE68	HUMAN	08ne68	homo sapien	483	35	54.7	127	1	CRCB	LEPIC	Q72v37	leptospira
411	36	56.2	886	2	Q4MOW6	9BURK	04mow6	burkholderi	484	35	54.7	127	1	CRCB	LEPIC	Q72v37	leptospira
412	36	56.2	892	2	Q7SCM9	NEUCR	07scm9	neurospora	485	35	54.7	131	2	Q4F5F0	9GNAM	Q4f5f0	psychobact
413	36	56.2	899	2	Q7O1Z6	ARXAD	07o1z6	arxula aden	486	35	54.7	137	2	Q84W04	ARATH	Q84w04	arabidops
414	36	56.2	901	2	Q5N9R6	ORYSA	05n9r6	oryza sativ	487	35	54.7	138	1	HV48	MOUSE	P03980	mus musculu
415	36	56.2	901	2	Q5MAH5	9BACT	05mah5	prevotella	488	35	54.7	139	2	Q6ZUE7	HUMAN	Q6zue7	homo sapien
416	36	56.2	903	1	GLR36	ARATH	084w41	arabidopsis	489	35	54.7	145	2	Q9S274	ARATH	Q9s274	arabidopsis
417	36	56.2	908	1	MGR8	MOUSE	P47743	mus musculu	490	35	54.7	153	2	Q8EFL3	3HEON	Q8efl3	shewanella
418	36	56.2	908	1	MGR8	PAR	P70579	rattus norv	491	35	54.7	161	2	Q4H2S1	GIBZE	Q4h2s1	zymomonas m
419	36	56.2	908	1	Q6B964	MOUSE	Q6b964	mus musculu	492	35	54.7	164	2	Q4H2S1	GIBZE	Q4h2s1	gibberella
420	36	56.2	916	2	Q580L5	9TRYP	Q580l5	trypanosoma	493	35	54.7	175	2	CRG1	XENLA	Q06254	xenopus lae
421	36	56.2	934	2	Q4HSZ6	CAMP	Q4hsz6	campylobact	494	35	54.7	175	2	Q66KJ7	XENLA	Q66kj7	xenopus lae
422	36	56.2	972	2	Q8PB01	XANCP	Q8pbq1	xanthomonas	495	35	54.7	175	2	Q6L1L5	XENLA	Q6l1l5	xenopus lae
423	36	56.2	973	2	Q7S9Q4	NEUCR	Q7s9q4	neurospora	496	35	54.7	175	2	Q6DER7	XENTR	Q6der7	xenopus tro
424	36	56.2	981	2	Q4MMV4	ASAPU	Q4mmv4	aspergillus	497	35	54.7	186	2	Q20769	CAEEL	Q20769	caenorhabdi
425	36	56.2	981	2	Q4SP98	TETNG	Q4sp98	tetradon n	498	35	54.7	189	2	Q6KR5	XENLA	Q6kr5	xenopus lae
426	36	56.2	983	2	Q7VUH9	BORPE	Q7vuh9	botdettella	499	35	54.7	196	2	Q8IWC8	HUMAN	Q8iwc8	homo sapien
427	36	56.2	998	2	Q5L857	BACFN	Q5l857	bacteroides	500	35	54.7	196	2	Q92PH8	PHIME	Q92ph8	rhizobium m
428	36	56.2	998	2	Q64ND8	BACFR	Q64nd8	bacteroides	501	35	54.7	204	2	Q9H7R2	HUMAN	Q9h7r2	homo sapien
429	36	56.2	1000	2	Q5ULI0	MAGRC	Q5uli0	magnaporthe	502	35	54.7	207	2	Q9NKH4	HUMAN	Q9nkh4	homo sapien
430	36	56.2	1002	2	Q4QJ13	LEIMA	Q4qj13	leishmania	503	35	54.7	215	2	Q5BHG6	EMENI	Q5bhg6	aspergillus
431	36	56.2	1016	2	Q6PKK4	XANAC	Q6pkk4	xanthomonas	504	35	54.7	234	2	Q5T3I1	HUMAN	Q5t3i1	homo sapien
432	36	56.2	1030	2	Q5BCB0	EMENI	Q5bcbo	aspergillus	505	35	54.7	239	2	Q8Z243	PYRAE	Q8z243	pyrobaculum
433	36	56.2	1032	2	Q4UVCI	XANCP	Q4uvci	xanthomonas	506	35	54.7	239	2	Q57ZL9	9TRYP	Q57zl9	trypanosoma
434	36	56.2	1032	2	Q8PB80	XANCP	Q8pb80	xanthomonas	507	35	54.7	241	2	Q9ANJ6	BRALU	Q9anj6	bradyrhizob
435	36	56.2	1051	2	Q4IT06	AZOVIT	Q4it06	azotobacter	508	35	54.7	255	2	Q92IA6	MOUSE	Q92ia6	mus musculu
436	36	56.2	1076	2	Q7YWM1	BORPE	Q7ywm1	botdettella	509	35	54.7	258	2	Q39957	HELAN	Q39957	helianthus
437	36	56.2	1076	2	Q7MH61	BORBR	Q7mh61	botdettella	510	35	54.7	258	2	Q5L075	GEOKA	Q5l075	geobacillus
438	36	56.2	1230	2	Q5B4F9	EMENI	Q5b4f9	aspergillus	511	35	54.7	257	2	Q5X1X3	LEGPA	Q5x1x3	legionella
439	36	56.2	1330	2	Q6NRS1	XENLA	Q6nrsl	xenopus lae	512	35	54.7	261	2	Q4SA27	TETNG	Q4sa27	tetradon n
440	36	56.2	1379	2	Q5B6C2	EMENI	Q5b6c2	aspergillus	513	35	54.7	261	2	Q6L1P5	DROME	Q6l1p5	drosophila
441	36	56.2	1430	2	Q4UAA1	THHAN	Q4uaa1	theileria a	514	35	54.7	272	2	Q6HB21	BACCH	Q6hb21	bacillus ce
442	36	56.2	1635	2	Q17412	AARDAR	Q17412	aedes aegypt	515	35	54.7	272	2	Q72XJ4	BACCH	Q72xj4	bacillus ce
443	36	56.2	2068	2	Q4W382	9RHAB	Q4w382	lettuce nec	516	35	54.7	276	2	Q881P0	PRESM	Q881p0	pseudomonas
444	36	56.2	2286	2	Q7PL80	DROME	Q7pl80	drosophila	517	35	54.7	281	2	Q5ALW8	CANAL	Q5alw8	candida alb
445	36	56.2	2408	2	Q67AN2	BRARE	Q67an2	brachydantio	518	35	54.7	285	2	Q7NJ53	GLOVI	Q7nj53	gloeobacter
446	36	56.2	2500	2	Q58XP5	BRARE	Q58xp5	brachydantio	519	35	54.7	285	2	Q4MHW2	ASAPU	Q4mhw2	aspergillus
447	36	56.2	2838	2	Q8MP05	TENMO	Q8mp05	tenebrio mo	520	35	54.7	286	2	Q37921	CORBE	Q37921	corynebacte
448	36	56.2	5141	2	Q7S6D3	NEUCR	Q7s6d3	neurospora	521	35	54.7	286	2	Q6NK23	CORDI	Q6nk23	corynebacte
449	35.5	55.5	209	2	Q86QF0	9CARA	Q86qf0	carabus pun	522	35	54.7	287	2	Q6OX38	CABBR	Q6ox38	caenorhabdi
450	35.5	55.5	209	2	Q86QF1	9CARA	Q86qf1	carabus lin	523	35	54.7	296	2	Q6PBC9	XENTR	Q6pbc9	xenopus tro
451	35.5	55.5	209	2	Q86QF2	9CARA	Q86qf2	carabus his	524	35	54.7	300	2	Q4IHP0	GIBBE	Q4ihp0	gibberella
452	35.5	55.5	209	2	Q86QF4	9CARA	Q86qf4	carabus aur	525	35	54.7	304	2	Q82N92	STRAM	Q82n92	streptomyce
453	35.5	55.5	216	2	Q06074	BACME	Q06074	baecillus me	526	35	54.7	310	2	Q5LJ64	BACFN	Q5lj64	bacteroides
454	35.5	55.5	340	2	Q7MG39	VIBBY	Q7mg39	vibriio vuln	527	35	54.7	312	2	Q5B6N9	EMENI	Q5b6n9	aspergillus
455	35.5	55.5	340	2	Q8D4K5	VIBVU	Q8d4k5	vibriio vuln	528	35	54.7	312	2	Q5S101	ARATH	Q5s101	arabidops
456	35.5	55.5	365	2	Q7UTZ8	RHOBA	Q7utz8	rhodospirell	529	35	54.7	314	2	Q5LBER	BACFN	Q5lber	bacteroides
457	35.5	55.5	387	2	Q5N5D2	SYNPF	Q5n5d2	synecococc	530	35	54.7	314	2	Q64VQ2	BACFN	Q64vq2	bacteroides
458	35.5	55.5	392	2	Q22899	CAEEL	Q22899	caenorhabdi	531	35	54.7	314	2	Q5OXE6	IDILLO	Q5oxe6	idionaria
459	35.5	55.5	401	2	Q8Y881	ANASBP	Q8y881	anabaena sp	532	35	54.7	317	2	Q4KUR1	METAN	Q4kur1	metarhizium
460	35.5	55.5	482	2	Q7Z351	MOBAN	Q7z351	homo sapien	533	35	54.7	317	2	Q4KUR2	METAN	Q4kur2	metarhizium
461	35.5	55.5	511	2	Q97G39	CIOAB	Q97g39	ciostriidum	534	35	54.7	317	2	Q4KUR3	METAN	Q4kur3	metarhizium
462	35.5	55.5	614	2	Q4S7B6	TETNG	Q4s7b6	tetradon n	535	35	54.7	317	2	Q5DFM3	SCHUA	Q5dfm3	schistosoma
463	35.5	55.5	638	2	Q9V819	DROME	Q9v819	drosophila s	536	35	54.7	328	2	Q4WDZ6	ASAPU	Q4wdz6	aspergillus
464	35.5	55.5	779	2	Q8XOF6	RALSO	Q8xof6	raistonia s	537	35	54.7	338	2	Q4KDV5	PSEPF	Q4kdv5	pseudomonas
465	35	54.7	53	2	Q7OR18	DROSI	Q7ork4	drosophila	538	35	54.7	339	2	Q5AEF7	CANAL	Q5aef7	candida alb
466	35	54.7	53	2	Q7OR18	DROSI	Q7ork4	drosophila	539	35	54.7	344	2	Q02575	DROLT	Q02575	drosophila
467	35	54.7	75	2	Q47926	9ACTO	Q47926	frankia sp.	540	35	54.7	346	2	Q93YQ2	ARATH	Q93yq2	arabidops
468	35	54.7	85	2	Q7WS80	LEGN	Q7ws80	legionella	541	35	54.7	348	2	Q7OK49	ANOGA	Q7ok49	anopheles g
469	35	54.7	85	2	Q7WSA1	LEGN	Q7wsa1	legionella	542	35	54.7	348	2	Q72V58	LEPIC	Q72v58	leptospira

543	35	54.7	348	2	QBEZQ0	LEPIN	QBEZQ0	leptospira	616	35	54.7	530	1	SRVA	DROME	P07666	dtrosophila
544	35	54.7	355	2	Q4LMT8	9BURK	Q4LMT8	burkholderi	617	35	54.7	531	2	OO1927	CAEBL	OO1927	caenorhabdi
545	35	54.7	356	2	Q8TMT4	METKA	Q8TMT4	methanopyru	618	35	54.7	539	2	Q9F106	FIBSU	Q9F106	fibrobacter
546	35	54.7	361	1	SERC	XANAC	Q8BY17	xanthomonas	619	35	54.7	541	2	Q55FP9	DICDI	Q55FP9	dictyosteli
547	35	54.7	361	1	SERC	XANOR	Q5H079	xanthomonas	620	35	54.7	541	2	Q8K225	MOUSE	Q8K225	mus musculu
548	35	54.7	361	1	Q94GQ3	ORYSA	Q94GQ3	oryza sativ	621	35	54.7	546	2	Q8X1X6	CLOPE	Q8X1X6	clostridium
549	35	54.7	361	2	Q9FKR0	ARATH	Q9FKR0	arabidopsis	622	35	54.7	547	2	Q52PNT	9CAUD	Q52PNT	xanthomonas
550	35	54.7	370	2	Q5TJ10	HUMAN	Q5TJ10	homo sapien	623	35	54.7	560	2	Q560Y5	CRYNE	Q560Y5	cryptococcu
551	35	54.7	370	2	Q9WYB1	THEMA	Q9WYB1	thermocoga	624	35	54.7	561	2	Q5KPY6	CRYNE	Q5KPY6	cryptococcu
552	35	54.7	376	2	Q94516	SCHEP	Q94516	schizosacch	625	35	54.7	562	1	TR2M	PANAY	Q541P9	dictyosteli
553	35	54.7	380	2	Q7T140	BRARE	Q7T140	brachydantio	626	35	54.7	564	2	Q541P9	DICDI	Q541P9	dictyosteli
554	35	54.7	383	1	YUKR	YEAST	Q42946	saccharomyc	627	35	54.7	568	2	Q3HBX5	HUMAN	Q3HBX5	homo sapien
555	35	54.7	383	2	Q6Q5N7	YEAST	Q6Q5N7	saccharomyc	628	35	54.7	568	2	Q53G59	HUMAN	Q53G59	homo sapien
556	35	54.7	389	2	Q6BFI6	PARTTE	Q6BFI6	paramecium	629	35	54.7	568	2	Q8B2M0	MOUSE	Q8B2M0	mus musculu
557	35	54.7	394	2	Q6FXB4	CANGA	Q6FXB4	candida gla	630	35	54.7	568	2	Q8R2H4	RAT	Q8R2H4	rattus norv
558	35	54.7	406	2	Q4MKV0	ASPFU	Q4MKV0	aspergillus	631	35	54.7	577	2	Q5YXU8	ORYSA	Q5YXU8	oryza sativ
559	35	54.7	409	2	Q86K12	DICDI	Q86K12	dictyosteli	632	35	54.7	585	2	Q41549	GIBZE	Q41549	gibberella
560	35	54.7	409	2	Q8A398	BACTN	Q8A398	bacteroides	633	35	54.7	586	2	Q4V9V8	MOUSE	Q4V9V8	mus musculu
561	35	54.7	409	2	Q7U231	MYCBO	Q7U231	mycobacteri	634	35	54.7	590	2	Q79097	ALLMI	Q79097	alligator m
562	35	54.7	409	2	P95207	MYCTU	P95207	mycobacteri	635	35	54.7	603	2	Q33790	ALLMI	Q33790	alligator m
563	35	54.7	411	2	Q7OSH7	GIATA	Q7OSH7	giardia lam	636	35	54.7	608	2	Q7UZ43	RHOBA	Q7UZ43	rhodospirell
564	35	54.7	415	2	Q50ZHO	ENTHI	Q50ZHO	entamoeba h	637	35	54.7	610	2	Q50W42	ENTHI	Q50W42	entamoeba h
565	35	54.7	417	2	Q67YU7	ARATH	Q67YU7	arabidopsis	638	35	54.7	613	2	Q8WCX7	MOUSE	Q8WCX7	mus musculu
566	35	54.7	420	2	Q4QG23	LEIMA	Q4QG23	leishmania	639	35	54.7	613	2	Q93R69	PMICO	Q93R69	microbacter
567	35	54.7	423	2	Q14456	METAN	Q14456	metarhizium	640	35	54.7	620	2	Q5HY00	GLUOX	Q5HY00	glucobacter
568	35	54.7	424	2	Q9Y841	9HYPO	Q9Y841	metarhizium	641	35	54.7	620	2	Q5HY00	GLUOX	Q5HY00	glucobacter
569	35	54.7	424	2	Q4UAM9	METAN	Q4UAM9	metarhizium	642	35	54.7	630	2	V70K	PURV	V70K	purv
570	35	54.7	427	2	Q9CAX1	ARATH	Q9CAX1	arabidopsis	643	35	54.7	639	1	V70K	PURV	V70K	purv
571	35	54.7	428	2	Q5AR60	EMENI	Q5AR60	aspergillus	644	35	54.7	639	1	V70K	PURV	V70K	purv
572	35	54.7	430	2	Q6C8R8	YARLI	Q6C8R8	yarrowia li	645	35	54.7	639	1	V70K	PURV	V70K	purv
573	35	54.7	430	2	Q57X89	9TRYP	Q57X89	trypanosoma	646	35	54.7	639	2	Q8QYNI	PURV	Q8QYNI	purv
574	35	54.7	430	2	Q5SL50	THEB8	Q5SL50	thermus the	647	35	54.7	639	2	Q8QYNI	PURV	Q8QYNI	purv
575	35	54.7	430	2	Q72L14	THEB2	Q72L14	thermus the	648	35	54.7	639	2	Q8QYNI	PURV	Q8QYNI	purv
576	35	54.7	436	2	Q6AK99	DESPS	Q6AK99	desulfotale	649	35	54.7	639	2	Q8QYNI	PURV	Q8QYNI	purv
577	35	54.7	436	1	VE2	HPV22	VE2	human papil	650	35	54.7	639	2	Q8QYNI	PURV	Q8QYNI	purv
578	35	54.7	440	2	Q80W26	MOUSE	Q80W26	mus musculu	651	35	54.7	639	2	Q8QYNI	PURV	Q8QYNI	purv
579	35	54.7	446	2	Q6P6P2	HUMAN	Q6P6P2	homo sapien	652	35	54.7	639	2	Q8QYNI	PURV	Q8QYNI	purv
580	35	54.7	446	2	Q61KZ7	CABBR	Q61KZ7	caenorhabdi	653	35	54.7	639	2	Q8QYNI	PURV	Q8QYNI	purv
581	35	54.7	447	1	HST3	YEA8T	HST3	saccharomyc	654	35	54.7	654	2	Q4TKB3	ERYPHN	Q4TKB3	erythrobact
582	35	54.7	447	2	Q6ER16	YEAST	Q6ER16	saccharomyc	655	35	54.7	654	2	Q4TKB3	ERYPHN	Q4TKB3	erythrobact
583	35	54.7	448	2	Q9W648	FUGRU	Q9W648	fugu rubrip	656	35	54.7	657	2	Q8LH44	ORYSA	Q8LH44	oryza sativ
584	35	54.7	450	1	CIMH	BACSU	P94363	bacillus su	657	35	54.7	657	2	Q8LH44	ORYSA	Q8LH44	oryza sativ
585	35	54.7	451	2	Q4L1Z7	9BURK	Q4L1Z7	burkholderi	658	35	54.7	661	2	Q6ZNC5	HUMAN	Q6ZNC5	homo sapien
586	35	54.7	451	2	Q4SRS1	TEING	Q4SRS1	tetradodon n	659	35	54.7	705	2	Q50PPE	ENTHI	Q50PPE	entamoeba h
587	35	54.7	454	2	Q6Y2Y8	9ARPA	Q6Y2Y8	huanaqa sac	660	35	54.7	710	2	Q4Q5P3	LEIMA	Q4Q5P3	leishmania
588	35	54.7	455	2	Q9LMB1	ARATH	Q9LMB1	arabidopsis	661	35	54.7	718	2	Q8Y1B6	PURV	Q8Y1B6	purv
589	35	54.7	464	2	Q5BPJ0	ARATH	Q5BPJ0	arabidopsis	662	35	54.7	721	2	Q8Y1B6	PURV	Q8Y1B6	purv
590	35	54.7	465	2	Q6UY53	MOUSE	Q6UY53	mus musculu	663	35	54.7	724	2	Q6Z4D2	ORYSA	Q6Z4D2	oryza sativ
591	35	54.7	467	2	Q4VBH1	RAT	Q4VBH1	rattus norv	664	35	54.7	749	2	Q82C96	STRAM	Q82C96	streptomyc
592	35	54.7	468	2	Q6D9P1	BRMCT	Q6D9P1	erwinia car	665	35	54.7	763	2	Q82C96	STRAM	Q82C96	streptomyc
593	35	54.7	469	2	Q9LDG2	ARATH	Q9LDG2	arabidopsis	666	35	54.7	763	2	Q82C96	STRAM	Q82C96	streptomyc
594	35	54.7	470	2	Q4QJ74	LEIMA	Q4QJ74	leishmania	667	35	54.7	764	2	Q8Y1B6	PURV	Q8Y1B6	purv
595	35	54.7	473	2	Q6P055	HUMAN	Q6P055	homo sapien	668	35	54.7	779	2	Q5B822	EMENI	Q5B822	emmeni
596	35	54.7	473	2	Q9DB14	MOUSE	Q9DB14	mus musculu	669	35	54.7	798	2	Q5LJL5	BACFN	Q5LJL5	bacteroides
597	35	54.7	475	2	Q5PQ81	RAT	Q5PQ81	rattus norv	670	35	54.7	803	2	Q64UN7	BACFN	Q64UN7	bacteroides
598	35	54.7	476	1	Y099	CAEBL	P41649	caenorhabdi	671	35	54.7	803	2	Q64UN7	BACFN	Q64UN7	bacteroides
599	35	54.7	483	2	Q4VAB6	MOUSE	Q4VAB6	mus musculu	672	35	54.7	863	2	Q6D5N8	BRMCT	Q6D5N8	erwinia car
600	35	54.7	484	2	Q4S0T9	TEING	Q4S0T9	tetradodon n	673	35	54.7	870	2	Q6D5N8	BRMCT	Q6D5N8	erwinia car
601	35	54.7	491	2	Q8TEK5	HUMAN	Q8TEK5	homo sapien	674	35	54.7	871	2	Q6KAO8	MOUSE	Q6KAO8	mouse
602	35	54.7	492	2	P91725	DROYA	P91725	dtrosophila	675	35	54.7	888	2	Q8A5C3	BACTN	Q8A5C3	bactn
603	35	54.7	493	2	Q6B1Q7	DEBHA	Q6B1Q7	debaromyce	676	35	54.7	908	2	Q6J165	HUMAN	Q6J165	homo sapien
604	35	54.7	494	2	P91653	DROMA	P91653	dtrosophila	677	35	54.7	908	2	Q6J165	HUMAN	Q6J165	homo sapien
605	35	54.7	495	2	Q23156	ARATH	Q23156	arabidopsis	678	35	54.7	932	2	Q6O126	MOUSE	Q6O126	mouse
606	35	54.7	497	2	P91708	DROSE	P91708	dtrosophila	679	35	54.7	938	2	Q6O126	MOUSE	Q6O126	mouse
607	35	54.7	498	2	P91690	DROOR	P91690	dtrosophila	680	35	54.7	952	2	Q8K468	MOUSE	Q8K468	mouse
608	35	54.7	498	2	Q9DGO0	XENIA	Q9DGO0	xenopus lae	681	35	54.7	953	2	Q6O127	SWYTH	Q6O127	syndyobacte
609	35	54.7	498	2	Q5XG13	XENIA	Q5XG13	xenopus lae	682	35	54.7	977	1	ZNF31	HUMAN	ZNF31	human
610	35	54.7	506	2	Q5AEU3	CANAL	Q5AEU3	candida alb	683	35	54.7	977	1	ZNF31	HUMAN	ZNF31	human
611	35	54.7	506	2	Q59SR2	CANAL	Q59SR2	candida alb	684	35	54.7	977	1	ZNF31	HUMAN	ZNF31	human
612	35	54.7	506	2	Q8YVB4	ANASP	Q8YVB4	anaeabada ep	685	35	54.7	1035	2	Q4PAX3	USTMA	Q4PAX3	ustilago ma
613	35	54.7	524	2	Q82169	STRAM	Q82169	streptomyc	686	35	54.7	1043	2	Q6ZNI3	HUMAN	Q6ZNI3	human
614	35	54.7	529	2	Q5R168	BRARE	Q5R168	brachydantio	687	35	54.7	1050	2	Q89UAI	BRAJA	Q89UAI	bradyrhizob
615	35	54.7	529	2	Q5R168	BRARE	Q5R168	brachydantio	688	35	54.7	1050	2	Q89UAI	BRAJA	Q89UAI	bradyrhizob

689	35	54.7	1065	2	O9LG15_ORYSA	O9LG15_oryza sativ	762	34	53.1	234	2	O5PMF2_SALPA	O5PMF2_salmonella
690	35	54.7	1171	2	O4RLR5_TERTNG	O4RLR5_tetradon n	763	34	53.1	235	2	O7UPF3_RHOBA	O7UPF3_rhodopirell
691	35	54.7	1379	2	O54MT3_DICDI	O54mt3 dictyosteli	764	34	53.1	237	2	O82PB0_STRAW	O82PB0_streptococc
692	35	54.7	1465	2	O4SB89_TERTNG	O4sb89 tetradon n	765	34	53.1	241	1	6RGL_TREPA	O83490_treponema p
693	35	54.7	1579	2	O9BH56_CABEL	O9bh56 caenorhabdi	766	34	53.1	248	2	O8UUA3_AGRTS	O8UUA3_agrobacteri
694	35	54.7	1608	2	O4SH88_TERTNG	O4sh88 tetradon n	767	34	53.1	249	2	O9LKK3_HORVU	O9LKK3_hordeum vul
695	35	54.7	2078	2	O4Z380_PLABA	O4z380 plasmodium	768	34	53.1	251	2	O82MW3_NITEU	O82MW3_nitrosomona
696	35	54.7	2139	2	O88Y66_LACPL	O88y66 lactobacilli	769	34	53.1	251	2	O89KV8_BRAYU	O89KV8_bradyrhizob
697	35	54.7	2156	2	O7R036_PLAYO	O7r036 plasmodium	770	34	53.1	251	2	O7W0E8_BORBR	O7W0E8_bordetella
698	35	54.7	2352	2	O61240_HALRO	O61240 halocynthia	771	34	53.1	253	2	O567H6_BRARE	O567H6_brachydantio
699	35	54.7	2482	2	O61G60_CABBR	O61g60 caenorhabdi	772	34	53.1	261	2	O9HOK8_TALSA	O9HOK8_halobacteri
700	35	54.7	2566	2	O8TSE7_METAC	O8tse7 methanobarc	773	34	53.1	263	2	O9RYG2_DEIRA	O9RYG2_deinococcus
701	35	54.7	3202	2	O6PYM6_BCMVN	O6pym6 blackeaye co	774	34	53.1	265	2	O9U4Z8_MANSE	O9U4Z8_manduca sex
702	35	54.7	3222	2	O85057_BCMVN	O85057 peanut scri	775	34	53.1	270	2	O9H1W8_THIAC	O9H1W8_thioplasm
703	35	54.7	3222	2	O85071_BCMVN	O85071 peanut scri	776	34	53.1	270	2	O7W022_BORPE	O7W022_bordetella
704	34.5	53.9	209	2	O9MHT0_9CARA	O9mht0 carabus deh	777	34	53.1	270	2	O7WC82_BORPA	O7WC82_bordetella
705	34.5	53.9	344	2	O83B45_COXBU	O83b45 coxiella bu	778	34	53.1	272	2	O8PYU8_BRUSU	O8PYU8_brucella su
706	34.5	53.9	346	2	O6MQ87_BDEBA	O6mq87 bdeilovibri	779	34	53.1	272	2	O8Y1Z7_BRUME	O8Y1Z7_brucella me
707	34.5	53.9	370	2	O16719_CAEHL	O16719 caenorhabdi	780	34	53.1	274	2	O8R8B3_THIETN	O8R8B3_thiomanar
708	34.5	53.9	375	2	O91YR3_MOUSE	O91yr3 mus musculu	781	34	53.1	280	2	O5BGN1_EMENTI	O5BGN1_aspergillus
709	34.5	53.9	481	2	O4WQW3_ASPFU	O4wqw3 aspergillus	782	34	53.1	281	2	O68076_RHOCA	O68076_rhodobacter
710	34.5	53.9	487	2	O9N548_CABEL	O9n548 caenorhabdi	783	34	53.1	289	2	O75T28_DSIOC	O75T28_pseudomonas
711	34.5	53.9	520	2	O4LHRO_9BORK	O4lhr0 burkholderi	784	34	53.1	289	2	O8RNX9_COMTE	O8RNX9_comamonas t
712	34.5	53.9	671	2	O98DL4_RAILO	O98dl4 rhizobium i	785	34	53.1	289	2	O93P85_COMTE	O93P85_comamonas t
713	34.5	53.9	1143	2	O5TZX0_BRARE	O5tzh0 brachydanio	786	34	53.1	294	2	O526W7_MAGGR	O526W7_magnaporthe
714	34	53.1	77	2	O99QO0_STRCC	O99qo0 streptomyces	787	34	53.1	297	2	O7PYO8_ANOGA	O7PYO8_anopheles g
715	34	53.1	84	2	O72923_9HEPC	O72923 hepatitis c	788	34	53.1	298	2	O762F6_RHORG	O762F6_rhodococcus
716	34	53.1	84	2	O72924_9HEPC	O72924 hepatitis c	789	34	53.1	302	1	Y1375_HAVIN	P44169_haemophilus
717	34	53.1	84	2	O72925_9HEPC	O72925 hepatitis c	790	34	53.1	302	2	O57BD1_BRUAB	O57BD1_brucella ab
718	34	53.1	85	2	O6E8N8_LEGMI	O6e8n8 legionella	791	34	53.1	302	2	O4QK87_HAE18	O4QK87_haemophilus
719	34	53.1	86	2	O8WMP9_PIG	O8wmf9 sus scrofa	792	34	53.1	308	2	O7RUT2_HUMAN	O7RUT2_homo sapien
720	34	53.1	89	2	O9XK07_VIBCH	O9xk07 vibrio chol	793	34	53.1	312	2	O60X80_CAEBR	O60X80_caenorhabdi
721	34	53.1	124	2	O5H318_XANOR	O5h318 xanthomonas	794	34	53.1	314	2	O9DA78_MOUSE	O9DA78_mus musculu
722	34	53.1	126	2	O9LO18_ARATH	O9l018 arabidopsis	795	34	53.1	315	2	O8M9U2_CHAGL	O8M9U2_chlamydomon
723	34	53.1	127	2	O5UTM5_9CAUD	O5utms lactobacilli	796	34	53.1	317	2	O6HG36_BACHK	O6HG36_bacillus th
724	34	53.1	128	1	O8XTU0_RALSO	O8xtu0 ralstonia s	797	34	53.1	317	2	O8IMT3_BACAN	O8IMT3_bacillus an
725	34	53.1	128	1	AZUR_ALCPA	AZUR281 alcaligenes	798	34	53.1	317	2	O638U4_BACC2	O638U4_bacillus ce
726	34	53.1	129	1	AZUR2_ALCPA	AZUR281 alcaligenes	799	34	53.1	320	2	O9XDT2_9BACI	O9XDT2_bacillus sp
727	34	53.1	129	1	O977C8_SUITCO	P56275 sulfolobus	800	34	53.1	320	2	O81B18_BACRC	O81B18_bacillus ce
728	34	53.1	131	2	O6LX75_METMP	O6lx75 methanococc	801	34	53.1	320	2	O5FU46_GLUOX	O5FU46_glucosinolat
729	34	53.1	135	2	O5LDT6_BACFN	O5ldt6 bacteroides	802	34	53.1	322	2	O98TB6_ONCKE	O98TB6_oncortophicu
730	34	53.1	137	2	O8GWT5_ARATH	O8gwt5 arabidopsis	803	34	53.1	323	1	O8SO_SALSA	O8SO_salmo balat
731	34	53.1	139	2	O572E3_PHYIN	O572e3 phytophthor	804	34	53.1	323	2	O4ICR4_GIBZE	O4ICR4_gibberella
732	34	53.1	142	1	HV01_RAT	P01805 rattus norv	805	34	53.1	325	2	O9XKY8_AGRAR	O9XKY8_agricolpe ae
733	34	53.1	145	2	O9ZAT4_ACIBA	O9zat4 acinetobact	806	34	53.1	327	2	O7N3Y5_PHOLL	O7N3Y5_photobactdu
734	34	53.1	145	2	O7WYD9_ACIBA	O7wyd9 acinetobact	807	34	53.1	329	1	PDXAL_SATRY	P58713_salmonella
735	34	53.1	146	2	O9ZRF61_ACICA	O9zf61 acinetobact	808	34	53.1	329	2	O57TG3_SALCH	O57TG3_salmonella
736	34	53.1	146	2	O6FDQ2_ACICAD	O6fdq2 acinetobact	809	34	53.1	338	2	O5EN96_9BACT	O5EN96_uncultured
737	34	53.1	149	1	AZUR_ALCPA	P00280 alcaligenes	810	34	53.1	339	2	O989A6_RHILO	O989A6_rhizobium i
738	34	53.1	149	2	O4UYA9_XANCP	O4uya9 xanthomonas	811	34	53.1	340	2	O8RVB8_CHLRE	O8RVB8_chlamydomon
739	34	53.1	149	2	O8P5R2_XANCP	O8p5r2 xanthomonas	812	34	53.1	340	2	O8H2C1_CHLRE	O8H2C1_chlamydomon
740	34	53.1	149	2	O8PH38_XANAC	O8ph38 xanthomonas	813	34	53.1	340	2	O8H762_CHLRE	O8H762_chlamydomon
741	34	53.1	150	2	O8TGB8_VIBPA	O8tgb8 vibrio para	814	34	53.1	340	2	O6EBV5_YERPS	O6EBV5_yersinia ps
742	34	53.1	151	2	O9PFTV0_XYLFA	O9pftv0 xyella fas	815	34	53.1	342	2	O6TWE7_ORYSA	O6TWE7_oryza sativ
743	34	53.1	151	2	O87B74_XYLFT	O87b74 xyella fas	816	34	53.1	343	2	O9V190_PYPAB	O9V190_pyrococcus
744	34	53.1	159	2	O5H5B2_XANOR	O5h5b2 xanthomonas	817	34	53.1	343	2	O86GU6_CAEEL	O86GU6_caenorhabdi
745	34	53.1	174	2	O6ANZ9_DSPPS	O6anz9 denulfolate	818	34	53.1	346	2	O59293_PYRHO	O59293_pyrococcus
746	34	53.1	189	2	O6VZG3_CNPFV	O6vzg3 canarypox v	819	34	53.1	354	2	O5UJC2_PYRKO	O5UJC2_pyrococcus
747	34	53.1	190	2	O9V591_FOWPV	O9v591 fowlpox vir	820	34	53.1	354	2	O5IMN5_MAGGR	O5IMN5_magnaporthe
748	34	53.1	193	1	O7OHI5_FOWPV	O7ohi5 fowlpox vir	821	34	53.1	357	2	O5LXO9_STLPO	O5LXO9_silicibacte
749	34	53.1	193	1	PGRP_CAMDR	O9gk12 camelus dfo	822	34	53.1	358	2	O5ENAI_9BACT	O5ENAI_uncultured
750	34	53.1	194	2	O6PKY6_PIG	O6pkv6 sus scrofa	823	34	53.1	362	1	SERC_XYLFA	SERC_xyella fas
751	34	53.1	198	2	O5ASR5_EMENTI	O5asr5 aspergillus	824	34	53.1	362	1	SERC_XYLFA	SERC_xyella fas
752	34	53.1	202	2	O6AL51_DSPPS	O6al51 denulfolate	825	34	53.1	363	2	O7XV00_ORYSA	O7XV00_oryza sativ
753	34	53.1	202	2	O7N6Z6_PHOLA	O7n6z6 photorhabdu	826	34	53.1	365	2	O8AAU2_BACTN	O8AAU2_bacteroides
754	34	53.1	203	2	O5DAP3_SCHJA	O5dap3 schistosoma	827	34	53.1	366	2	O9W6B4_9SAUR	O9W6B4_plethsuma ma
755	34	53.1	222	2	O6UTZ8_ORNHU	O6utz8 ornithiocton	828	34	53.1	371	2	O661I2_BORGA	O661I2_borrelia ga
756	34	53.1	223	2	O6ZUL3_HUMAN	O6zul3 homo sapien	829	34	53.1	374	2	O9XO50_THIEMA	O9XO50_thiemoega
757	34	53.1	225	2	O6O5X3_METCA	O6o5x3 methylococc	830	34	53.1	382	2	O4SDX9_TERTNG	O4SDX9_tetradon n
758	34	53.1	228	2	O4NIV4_9MICA	O4niv4 arthrobacte	831	34	53.1	383	2	O8ERB5_OCEIH	O8ERB5_oceanobacil
759	34	53.1	228	2	O8YDV5_BRUME	O8ydv5 brucella me	832	34	53.1	386	1	GALL_VIBU	O8bhn9_vibrio vuln
760	34	53.1	232	2	O8LPV1_DSANCA	O8lpv1 deschampsia	833	34	53.1	386	2	O4WUZO_ASPFU	O4WUZO_aspergillus
761	34	53.1	232	2	O4MW37_BACCE	O4mw37 bacillus ce	834	34	53.1	392	2	O5YXJ7_NOCFA	O5YXJ7_nocardia fa

835	34	53.1	394	2	Q740A3 MYCPA	Q740a3 mycobacteri	908	34	53.1	598	2	Q5WKC0_BACSK	Q5wkc0 bacillus ci
836	34	53.1	405	2	Q4PIH1_USMTA	Q4phi1 usfilago ma	909	34	53.1	599	2	Q9KED7_BACHD	Q9ked7 bacillus ha
837	34	53.1	410	2	Q9PW33_TYRNA	Q9pw33 typhloeco	910	34	53.1	600	2	Q53521_MYCTU	Q53521 mycobacteri
838	34	53.1	413	1	CSD_STIAM	P63518 staphylococ	911	34	53.1	603	2	Q7D7D8_MYCTU	Q7d7d8 mycobacteri
839	34	53.1	413	1	CSD_STIAM	P99177 staphylococ	912	34	53.1	603	2	Q7WNA3_BORPA	Q7wna3 bordetella
840	34	53.1	413	1	CSD_STIAM	P69177 staphylococ	913	34	53.1	603	2	Q8HG39_ALLST	Q8hg39 alligator b
841	34	53.1	413	1	CSD_STIAM	P69177 staphylococ	914	34	53.1	605	2	Q9AH41_NEICI	Q9ah41 neisseria c
842	34	53.1	413	1	CSD_STIAM	P69177 staphylococ	915	34	53.1	605	2	Q7WJ16_BORBR	Q7wj16 bordetella
843	34	53.1	413	1	CSD_STIAM	P69177 staphylococ	916	34	53.1	607	1	Q96G18_RHIL0	Q96g18 rhizobium l
844	34	53.1	413	1	Q5HQ00_STAEQ	Q5hq00 staphylococ	917	34	53.1	608	2	Q96G18_RHIL0	Q96g18 streptococc
845	34	53.1	413	2	Q5HHH0_STIAC	Q5hhh0 staphylococ	918	34	53.1	614	2	Q9AHT8_STRPN	Q9aht8 streptococc
846	34	53.1	417	2	Q5NXL6_AZOSE	Q5nxl6 azaracus sp	919	34	53.1	614	2	Q4W123_STRPN	Q4w123 streptococ
847	34	53.1	417	2	Q93H89_STIAM	Q93h89 streptomyc	920	34	53.1	614	2	Q4W123_STRPN	Q4w123 streptococ
848	34	53.1	418	2	Q9KAS5_VIBCH	Q9kas5 vibrio chol	921	34	53.1	615	2	Q4W126_STRPN	Q4w126 streptococ
849	34	53.1	419	2	Q9CTA3_VIBCH	Q9cta3 lactococcus	922	34	53.1	615	2	Q5XIO6_RAT	Q5xio6 rat
850	34	53.1	421	2	Q9CAP2_ARATH	Q9cap2 arabidopsis	923	34	53.1	620	1	Q9WNA3_BORPE	Q9wna3 bordetella
851	34	53.1	423	2	Q5MNU1_VERLE	Q5mnu1 verticilliu	924	34	53.1	620	1	Q9WNA3_BORPE	Q9wna3 bordetella
852	34	53.1	423	2	Q5MNU2_VERLE	Q5mnu2 verticilliu	925	34	53.1	625	1	Q9WNA3_BORPE	Q9wna3 bordetella
853	34	53.1	425	2	Q88VK0_LACPL	Q88vk0 lactobacill	926	34	53.1	627	2	Q7XPO0_ORYSA	Q7xpo0 oryza sativ
854	34	53.1	427	2	Q5ARN1_DICDI	Q5arn1 dictyosteli	927	34	53.1	630	2	Q7P5J7_FUSNV	Q7p5j7 fusobacteri
855	34	53.1	427	2	Q7WYN8_CHRYO	Q7wyn8 chromobact	928	34	53.1	640	2	Q5NM84_AZOSE	Q5nm84 azaracus sp
856	34	53.1	438	2	Q5TINO_MEDTR	Q5tino medicago tr	929	34	53.1	642	1	Q9WNA3_BORPE	Q9wna3 bordetella
857	34	53.1	438	2	Q9SSA9_ARATH	Q9ssa9 arabidopsis	930	34	53.1	642	1	Q9WNA3_BORPE	Q9wna3 bordetella
858	34	53.1	441	2	Q73RR9_TREDE	Q73rr9 treponema d	931	34	53.1	645	2	Q8IH08_PLAF7	Q8ih08 plasmodium
859	34	53.1	442	2	Q6DBE3_ARATH	Q6dbe3 arabidopsis	932	34	53.1	645	2	Q9S9N1_ARATH	Q9s9n1 arabidopsi
860	34	53.1	442	2	Q9CKS9_PASMU	Q9cks9 pasteurella	933	34	53.1	646	2	Q5IIP7_MAGGR	Q5iip7 magnetarthe
861	34	53.1	444	2	Q4WDL5_ASPFU	Q4wdl5 aspergillus	934	34	53.1	653	2	Q5IIP7_MAGGR	Q5iip7 magnetarthe
862	34	53.1	444	2	Q6SMN7_BACLD	Q6smn7 bacillus li	935	34	53.1	658	1	LYTB_STRPN	Q4W126_STRPN
863	34	53.1	445	2	Q7VQ09_CHLPH	Q7vq09 chlamydia p	936	34	53.1	658	2	Q4W126_STRPN	Q4w126 streptococ
864	34	53.1	445	2	Q9RB67_CHLPH	Q9rb67 chlamydia p	937	34	53.1	658	2	Q4W126_STRPN	Q4w126 streptococ
865	34	53.1	446	2	Q9S115_STRPN	Q9s115 streptococ	938	34	53.1	664	2	Q5A285_EMENT	Q5a285 aspergillus
866	34	53.1	447	2	Q8BU78_OCEBH	Q8bu78 oceanobacil	939	34	53.1	669	2	Q5A285_EMENT	Q5a285 aspergillus
867	34	53.1	450	2	Q5SSU3_CRYNE	Q5ssu3 cryptococcu	940	34	53.1	676	1	Q9WNA3_BORPE	Q9wna3 bordetella
868	34	53.1	450	2	Q5KH78_CRYNE	Q5kh78 cryptococcu	941	34	53.1	688	2	Q9WNA3_BORPE	Q9wna3 bordetella
869	34	53.1	451	2	Q5O652_PARHA	Q5o652 paracoccus	942	34	53.1	692	2	Q6D733_ERWCT	Q6d733 erwinia car
870	34	53.1	454	1	Q9KEG6_BACHD	Q9keg6 bacillus ha	943	34	53.1	692	2	Q8X5J2_ECOS7	Q8x5j2 escherichia
871	34	53.1	454	1	Q9KEG6_BACHD	Q9keg6 bacillus ha	944	34	53.1	697	2	Q741W7_MYCPA	Q741w7 mycobacteri
872	34	53.1	456	2	Q4PIH2_USMTA	Q4phi2 usfilago ma	945	34	53.1	700	2	Q9KLO6_VIBCH	Q9klo6 vibrio chol
873	34	53.1	461	1	Q9KLO6_VIBCH	Q9klo6 vibrio chol	946	34	53.1	702	1	LYTB_STR6	Q9KLO6_VIBCH
874	34	53.1	467	2	Q7SD34_NEUCR	Q7sd34 neurospora	947	34	53.1	702	2	Q4W122_STRPN	Q4w122 streptococ
875	34	53.1	470	1	Q5Y7A58_BRUBA	Q5y7a58 brucella ab	948	34	53.1	702	2	Q4W122_STRPN	Q4w122 streptococ
876	34	53.1	471	2	Q8FXP1_BRUSU	Q8fxp1 brucella su	949	34	53.1	702	2	Q4W122_STRPN	Q4w122 streptococ
877	34	53.1	481	2	Q7S7L7_NEUCR	Q7s7l7 neurospora	950	34	53.1	705	2	Q6H798_ORYSA	Q6h798 oryza sativ
878	34	53.1	484	2	Q4W976_ASPFU	Q4w976 aspergillus	951	34	53.1	705	2	Q8BU78_OCEBH	Q8bu78 oceanobacil
879	34	53.1	484	2	Q6STY3_BACNM	Q6sty3 mannheimia	952	34	53.1	726	2	Q8BDW8_SHRON	Q8bdw8 streptococ
880	34	53.1	486	2	Q6STY3_BACNM	Q6sty3 mannheimia	953	34	53.1	733	2	Q9UG70_VYIRU	Q9ug70 varicella
881	34	53.1	488	2	Q4MXX3_BACCN	Q4mxx3 bacillus ce	954	34	53.1	733	2	Q9UG70_VYIRU	Q9ug70 varicella
882	34	53.1	488	2	Q8IMU8_BACCN	Q8imu8 bacillus ce	955	34	53.1	733	2	Q9UG70_VYIRU	Q9ug70 varicella
883	34	53.1	497	2	Q6HGM5_BACHK	Q6hgm5 bacillus th	956	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
884	34	53.1	499	2	Q6HGM5_BACHK	Q6hgm5 bacillus th	957	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
885	34	53.1	499	2	Q6HGM5_BACHK	Q6hgm5 bacillus th	958	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
886	34	53.1	500	2	Q6HGM5_BACHK	Q6hgm5 bacillus th	959	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
887	34	53.1	500	2	Q6HGM5_BACHK	Q6hgm5 bacillus th	960	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
888	34	53.1	504	2	Q5ARL5_EMENT	Q5arl5 aspergillus	961	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
889	34	53.1	506	2	Q73801_FUGUR	Q73801 fuqu rbrirp	962	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
890	34	53.1	508	2	Q73801_FUGUR	Q73801 fuqu rbrirp	963	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
891	34	53.1	508	2	Q73801_FUGUR	Q73801 fuqu rbrirp	964	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
892	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	965	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
893	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	966	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
894	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	967	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
895	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	968	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
896	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	969	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
897	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	970	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
898	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	971	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
899	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	972	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
900	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	973	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
901	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	974	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
902	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	975	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
903	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	976	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
904	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	977	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
905	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	978	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
906	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	979	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella
907	34	53.1	514	2	Q6MY80_ASPFU	Q6my80 aspergillus	980	34	53.1	734	1	Q9UG70_VYIRU	Q9ug70 varicella


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DR PROSITE; P600290; IG_MHC; UNKNOWN_2.
SQ Immunoglobulin domain.
SEQUENCE 481 AA; 5203 MW; 4EBB5C53038B718 CRC64;

Query Match
Best Local Similarity 75.0%; Score 48; DB 2; Length 481;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
DB 45 GYFTDYNN 54

RESULT 3
Q9ULB1_MOUSE PRELIMINARY; PRT; 114 AA.
ID Q9ULB1_MOUSE PRELIMINARY; PRT; 114 AA.
AC Q9ULB1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
   (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20448942; PubMed=10992488;
RA DOI=10.1128/JAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
   with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206025; AAF69323.1; -; mRNA.
DR HSSP; P01751; 1NOB.
DR SMR; Q9ULB1; 2-114.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match
Best Local Similarity 73.4%; Score 47; DB 2; Length 114;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
DB 18 GYSFTSYMM 27

RESULT 4
Q9Z1C6_MOUSE PRELIMINARY; PRT; 117 AA.
ID Q9Z1C6_MOUSE PRELIMINARY; PRT; 117 AA.
AC Q9Z1C6;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mab 2A2 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN-Balb/c;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
   RT IgG3/G4 constant regions block human leukocyte binding to porcine
   endothelial cells."
RL Mol. Immunol. 34:441-452(1997).
DR EMBL; U78799; AAD00291.1; -; mRNA.
DR HSSP; P01820; 1G7J.
DR SMR; Q9Z1C6; 1-116.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;

Query Match
Best Local Similarity 73.4%; Score 47; DB 2; Length 117;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
DB 26 GYSFTSYMM 35

RESULT 5
Q5ZL51_MOUSE PRELIMINARY; PRT; 483 AA.
ID Q5ZL51_MOUSE PRELIMINARY; PRT; 483 AA.
AC Q5ZL51;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Caavaant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marrs M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RG NIH MGC Project;
RG Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC094065; AAH94065.1; -, mRNA.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 483 AA; 52167 MW; CQFDB9168795FEB4 CRC64;

Query Match 73.4%; Score 47; DB 2; Length 483;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMNN 10
DB 45 GYAFSGPMNN 54

RESULT 6
O9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.
ID O9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.
AC O9GYZ2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AA01452.1; -, mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; O9GYZ2; 1-119.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA983873FDF5FA6AB CRC64;

Query Match 71.9%; Score 46; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 8.3;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGHMNN 10
DB 26 GYTFGTGYNN 35

RESULT 7
O6GPX4_XENLA PRELIMINARY; PRT; 585 AA.
ID O6GPX4_XENLA PRELIMINARY; PRT; 585 AA.
AC O6GPX4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.

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OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OC NCBI_TaxID=8335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullanb S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072981; AAH72981.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IG_C1; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KM Hypothetical protein.
SQ SEQUENCE 585 AA; 64854 MW; 05A3D91B29E566A3 CRC64;

Query Match 71.9%; Score 46; DB 2; Length 585;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMNN 10
DB 45 GYTFSDHMNN 54

RESULT 8
HV04_MOUSE STANDARD; PRT; 117 AA.
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;

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 CC removed.
 CC -----
 CC PIR; A02032; HWS02.
 DR PDB; 1QNZ; NMR; H=21-117.
 DR Ensembl; ENSMUSG0000062849; Mus musculus.
 DR InterPro; IPR007110; IG-1-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 Ig heavy chain V region 102.
 FT REGION 20 49 Framework-1.
 FT REGION 50 54 Complementarity-determining-1.
 FT REGION 55 68 Framework-2.
 FT REGION 69 85 Complementarity-determining-2.
 FT REGION 86 117 Framework-3.
 FT DISULFID 41 115 By similarity.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12867 MW; 740A65DD651FCA8C CRC64;
 Query Match 68.8%; Score 44; DB 1; Length 117;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYSFTGHMNN 10
 DB 45 GYFTSYWMH 54
 RESULT 11
 HV09_MOUSE STANDARD; PRT; 117 AA.
 ID HV09_MOUSE
 AC P01753; P11271;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region 186-1 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
 RA Boehwell A.L.M., Paekind M., Reith M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MSCHELANE0US: This germline gene belongs to a set of closely
 CC related genes that could encode V regions of NPB antibodies.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC PIR; D90809; HWS61.
 DR HSSP; P01751; 1A6W.
 DR SMR; P01753; 20-117.
 DR Ensembl; ENSMUSG0000063737; Mus musculus.
 DR InterPro; IPR007110; IG-1-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19

FT CHAIN 20 117 Ig heavy chain V region 186-1.
 FT REGION 20 49 Framework-1.
 FT REGION 50 54 Complementarity-determining-1.
 FT REGION 55 68 Framework-2.
 FT REGION 69 85 Complementarity-determining-2.
 FT REGION 86 117 Framework-3.
 FT DISULFID 41 115 By similarity.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;
 Query Match 68.8%; Score 44; DB 1; Length 117;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GYSFTGHMNN 10
 DB 45 GYFTSYWMH 54
 RESULT 12
 HV10_MOUSE STANDARD; PRT; 117 AA.
 ID HV10_MOUSE
 AC P01754; P11270;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region 145 precursor.
 ON Name=IGH-VJ558;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
 RA Boehwell A.L.M., Paekind M., Reith M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MSCHELANE0US: This germline gene belongs to a set of closely
 CC related genes that could encode V regions of NPB antibodies.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; J00533; AAA38602.1; -; Genomic_DNA.
 DR PIR; C90809; HWS45.
 DR HSSP; P01751; 1A6W.
 DR SMR; P01754; 20-117.
 DR Ensembl; ENSMUSG0000063737; Mus musculus.
 DR MGI; MGI:96486; IGH-VJ558.
 DR InterPro; IPR007110; IG-1-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 Ig heavy chain V region 145.
 FT REGION 20 49 Framework-1.
 FT REGION 50 54 Complementarity-determining-1.
 FT REGION 55 68 Framework-2.
 FT REGION 69 85 Complementarity-determining-2.
 FT REGION 86 117 Framework-3.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12921 MW; D37DEBA3F543B996 CRC64;
 Query Match 68.8%; Score 44; DB 1; Length 117;

Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||:|:|:
45 GYFTSYMMH 54

RESULT 13
HV49 MOUSE

ID HV49 MOUSE STANDARD; PRT; 117 AA.

AC P06328;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig heavy chain V region VH558 B4 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

OK NCB1_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;

RT Yancopoulos G.D., Alt F.W.;

RT "Developmentally controlled and tissue-specific expression of

unrearranged VH gene segments."

Cell 40:271-281(1985).

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use as long as its content is in no way modified and this statement is not

removed.

CC EMBL; M13788; AAA38506.1; -, mRNA.

DR PIR; A02035; MEMSB4.

DR HSSP; P01751; 1A6W.

DR Ensembl; ENSMUSG00000063737; Mus musculus.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

OK NCB1_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=84182519; PubMed=6201362;

RT Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

RT "A V region determinant (idiotope) expressed at high frequency in B

lymphocytes is encoded by a large set of antibody structural genes."

EMBO J. 3:517-523(1984).

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CC PIR; A02037; MEMS15.

DR HSSP; P01751; 1A6W.

DR SMR; P06329; 1-120.

DR Ensembl; ENSMUSG00000021155; Mus musculus.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

OK NCB1_TaxID=10090;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

OK NCB1_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=85230574; PubMed=3924600;

RT Schiff C., Millil M., Pongereau M.;

RT "Functional and pseudogenes are similarly organized and may equally

contribute to the extensive antibody diversity of the IghH1 family."

EMBO J. 4:1225-1230(1985).

DR EMBL; X02462; CAA26299.1; -, Genomic_DNA.

DR SMR; OSR3X0; 20-116.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

OK NCB1_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=84182519; PubMed=6201362;

RT Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

RT "A V region determinant (idiotope) expressed at high frequency in B

lymphocytes is encoded by a large set of antibody structural genes."

EMBO J. 3:517-523(1984).

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CC PIR; A02037; MEMS15.

DR HSSP; P01751; 1A6W.

DR SMR; P06329; 1-120.

DR Ensembl; ENSMUSG00000021155; Mus musculus.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

OK NCB1_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=84182519; PubMed=6201362;

RT Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;

RT "A V region determinant (idiotope) expressed at high frequency in B

lymphocytes is encoded by a large set of antibody structural genes."

EMBO J. 3:517-523(1984).

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CC PIR; A02037; MEMS15.

DR HSSP; P01751; 1A6W.

DR SMR; P06329; 1-120.

DR Ensembl; ENSMUSG00000021155; Mus musculus.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

OK NCB1_TaxID=10090;

FT REGION 106 120 J segment.
 FT DISULFID 22 96 By similarity.
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA; 13311 MW; 91453P426F09834 CRC64;

Query Match 68.8%; Score 44; DB 1; Length 120;
 Best Local Similarity 60.0%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Gy 1 GYSFTGHMMN 10
 ||:|:|:|:
 Db 26 GYFTSYMMH 35

RESULT 16

O924R6_MOUSE PRELIMINARY; PRT; 137 AA.

ID O924R6_MOUSE PRELIMINARY; PRT; 137 AA.
 AC O924R6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 GN Name=VH186.2-D-J-C mu;

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6;

RA Kozono Y., Kozono H., Azuma T.;

RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC PubMed=315311;

RA Corbett S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.;

RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of

RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-

RT specific V genes as the original antigen.";

RL J. Immunol. 141:779-784(1988).

DR EMBL; AB067783; BAB63268.1; -; mRNA.

DR PIR; F28833; F28833.

DR PIR; PH1105; PH1105.

DR PIR; PH1108; PH1108.

DR PIR; PH1112; PH1112.

DR PIR; PH1114; PH1114.

DR PIR; PH1118; PH1118.

DR PIR; PH1119; PH1119.

DR PIR; PH1122; PH1122.

DR PIR; PH1123; PH1123.

DR PIR; PH1124; PH1124.

DR PIR; PH1125; PH1125.

DR PIR; PH1126; PH1126.

DR PIR; PH1128; PH1128.

DR PIR; PH1129; PH1129.

DR PIR; PH1131; PH1131.

DR PIR; PH1133; PH1133.

DR PIR; PH1137; PH1137.

DR PIR; PH1139; PH1139.

DR PIR; PH1142; PH1142.

DR PIR; PH1144; PH1144.

DR PIR; PH1147; PH1147.

DR PIR; PH1149; PH1149.

DR PIR; PH1150; PH1150.

DR PIR; PH1151; PH1151.

DR PIR; PH1152; PH1152.

DR PIR; PH1153; PH1153.

DR HSSP; P01751; 1A6W.

DR SMR; Q924R6; 1-128.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR NON_TER 1 1
 FT NON_TER 137 137
 SQ SEQUENCE 137 AA; 15171 MW; 5C3BD966DC6A124 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 137;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Gy 1 GYSFTGHMMN 10
 ||:|:|:|:
 Db 26 GYFTSYMMH 35

RESULT 17

HY07_MOUSE STANDARD; PRT; 139 AA.

ID HY07_MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region BI-8/186-2 precursor.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6;

RA MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;

RA Botchwell A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,

RA Baltimore D.;

RT "Heavy chain variable region contribution to the NpB family of

RT antibodies: somatic mutation evident in a gamma 2a variable region.";

RL Cell 24:625-637(1981).

CC -I- MSCERIANBOUS: The BI-8 mu chain mRNA was cloned from a hybridoma

CC making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl

CC (NpB antibodies).

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CC EMBL; J00529; AAA38170.1; -; mRNA.

DR PIR; A90809; MEMS18.

DR PDB; 1A6V; X-ray; H=20-139.

DR PDB; 1A6V; X-ray; H/I/U=20-139.

DR PDB; 1A6W; X-ray; H=20-139.

DR PDB; 1NGQ; X-ray; H=20-139.

DR PDB; 1NGQ; X-ray; H=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.

DR PDB; 1NGQ; X-ray; A/C=20-139.


```

FT STRAND 28 31
FT TURN 33 34
FT STRAND 37 44
FT HELIX 48 50
FT STRAND 52 58
FT TURN 60 61
FT STRAND 64 70
FT TURN 72 74
FT STRAND 77 79
FT HELIX 81 83
FT TURN 84 86
FT STRAND 87 92
FT TURN 93 96
FT STRAND 97 102
FT HELIX 107 109
FT STRAND 111 118
FT TURN 120 123
FT STRAND 129 137
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

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Query Match 68.8%; Score 44; DB 1; Length 139;
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 GYSFTGHMMN 10
Db 45 GYFTSYMMH 54

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RESULT 18

```

Q924R5_MOUSE PRELIMINARY; PRT; 139 AA.
AC Q924R5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHI86.2-D-J-C mu protein (Fragment).
GN Name=VHI86.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067784; BAB63269.1; -; mRNA.
DR PIR; PH1137; PH1137.
DR HSSP; P01751; 1A6V.
DR SMR; Q924R5; 1-125.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 139
SQ SEQUENCE 139 AA; 15221 MW; 8491E2F85614736A CRC64;

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Query Match 68.8%; Score 44; DB 2; Length 139;
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GYSFTGHMMN 10
Db 26 GYFTSYMMH 35

```

```

RESULT 19
Q924P8_MOUSE
ID Q924P8_MOUSE PRELIMINARY; PRT; 140 AA.

```

```

AC Q924P8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN Name=AB069917; Synonyms=V23-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784 (1988).
DR EMBL; AB069917; BAB63933.1; -; mRNA.
DR PIR; PH156; PH156.
DR PIR; PH156; PH156.
DR HSSP; P01751; 1A6V.
DR SMR; Q924P8; 1-126.
DR MGI; MGI:3576502; AB069917.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;

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Query Match 68.8%; Score 44; DB 2; Length 140;
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 GYSFTGHMMN 10
Db 26 GYFTSYMMH 35

```

RESULT 20

```

Q924R2_MOUSE
ID Q924R2_MOUSE PRELIMINARY; PRT; 140 AA.
AC Q924R2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VHI86.2-D-J-C mu protein (Fragment).
GN Name=VHI86.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";

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RL J. Immunol. 141:779-784(1988).
DR EMBL: AB067788; BAB63273.1; -, mRNA.
DR PIR: F28833; F28833.
DR PIR: PH1105; PH1105.
DR PIR: PH1108; PH1108.
DR PIR: PH1114; PH1114.
DR PIR: PH1118; PH1118.
DR PIR: PH1119; PH1119.
DR PIR: PH1125; PH1125.
DR PIR: PH1126; PH1126.
DR PIR: PH1128; PH1128.
DR PIR: PH1129; PH1129.
DR PIR: PH1131; PH1131.
DR PIR: PH1134; PH1134.
DR PIR: PH1137; PH1137.
DR PIR: PH1139; PH1139.
DR PIR: PH1142; PH1142.
DR PIR: PH1144; PH1144.
DR PIR: PH1147; PH1147.
DR PIR: PH1149; PH1149.
DR PIR: PH1150; PH1150.
DR PIR: PH1151; PH1151.
DR PIR: PH1152; PH1152.
DR PIR: PH1153; PH1153.
DR HSSP: P01751; 1A6W.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 140;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
Db 26 GYTFSTYMMH 35

RESULT 21
Q924Q4_MOUSE PRELIMINARY; PRT; 141 AA.
ID Q924Q4_MOUSE PRELIMINARY;
AC Q924Q4_
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=315311;
RA Corbet S., Hirn M., Roth C., These J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
DR EMBL: AB067796; BAB63281.1; -, mRNA.
DR PIR: F28833; F28833.
DR PIR: PH105; PH105.
DR PIR: PH108; PH108.

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DR PIR: PH1114; PH1114.
DR PIR: PH1118; PH1118.
DR PIR: PH1119; PH1119.
DR PIR: PH1125; PH1125.
DR PIR: PH1126; PH1126.
DR PIR: PH1128; PH1128.
DR PIR: PH1129; PH1129.
DR PIR: PH1131; PH1131.
DR PIR: PH1134; PH1134.
DR PIR: PH1137; PH1137.
DR PIR: PH1139; PH1139.
DR PIR: PH1142; PH1142.
DR PIR: PH1144; PH1144.
DR PIR: PH1147; PH1147.
DR PIR: PH1149; PH1149.
DR PIR: PH1150; PH1150.
DR PIR: PH1151; PH1151.
DR PIR: PH1152; PH1152.
DR PIR: PH1153; PH1153.
DR HSSP: P01751; 1A6W.
DR SMR: Q924Q4; 1-132.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 141
SQ SEQUENCE 141 AA; 15561 MW; DDD80482D66B76A0 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 141;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
Db 26 GYTFSTYMMH 35

RESULT 22
Q924Q1_MOUSE PRELIMINARY; PRT; 142 AA.
ID Q924Q1_MOUSE PRELIMINARY;
AC Q924Q1_
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN Name=AB069917; Synonyms=V23-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Terynck T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=315311;
RA Corbet S., Hirn M., Roth C., These J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
RN [4]

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RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE:92381444; PubMed:1512540; DOI:10.1064/jem.176.3.761;
 RA Tillman D.M., Jout N.T., Hill R.J., Marion T.N.,
 RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
 selective B cell stimulation in (NZB x NZW)F1 mice."
 RL J. Exp. Med. 176:761-779(1992).
 DR EMBL: AB069913; BAB63929.1; -; mRNA.
 DR PIR: F33932; F33932.
 DR PIR: I28833; I28833.
 DR PIR: PH0985; PH0985.
 DR PIR: PH1155; PH1155.
 DR PIR: PH1156; PH1156.
 DR PIR: PH1157; PH1157.
 DR PIR: PH1158; PH1158.
 DR HSSP: P01751; 1A6W.
 DR SMR: Q924Q1; 1-128.
 DR Ensembl: ENSMUSG0000021155; Mus musculus.
 DR MGI: MGI:3576502; AB069917.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG-LIKE; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
 Query Match 68.8%; Score 44; DB 2; Length 142;
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNM 10
 Db 26 GYFTSYMMH 35

RESULT 23
 Q91V67_MOUSE PRELIMINARY; PRT; 143 AA.
 ID Q91V67_MOUSE PRELIMINARY; PRT; 143 AA.
 AC Q91V67;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
 GN Name:VH186.2-D-J-C mu; Synonyms:V304-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.,
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB069914; BAB63928.1; -; mRNA.
 DR EMBL: AB069914; BAB63930.1; -; mRNA.
 DR PIR: S26744; S26744.
 DR HSSP: P01751; 1A6W.
 DR SMR: Q91V67; 1-129.
 DR Ensembl: ENSMUSG0000021155; Mus musculus.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG-LIKE; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;

Query Match 68.8%; Score 44; DB 2; Length 143;
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNM 10
 Db 26 GYFTSYMMH 35

Db 26 GYFTSYMMH 35

RESULT 24
 Q91VA2_MOUSE PRELIMINARY; PRT; 143 AA.
 ID Q91VA2_MOUSE PRELIMINARY; PRT; 143 AA.
 AC Q91VA2;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 GN Name:VH186.2-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.,
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB067786; BAB63271.1; -; mRNA.
 DR EMBL: AB069911; BAB63927.1; -; mRNA.
 DR PIR: PH1105; PH1105.
 DR PIR: PH1114; PH1114.
 DR PIR: PH1118; PH1118.
 DR PIR: PH1119; PH1119.
 DR PIR: PH1125; PH1125.
 DR PIR: PH1126; PH1126.
 DR PIR: PH1128; PH1128.
 DR PIR: PH1134; PH1134.
 DR PIR: PH1137; PH1137.
 DR PIR: PH1142; PH1142.
 DR PIR: PH1149; PH1149.
 DR PIR: PH1150; PH1150.
 DR PIR: PH1151; PH1151.
 DR PIR: PH1152; PH1152.
 DR HSSP: P01751; 1A6W.
 DR SMR: Q91VA2; 1-134.
 DR Ensembl: ENSMUSG0000021155; Mus musculus.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PSS0835; IG-LIKE; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 143 AA; 15617 MW; 51952152F6F3AD47 CRC64;
 Query Match 68.8%; Score 44; DB 2; Length 143;
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNM 10
 Db 26 GYFTSYMMH 35

RESULT 25
 Q924R7_MOUSE PRELIMINARY; PRT; 143 AA.
 ID Q924R7_MOUSE PRELIMINARY; PRT; 143 AA.
 AC Q924R7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE VH186.2-D-J-C mu protein (Fragment).
 GN Name:VH186.2-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067782; BAB63267.1; -, mRNA.
DR PIR; PH105; PH105.
DR PIR; PH108; PH108.
DR PIR; PH114; PH114.
DR PIR; PH118; PH118.
DR PIR; PH119; PH119.
DR PIR; PH125; PH125.
DR PIR; PH126; PH126.
DR PIR; PH128; PH128.
DR PIR; PH131; PH131.
DR PIR; PH134; PH134.
DR PIR; PH137; PH137.
DR PIR; PH139; PH139.
DR PIR; PH142; PH142.
DR PIR; PH149; PH149.
DR PIR; PH150; PH150.
DR PIR; PH151; PH151.
DR PIR; PH152; PH152.
DR PIR; PH153; PH153.
DR HSSP; P01751; 1A6W.
DR SMR; Q924R7; 1-134.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 143 AA; 15648 MW; 51894D22EA9FDD47 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 143;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
Db 26 GTFTSYMMH 35

RESULT 26
Q924P6 MOUSE PRELIMINARY; PRT; 143 AA.
ID Q924P6_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924P6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067795; BAB63260.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; PH105; PH105.
DR PIR; PH108; PH108.
DR PIR; PH114; PH114.
DR PIR; PH118; PH118.
DR PIR; PH119; PH119.
DR PIR; PH125; PH125.
DR PIR; PH126; PH126.
DR PIR; PH128; PH128.
DR PIR; PH129; PH129.
DR PIR; PH131; PH131.
DR PIR; PH134; PH134.
DR PIR; PH137; PH137.
DR PIR; PH139; PH139.
DR PIR; PH142; PH142.
DR PIR; PH144; PH144.
DR PIR; PH147; PH147.
DR PIR; PH149; PH149.
DR PIR; PH150; PH150.
DR PIR; PH151; PH151.
DR PIR; PH152; PH152.
DR PIR; PH153; PH153.
DR HSSP; P01751; 1A6W.
DR SMR; Q924O5; 1-134.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
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DR Ensemble; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 143 AA; 15714 MW; 523385316C345A93 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 143;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
Db 26 GTFTSYMMH 35

RESULT 27
Q924O5 MOUSE PRELIMINARY; PRT; 143 AA.
ID Q924O5_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q924O5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067795; BAB63260.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; PH105; PH105.
DR PIR; PH108; PH108.
DR PIR; PH114; PH114.
DR PIR; PH118; PH118.
DR PIR; PH119; PH119.
DR PIR; PH125; PH125.
DR PIR; PH126; PH126.
DR PIR; PH128; PH128.
DR PIR; PH129; PH129.
DR PIR; PH131; PH131.
DR PIR; PH134; PH134.
DR PIR; PH137; PH137.
DR PIR; PH139; PH139.
DR PIR; PH142; PH142.
DR PIR; PH144; PH144.
DR PIR; PH147; PH147.
DR PIR; PH149; PH149.
DR PIR; PH150; PH150.
DR PIR; PH151; PH151.
DR PIR; PH152; PH152.
DR PIR; PH153; PH153.
DR HSSP; P01751; 1A6W.
DR SMR; Q924O5; 1-134.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.

"Allogeneic manipulation of the GAT idiotype cascade. Immunization of
C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
specific V genes as the original antigen."
J. Immunol. 141:779-784(1988).
RL EMBL; AB067795; BAB63260.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; PH105; PH105.
DR PIR; PH108; PH108.
DR PIR; PH114; PH114.
DR PIR; PH118; PH118.
DR PIR; PH119; PH119.
DR PIR; PH125; PH125.
DR PIR; PH126; PH126.
DR PIR; PH128; PH128.
DR PIR; PH129; PH129.
DR PIR; PH131; PH131.
DR PIR; PH134; PH134.
DR PIR; PH137; PH137.
DR PIR; PH139; PH139.
DR PIR; PH142; PH142.
DR PIR; PH144; PH144.
DR PIR; PH147; PH147.
DR PIR; PH149; PH149.
DR PIR; PH150; PH150.
DR PIR; PH151; PH151.
DR PIR; PH152; PH152.
DR PIR; PH153; PH153.
DR HSSP; P01751; 1A6W.
DR SMR; Q924O5; 1-134.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
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DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON_TER 1
 SQ SEQUENCE 143 AA; 15908 MW; 55A2372870FD0568 CRC64;

Query Match
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
 ||:|:|:|:
 Db 26 GYFTSYMMH 35

RESULT 28

O924R0_MOUSE PRELIMINARY; PRT; 143 AA.

AC O924R0;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE VHL16.2-D-J-C mu protein (Fragment).
 GN Name=VHL16.2-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC Pubmed=3135311;
 RA Corbet S., Hitt M., Roth C., Theze J., Fougereau M., Schiff C.;
 RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
 C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
 specific V genes as the original antigen.";
 RL J. Immunol. 141:779-784 (1988).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC Pubmed=2499887;
 RA Bacala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polypeptide autoantibodies are encoded by
 RT Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
 RL EMBL; AB067790; BAB63275.1; -, mRNA.
 DR PIR; F28833; F28833.
 DR PIR; F33932; F33932.
 DR PIR; PH105; PH105.
 DR PIR; PH108; PH108.
 DR PIR; PH114; PH114.
 DR PIR; PH116; PH116.
 DR PIR; PH119; PH119.
 DR PIR; PH125; PH125.
 DR PIR; PH126; PH126.
 DR PIR; PH128; PH128.
 DR PIR; PH129; PH129.
 DR PIR; PH131; PH131.
 DR PIR; PH134; PH134.
 DR PIR; PH137; PH137.
 DR PIR; PH139; PH139.
 DR PIR; PH142; PH142.
 DR PIR; PH144; PH144.
 DR PIR; PH147; PH147.
 DR PIR; PH149; PH149.
 DR PIR; PH150; PH150.
 DR PIR; PH151; PH151.
 DR PIR; PH152; PH152.
 DR PIR; PH153; PH153.
 DR HSSP; P01751; 1A6W.

DR SMR; Q924R0; 1-134.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 SQ SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

Query Match
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
 ||:|:|:|:
 Db 26 GYFTSYMMH 35

RESULT 29

O924P5_MOUSE PRELIMINARY; PRT; 144 AA.

AC O924P5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE VHL16.2-D-J-C mu protein (Fragment).
 GN Name=VHL16.2-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB069920; BAB63936.1; -, mRNA.
 DR PIR; PH137; PH137.
 DR PIR; S26744; S26744.
 DR HSSP; P01751; 1A6W.
 DR SMR; Q924P5; 1-135.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 SQ SEQUENCE 144 AA; 15865 MW; CD07BB97E95C1B27 CRC64;

Query Match
 Best Local Similarity 60.0%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
 ||:|:|:|:
 Db 26 GYFTSYMMH 35

RESULT 30

O924P7_MOUSE PRELIMINARY; PRT; 145 AA.

AC O924P7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE VHL16.2-D-J-C mu protein (Fragment).
 GN Name=VHL16.2-D-J-C mu;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:315311;
RA Corbet S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
  C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
  specific V genes as the original antigen.";
  J. Immunol. 141:779-784(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:249987;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyclonal autoantibodies are encoded by
  RT Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
  RL EMBL; AB069918; BAB63934.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1142; PH1142.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMR; Q924P7; 1-136.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 145 AA; 15988 MW; FB73958704796C9A CRC64;

Query Match 68.8%; Score 44; DB 2; Length 145;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
DB 26 GYFTSYMMH 35

RESULT 31
O92406_MOUSE PRELIMINARY; PRT; 145 AA.
ID O92406_MOUSE PRELIMINARY;
AC O92406;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:315311;
RA Corbet S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
  RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
  specific V genes as the original antigen.";
  J. Immunol. 141:779-784(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:249987;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyclonal autoantibodies are encoded by
  RT Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
  RL EMBL; AB067794; BAB63279.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMR; Q924O6; 1-136.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 145 AA; 16011 MW; 98C0846D40DF97EA CRC64;

Query Match 68.8%; Score 44; DB 2; Length 145;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
DB 26 GYFTSYMMH 35

RESULT 32
O92407_MOUSE PRELIMINARY; PRT; 145 AA.
ID O92407_MOUSE PRELIMINARY;
AC O92407;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

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OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbet S., Hirth M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
DR EMBL; AB067793; BAB63278.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMR; Q92407; 1-136.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 68.8%; Score 44; DB 2; Length 145;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNM 10
DB 26 GYFTSYMMH 35

RESULT 33
Q92409 MOUSE
ID Q92409 MOUSE PRELIMINARY; PRT; 145 AA.
AC Q92409;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vhl86.2-D-J-C mu protein (Fragment).
GN Name=Vhl86.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbet S., Hirth M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RL "Two murine natural polyclonal autoantibodies are encoded by
nonmutated germ-line genes.";
DR EMBL; AB067791; BAB63276.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMR; Q92409; 1-136.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 145;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNM 10
DB 26 GYFTSYMMH 35

RESULT 34
Q924R1 MOUSE
ID Q924R1 MOUSE PRELIMINARY; PRT; 145 AA.
AC Q924R1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vhl86.2-D-J-C mu protein (Fragment).
GN Name=Vhl86.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

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OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6;
RN Kozono Y., Kozono H., Azuma T.,
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA PubMed:315311;
RC Corbet S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.,
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.,
RT "Two murine natural polyclonal autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR EMBL; AB067789; BAB63274.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; 1A6W.
DR SMR; Q924R1; 1-136.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON-TER 1
FT NON-TER 145
SQ SEQUENCE 145 AA; 15979 MW; 0162D0A26C746C04 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 145;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6;
RN Kozono Y., Kozono H., Azuma T.,
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA PubMed:315311;
RC Corbet S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.,
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Kaartinen M., Rocca-Serra J., Makela O.,
RT "Combinatorial association of V genes: one VH gene codes for three
RT non-cross-reactive monoclonal antibodies each specific for a different
RT antigen (phoxazalone, NP or gat).";
RL Mol. Immunol. 25:859-865(1988).
DR EMBL; AB067787; BAB63272.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; J10078; J10078.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR PIR; S26744; S26744.
DR HSSP; P01751; 1A6W.
DR SMR; Q924R3; 1-136.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON-TER 1
FT NON-TER 145
SQ SEQUENCE 145 AA; 15996 MW; 35B1A36A4280BA81 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 145;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 35
Q924R3 MOUSE PRELIMINARY; PRT; 145 AA.
AC Q924R3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).

RESULT 36
Q924R4 MOUSE
Q924R4 MOUSE PRELIMINARY; PRT; 145 AA.
AC Q924R4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).


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ID 0924R4 MOUSE PRELIMINARY; PRT: 145 AA.
AC 0924R4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu Protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Pubmed=3135311;
RA Corbet S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Pubmed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR EMBL; AB067785; BAB63270.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; IAGW.
DR SMR; Q924R4; 1-136.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16081 MW; ECDBIAL35E05B8AA CRC64;

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Query Match 68.8%; Score 44; DB 2; Length 145;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GVSFTGHMNN 10
Db 26 GYFTSYMMH 35

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RESULT 37
ID 0924Q3 MOUSE PRELIMINARY; PRT: 146 AA.
AC 0924Q3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Pubmed=3135311;
RA Corbet S., Hirm M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotypic cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC Pubmed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR EMBL; AB067797; BAB63282.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR HSSP; P01751; IAGW.
DR SMR; Q924Q3; 1-137.
DR Ensemble; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16136 MW; CEA8DDE1955807F CRC64;

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Query Match 68.8%; Score 44; DB 2; Length 146;
Best Local Similarity 60.0%; Pred. No. 22;

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Mix FVB/N;
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
 RA Strusberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 RT nonmutated germ-line genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
 DR EMBL; BC028245; AAH28249.1; -, mRNA.
 DR PIR; F33932; F33932.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR HSSP; P01751; 1A6W.
 DR SMR; Q8K172; 20-239.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Immunoglobulin domain.
 SQ SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 482;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 DB 45 GYFTSYMMH 54

RESULT 41
 Q8R0F2_MOUSE
 ID Q8R0F2_MOUSE PRELIMINARY; PRT; 488 AA.
 AC Q8R0F2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 OS 1gh-VJ558 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RC Strusberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC031703; AAH31703.1; -, mRNA.
 DR HSSP; P01751; 1A6W.
 DR Ensembl; ENSMUSG00000021155; Mus musculus.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 488 AA; 53127 MW; 0E3B156E15573F0 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 488;
 Best Local Similarity 60.0%; Pred. No. 71;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 DB 45 GYFTSYMMH 54

RESULT 42
 Q4KML5_MOUSE
 ID Q4KML5_MOUSE PRELIMINARY; PRT; 617 AA.
 AC Q4KML5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Datchenko L., Matusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinck P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC098504; AA098504.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 617 AA; 68520 MW; BCF2AEC857CD3D12 CRC64;

Query Match 68.8%; Score 44; DB 2; Length 617;
 Best Local Similarity 60.0%; Pred. No. 90;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
 |||:|:|:
 45 GYFTSYMMH 54

RESULT 43
 O6FT92 CANGA PRELIMINARY; PRT; 766 AA.
 ID O6FT92_2
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Similar to sp|P42946 Saccharomyces cerevisiae YJL108c PRM10.
 GN OrderedLocustNames=CAG10G044339;
 OS Candida glabrata (Yeast) (Torulopsis glabrata).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5478;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 2001 / CBS 138.
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Francaul L., Aigle M., Anthouard V., Babori A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Blyksten C.,
 RA Boissarie A., Boyer J., Catolico L., Confaniolero F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantuya F., Hennequin C., Jauniaux N., Joyet P., Kachouti A.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicard J.-M., Nikolski M., Ozias S., Ozier-Kalodergopoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala P., Wesolowski-Louvel M., Weethof E., Wirth B.,
 RA Zenhou-Meyer M., Zivanovic Y., Boletoin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 DR EMBL; CR380953; CAGS9479.1; -; Genomic_DNA.
 DR InterPro; IPR010619; DUF1212.
 DR Pfam; PF06738; DUF1212; 1.

KW Complete proteome.
 SQ SEQUENCE 766 AA; 85390 MW; 92FA5C783810441E CRC64;
 Query Match 68.8%; Score 44; DB 2; Length 766;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 YSFTGHMMN 10
 |||:|:|:
 485 YAFGHHMN 493

RESULT 44
 O920E8 MOUSE PRELIMINARY; PRT; 120 AA.
 ID O920E8_MOUSE
 AC O920E8;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Pterin-mimicking anti-idiotypic heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Atkin J.D., Tape A., Jennings I.G., Horatis O., Cotton R.G.H.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF307936; AAL09420.1; -; Genomic_DNA.
 DR HSSP; P01751; INOB.
 DR SMR; Q920E8; 1-120.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 120
 SQ SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 67.2%; Score 43; DB 2; Length 120;
 Best Local Similarity 80.0%; Pred. No. 26;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMMN 10
 |||:|:|:
 26 GYSFTGHMMN 35

RESULT 45
 O8VJL1 MOUSE PRELIMINARY; PRT; 123 AA.
 ID O8VJL1_MOUSE
 AC O8VJL1;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Anti-DNA heavy chain (Fragment).
 GN Name=J558;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C3H/HeJ-1pr/1pr;
 RX MEDLINE=96409289; PubMed=8814271;
 RT Wlloch M.K., Alexander A.L., Pippen A.M., Pisecky D.S., Gillespie G.S.;
 RT "Differences in V kappa gene utilization and VH CDR3 sequence among
 RT anti-DNA from C3H-1pr mice and lupus mice with nephritis.";
 RL Eur. J. Immunol. 26:2225-2233(1996).
 DR EMBL; U59154; AAB02916.1; -; mRNA.

DR HSSP; P01751; 1NOB.
DR SMR; Q8V1U1; 1-123.
DR Ensembl; ENSMUSG00000057521; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR NON_TER 1 123
FT NON_TER 123
SQ SEQUENCE 123 AA; 13806 MW; CC0037A806E9911E CRC64;

Query Match
Best Local Similarity 80.0%; Score 43; DB 2; Length 123;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
DB 26 GYSFTGYMMN 35

RESULT 46
Q924Q2_MOUSE PRELIMINARY; PRT; 142 AA.
AC Q924Q2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR V303-D-J-C mu protein (Fragment).
GN Name=V303-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069910; BAB63926.1; -, mRNA.
DR HSSP; P01751; 1A6W.
DR Ensembl; ENSMUSG00000061773; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR NON_TER 1 142
FT NON_TER 142
SQ SEQUENCE 142 AA; 15684 MW; 048809F90C0FBD7B CRC64;

Query Match
Best Local Similarity 67.2%; Score 43; DB 2; Length 142;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMM 9
DB 26 GYFTSYMM 34

RESULT 47
Q924P9_MOUSE PRELIMINARY; PRT; 143 AA.
ID Q924P9_MOUSE
AC Q924P9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE V303-D-J-C mu protein (Fragment).
GN Name=V303-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=7523684;
RT Pokkuluri P.R., Bouthillier F., Li Y., Kuderova A., Lee J., Cygler M.;
RT "Preparation, characterization and crystallization of an antibody Fab
fragment that recognizes RNA. Crystal structures of native Fab and
three Fab-monomucleotide complexes.";
RT J. Mol. Biol. 243:283-297(1994).
RL EMBL; AB069916; BAB63932.1; -, mRNA.
DR PIR; PH160; PH160.
DR PIR; PH161; PH161.
DR PIR; PH162; PH162.
DR PIR; S53751; S53751.
DR HSSP; P01751; 1A6W.
DR Ensembl; ENSMUSG00000061773; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
DR NON_TER 1 143
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;

Query Match
Best Local Similarity 67.2%; Score 43; DB 2; Length 143;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMM 9
DB 26 GYFTSYMM 34

RESULT 48
Q924Q8_MOUSE PRELIMINARY; PRT; 146 AA.
ID Q924Q8_MOUSE
AC Q924Q8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE VHI86.2-D-J-C mu protein (Fragment).
GN Name=VHI86.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067792; BAB63277.1; -, mRNA.
DR PIR; PH105; PH105.
DR PIR; PH108; PH108.
DR PIR; PH114; PH114.
DR PIR; PH118; PH118.
DR PIR; PH119; PH119.
DR PIR; PH125; PH125.
DR PIR; PH126; PH126.
DR PIR; PH128; PH128.
DR PIR; PH131; PH131.
DR PIR; PH134; PH134.
DR PIR; PH137; PH137.
DR PIR; PH139; PH139.
DR PIR; PH142; PH142.
DR PIR; PH143; PH143.
DR PIR; PH149; PH149.
DR PIR; PH150; PH150.

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DR PIR; PH151; PH151.
DR PIR; PH152; PH152.
DR PIR; PH153; PH153.
DR HSSP; P01751; 1A6M.
DR SMR; Q924Q8; 1-137.
DR Ensembl; ENSMUSG0000063737; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; PS00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 146
SQ SEQUENCE 146 AA; 16023 MW; 4B04959991D49159 CRC64;

Query Match 67.2%; Score 43; DB 2; Length 146;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMM 9
   |||:|
Db 26 GYFTSYMM 34

RESULT 49
Q8RDG7 THETN PRELIMINARY; PRT; 349 AA.
ID Q8RDG7
AC Q8RDG7
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Nucleoside-diphosphate-sugar pyrophosphorylase.
GN Name=Gcd1; OrderedLocustNames=TTE0065;
OS Thermomicrobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermomicrobacteriales;
OC Thermomicrobacteriaceae; Thermomicrobacter.
OC NCBI_TaxID=119072;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=MB4.
RX MEDLINE=21992816; PubMed=11997336; DOI=10.1101/gr.219302;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of the T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE012981; AAM23372.1; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016779; F:nucleosidytransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR005835; NTP_transferase.
DR Pfam; PF00483; Hexapep_3.
DR Pfam; PF00483; NTP_transferase; 1.
KW Complete proteome.
SQ SEQUENCE 349 AA; 38891 MW; D577F7C5154D7AA8 CRC64;

Query Match 67.2%; Score 43; DB 2; Length 349;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 XSFTHMMN 10
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Db 210 YKFTSYMM 218

RESULT 50
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ID O504M7
AC O504M7
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

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DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshilyuk S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heaton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Merra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RX EMBL; BC094936; AAB94936.1; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-sec; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 616 AA; 67919 MW; 0FF4532BCD596A52 CRC64;

Query Match 67.2%; Score 43; DB 2; Length 616;
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Db 45 GYFTSYMM 53

Search completed: January 17, 2006, 12:04:43
Job time : 94.3636 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:50:24 ; Search time 17.2727 Seconds
(without alignments)
47.865 Million cell updates/sec

Title: US-10-665-658-10
Perfect score: 64
Sequence: 1 GYSFTGHHMN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/FCCTS_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/BE_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	64	100.0	121	2	US-08-974-899-4 Sequence 4, Appl
4	64	100.0	121	2	US-08-974-899-5 Sequence 5, Appl
5	64	100.0	121	2	US-08-974-899-24 Sequence 24, Appl
6	64	100.0	121	2	US-09-795-798-4 Sequence 4, Appl
7	64	100.0	121	2	US-09-795-798-5 Sequence 5, Appl
8	64	100.0	121	2	US-09-795-798-24 Sequence 24, Appl
9	60	93.8	116	2	US-09-127-449-50 Sequence 50, Appl
10	60	93.8	116	2	US-08-804-444A-50 Sequence 50, Appl
11	60	93.8	116	2	US-09-026-985-50 Sequence 50, Appl
12	60	93.8	116	2	US-09-121-952A-50 Sequence 50, Appl
13	60	93.8	116	2	US-09-334-340A-50 Sequence 50, Appl
14	60	93.8	116	2	US-09-355-014-50 Sequence 50, Appl
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16	52	81.2	118	2	US-08-767-128-2 Sequence 8, Appl
17	52	81.2	118	2	US-08-767-128-8 Sequence 8, Appl
18	52	81.2	138	2	US-09-948-004-14 Sequence 14, Appl
19	52	81.2	495	2	US-09-948-004-18 Sequence 18, Appl
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142	44	68.8	143	1	US-08-236-520-7	Sequence 7, Appl1	215	42	65.6	247	2	US-10-620-049-21	Sequence 21, Appl
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144	44	68.8	146	2	US-09-069-628-30	Sequence 30, Appl	217	42	65.6	258	2	US-09-315-574-5	Sequence 5, Appl1
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153	44	68.8	269	1	US-08-491-988-3	Sequence 3, Appl1	226	41	64.1	115	1	US-08-468-661-1	Sequence 1, Appl1
154	44	68.8	402	1	US-08-491-988-9	Sequence 9, Appl1	227	41	64.1	115	1	US-08-468-661-1	Sequence 1, Appl1
155	44	68.8	435	1	US-08-491-988-5	Sequence 5, Appl1	228	41	64.1	115	1	US-08-478-857-1	Sequence 1, Appl1
156	44	68.8	20	2	US-09-556-605-29	Sequence 29, Appl	229	41	64.1	115	2	US-08-471-771-1	Sequence 1, Appl1
157	43	67.2	111	2	US-08-881-037-20	Sequence 20, Appl	230	41	64.1	115	2	US-09-130-783-3	Sequence 3, Appl1
158	43	67.2	120	2	US-08-513-993C-7802	Sequence 7802, Ap	231	41	64.1	116	1	US-08-690-102A-4	Sequence 4, Appl1
159	43	67.2	130	2	US-09-556-605-3	Sequence 3, Appl1	232	41	64.1	116	1	US-08-690-102A-8	Sequence 8, Appl1
160	43	67.2	147	1	US-08-259-372A-8	Sequence 8, Appl1	233	41	64.1	116	1	US-08-690-102A-9	Sequence 9, Appl1
161	43	67.2	147	1	US-08-468-671-8	Sequence 8, Appl1	234	41	64.1	116	2	US-09-127-902-8	Sequence 8, Appl1
162	43	67.2	147	1	US-08-468-671-8	Sequence 8, Appl1	235	41	64.1	116	2	US-09-127-902-9	Sequence 9, Appl1
163	43	67.2	222	1	US-08-737-129A-6	Sequence 6, Appl1	236	41	64.1	116	2	US-09-127-902-8	Sequence 8, Appl1
164	43	67.2	241	1	US-08-235-838-11	Sequence 11, Appl	237	41	64.1	116	2	US-09-155-107-8	Sequence 4, Appl1
165	43	67.2	241	1	US-08-465-473B-11	Sequence 11, Appl	238	41	64.1	116	2	US-09-155-107-8	Sequence 8, Appl1
166	43	67.2	637	1	US-08-235-838-16	Sequence 16, Appl	239	41	64.1	116	2	US-09-155-107-8	Sequence 21, Appl
167	43	67.2	637	1	US-08-465-473B-16	Sequence 16, Appl	240	41	64.1	116	4	PCT-US95-09641-4	Sequence 4, Appl1
168	42.5	66.4	114	2	US-09-724-409-7	Sequence 7, Appl1	241	41	64.1	116	4	PCT-US95-09641-9	Sequence 9, Appl1
169	42.5	66.4	114	2	US-09-724-530-7	Sequence 7, Appl1	242	41	64.1	116	4	US-08-545-809A-90	Sequence 90, Appl
170	42.5	66.4	114	2	US-09-328-296-7	Sequence 76, Appl	243	41	64.1	117	2	US-10-194-975-118	Sequence 118, App
171	42.5	66.4	117	2	US-08-525-539A-76	Sequence 76, Appl	244	41	64.1	117	2	US-09-515-697-90	Sequence 90, Appl
172	42.5	66.4	117	2	US-08-525-539A-78	Sequence 78, Appl	245	41	64.1	117	2	US-09-515-697-90	Sequence 90, Appl
173	42.5	66.4	136	2	US-08-525-539A-47	Sequence 47, Appl	246	41	64.1	119	2	US-08-767-128-26	Sequence 26, Appl

247	41	64.1	119	2	US-09-920-262A-7	Sequence 7, Appl1	320	40	62.5	117	2	US-09-234-340A-48	Sequence 48, Appl1
248	41	64.1	120	2	US-08-767-128-28	Sequence 28, Appl1	321	40	62.5	117	2	US-09-234-340A-49	Sequence 49, Appl1
249	41	64.1	122	2	US-08-483-749A-2	Sequence 26, Appl1	322	40	62.5	117	2	US-09-355-014-48	Sequence 48, Appl1
250	41	64.1	122	2	US-08-957-001B-26	Sequence 26, Appl1	323	40	62.5	117	2	US-09-355-014-49	Sequence 49, Appl1
251	41	64.1	122	1	US-09-496-301-26	Sequence 94, Appl1	324	40	62.5	118	2	US-09-232-290-58	Sequence 58, Appl1
252	41	64.1	123	2	US-08-477-877B-94	Sequence 86, Appl1	325	40	62.5	119	2	US-08-737-560A-10	Sequence 10, Appl1
253	41	64.1	123	1	US-08-482-882-86	Sequence 86, Appl1	326	40	62.5	119	2	US-08-881-037-60	Sequence 60, Appl1
254	41	64.1	123	1	US-08-483-389-86	Sequence 86, Appl1	327	40	62.5	119	2	US-09-438-954-2	Sequence 2, Appl1
255	41	64.1	123	1	US-08-472-281A-94	Sequence 94, Appl1	328	40	62.5	119	2	US-09-438-954-4	Sequence 4, Appl1
256	41	64.1	123	1	US-08-487-113D-86	Sequence 86, Appl1	329	40	62.5	120	1	US-08-111-080-25	Sequence 25, Appl1
257	41	64.1	123	1	US-08-473-503-86	Sequence 86, Appl1	330	40	62.5	120	1	US-08-211-202-1	Sequence 1, Appl1
258	41	64.1	123	1	US-08-483-933-86	Sequence 86, Appl1	331	40	62.5	120	1	US-08-211-980-45	Sequence 25, Appl1
259	41	64.1	123	1	US-08-477-989B-94	Sequence 94, Appl1	332	40	62.5	120	1	US-08-211-980-45	Sequence 25, Appl1
260	41	64.1	123	1	US-08-720-420A-86	Sequence 86, Appl1	333	40	62.5	120	4	PCT-US93-07967-25	Sequence 25, Appl1
261	41	64.1	123	2	US-08-714-017-86	Sequence 86, Appl1	334	40	62.5	120	4	PCT-US93-07967-25	Sequence 25, Appl1
262	41	64.1	123	2	US-08-475-680-86	Sequence 86, Appl1	335	40	62.5	135	1	US-08-398-613A-50	Sequence 50, Appl1
263	41	64.1	123	2	US-09-462-140D-102	Sequence 102, App	336	40	62.5	135	1	US-08-398-612A-50	Sequence 50, Appl1
264	41	64.1	123	2	US-09-462-140D-105	Sequence 105, App	337	40	62.5	135	1	US-08-398-611A-50	Sequence 50, Appl1
265	41	64.1	129	2	US-09-471-276-864	Sequence 864, App	338	40	62.5	135	1	US-08-398-611A-50	Sequence 50, Appl1
266	41	64.1	138	1	US-08-482-882-78	Sequence 78, Appl1	339	40	62.5	135	2	US-08-491-334A-50	Sequence 50, Appl1
267	41	64.1	138	1	US-08-483-389-78	Sequence 78, Appl1	340	40	62.5	135	2	US-09-027-449-37	Sequence 37, Appl1
268	41	64.1	138	1	US-08-487-113D-78	Sequence 78, Appl1	341	40	62.5	135	2	US-09-027-449-37	Sequence 37, Appl1
269	41	64.1	138	1	US-08-473-503-78	Sequence 78, Appl1	342	40	62.5	135	2	US-09-026-985-37	Sequence 37, Appl1
270	41	64.1	138	1	US-08-483-933-78	Sequence 78, Appl1	343	40	62.5	135	2	US-09-121-952A-37	Sequence 37, Appl1
271	41	64.1	138	1	US-08-720-420A-78	Sequence 78, Appl1	344	40	62.5	141	2	US-09-234-340A-37	Sequence 37, Appl1
272	41	64.1	138	2	US-08-714-017-78	Sequence 78, Appl1	345	40	62.5	142	2	US-09-564-329A-13	Sequence 37, Appl1
273	41	64.1	138	2	US-08-475-680-78	Sequence 78, Appl1	346	40	62.5	142	2	US-09-564-329A-13	Sequence 37, Appl1
274	41	64.1	139	2	US-09-355-925-7	Sequence 7, Appl1	347	40	62.5	142	2	US-09-963-620-13	Sequence 13, Appl1
275	41	64.1	139	2	US-09-355-925-8	Sequence 8, Appl1	348	40	62.5	142	2	US-09-855-632-13	Sequence 13, Appl1
276	41	64.1	139	2	US-09-269-921-105	Sequence 105, App	349	40	62.5	142	2	US-09-934-773-13	Sequence 13, Appl1
277	41	64.1	139	2	US-09-269-921-108	Sequence 108, App	350	40	62.5	142	2	US-09-855-153-13	Sequence 13, Appl1
278	41	64.1	139	2	US-09-269-921-109	Sequence 109, App	351	40	62.5	142	2	US-09-855-153-13	Sequence 13, Appl1
279	41	64.1	139	2	US-09-269-921-110	Sequence 110, App	352	40	62.5	142	1	US-10-224-720-13	Sequence 2, Appl1
280	41	64.1	139	2	US-09-269-921-111	Sequence 111, App	353	40	62.5	142	1	US-08-737-129A-2	Sequence 14, Appl1
281	41	64.1	139	2	US-09-269-921-112	Sequence 112, App	354	40	62.5	242	1	US-08-392-338A-23	Sequence 23, Appl1
282	41	64.1	139	2	US-09-269-921-113	Sequence 113, App	355	40	62.5	242	1	US-08-92C-789-14	Sequence 14, Appl1
283	41	64.1	139	2	US-09-269-921-114	Sequence 114, App	356	40	62.5	242	2	US-09-166-750-23	Sequence 23, Appl1
284	41	64.1	139	2	US-09-269-921-115	Sequence 115, App	357	40	62.5	242	2	US-09-166-093-23	Sequence 23, Appl1
285	41	64.1	139	2	US-09-269-921-116	Sequence 116, App	358	40	62.5	242	2	US-09-166-094-23	Sequence 23, Appl1
286	41	64.1	139	2	US-09-269-921-117	Sequence 117, App	359	40	62.5	242	2	US-09-443-213-23	Sequence 23, Appl1
287	41	64.1	139	2	US-09-269-921-118	Sequence 118, App	360	40	62.5	242	6	5455030-17	Parent No. 5455030
288	41	64.1	139	2	US-09-269-921-119	Sequence 119, App	361	40	62.5	244	1	US-08-392-338A-13	Sequence 13, Appl1
289	41	64.1	139	2	US-09-269-921-120	Sequence 120, App	362	40	62.5	244	1	US-09-166-750-13	Sequence 13, Appl1
290	41	64.1	139	2	US-09-269-921-121	Sequence 121, App	363	40	62.5	244	2	US-09-166-093-13	Sequence 13, Appl1
291	41	64.1	139	2	US-09-269-921-122	Sequence 122, App	364	40	62.5	244	2	US-09-172-019-13	Sequence 13, Appl1
292	41	64.1	139	2	US-09-269-921-123	Sequence 123, App	365	40	62.5	244	2	US-09-172-019-13	Sequence 13, Appl1
293	41	64.1	139	2	US-09-269-921-124	Sequence 124, App	366	40	62.5	244	2	US-09-166-094-13	Sequence 13, Appl1
294	41	64.1	139	2	US-09-269-921-125	Sequence 125, App	367	40	62.5	244	2	US-09-443-213-13	Sequence 13, Appl1
295	41	64.1	139	2	US-09-269-921-126	Sequence 126, App	368	40	62.5	246	4	PCT-US93-11138-14	Sequence 14, Appl1
296	41	64.1	139	2	US-09-269-921-127	Sequence 127, App	369	40	62.5	246	1	US-08-469-658-57	Sequence 57, Appl1
297	41	64.1	139	2	US-09-269-921-128	Sequence 128, App	370	40	62.5	249	1	US-08-797-689-18	Sequence 18, Appl1
298	41	64.1	139	2	US-08-952-235-2	Sequence 2, Appl1	371	40	62.5	249	2	US-09-984-166-18	Sequence 18, Appl1
299	41	64.1	230	2	US-09-669-971-2	Sequence 2, Appl1	372	40	62.5	250	1	US-08-392-338A-15	Sequence 15, Appl1
300	41	64.1	230	2	US-10-620-049-23	Sequence 23, Appl1	373	40	62.5	250	1	US-09-166-750-13	Sequence 15, Appl1
301	41	64.1	247	2	US-10-620-049-25	Sequence 25, Appl1	374	40	62.5	250	2	US-09-172-019-15	Sequence 15, Appl1
302	41	64.1	389	2	US-09-802-540-12102	Sequence 12102, A	375	40	62.5	250	2	US-09-166-094-15	Sequence 15, Appl1
303	41	64.1	470	2	US-09-859-053-28	Sequence 28, Appl1	376	40	62.5	250	2	US-09-166-094-15	Sequence 15, Appl1
304	40	62.5	84	2	US-08-928-383B-16	Sequence 16, Appl1	377	40	62.5	250	2	US-09-443-213-15	Sequence 15, Appl1
305	40	62.5	97	1	US-08-211-202-127	Sequence 127, App	378	40	62.5	253	1	US-08-398-613A-58	Sequence 58, Appl1
306	40	62.5	97	1	US-08-211-202-129	Sequence 129, App	379	40	62.5	253	1	US-08-398-612A-58	Sequence 58, Appl1
307	40	62.5	108	2	US-08-477-347-7	Sequence 7, Appl1	380	40	62.5	253	1	US-08-398-611A-58	Sequence 58, Appl1
308	40	62.5	108	2	US-09-800-908-7	Sequence 7, Appl1	381	40	62.5	253	1	US-08-392-338A-17	Sequence 17, Appl1
309	40	62.5	109	1	US-07-942-245-21	Sequence 21, Appl1	382	40	62.5	253	1	US-08-491-334A-58	Sequence 58, Appl1
310	40	62.5	111	2	US-08-881-037-15	Sequence 15, Appl1	383	40	62.5	253	2	US-09-027-449-44	Sequence 44, Appl1
311	40	62.5	113	1	US-08-211-202-115	Sequence 115, App	384	40	62.5	253	2	US-09-027-449-52	Sequence 52, Appl1
312	40	62.5	117	2	US-09-027-449-48	Sequence 48, App	385	40	62.5	253	2	US-09-027-449-55	Sequence 55, Appl1
313	40	62.5	117	2	US-09-027-449-49	Sequence 49, App	386	40	62.5	253	2	US-09-166-750-17	Sequence 17, Appl1
314	40	62.5	117	2	US-08-804-444A-48	Sequence 48, App	387	40	62.5	253	2	US-09-166-093-17	Sequence 17, Appl1
315	40	62.5	117	2	US-08-804-444A-49	Sequence 49, App	388	40	62.5	253	2	US-09-172-019-17	Sequence 17, Appl1
316	40	62.5	117	2	US-09-026-985-48	Sequence 48, App	389	40	62.5	253	2	US-08-804-444A-14	Sequence 14, Appl1
317	40	62.5	117	2	US-09-026-985-49	Sequence 49, App	390	40	62.5	253	2	US-08-804-444A-52	Sequence 52, Appl1
318	40	62.5	117	2	US-09-121-952A-48	Sequence 48, App	391	40	62.5	253	2	US-08-804-444A-55	Sequence 55, Appl1
319	40	62.5	117	2	US-09-121-952A-49	Sequence 49, App	392	40	62.5	253	2	US-09-166-094-17	Sequence 17, Appl1

393	40	62.5	253	2	US-09-026-985-44	Sequence 44, Appl	466	39	60.9	119	2	US-09-406-532-2	Sequence 2, Appl
394	40	62.5	253	2	US-09-026-985-52	Sequence 52, Appl	467	39	60.9	119	2	US-09-254-180C-16	Sequence 16, Appl
395	40	62.5	253	2	US-09-026-985-55	Sequence 55, Appl	468	39	60.9	119	2	US-09-254-180C-18	Sequence 18, Appl
396	40	62.5	253	2	US-09-121-952A-44	Sequence 44, Appl	469	39	60.9	119	2	US-09-254-180C-19	Sequence 19, Appl
397	40	62.5	253	2	US-09-121-952A-52	Sequence 52, Appl	470	39	60.9	119	2	US-09-254-180C-149	Sequence 149, Appl
398	40	62.5	253	2	US-09-121-952A-55	Sequence 55, Appl	471	39	60.9	119	2	US-08-913-555-23	Sequence 23, Appl
399	40	62.5	253	2	US-09-234-340A-44	Sequence 44, Appl	472	39	60.9	121	1	US-08-480-434-79	Sequence 29, Appl
400	40	62.5	253	2	US-09-234-340A-52	Sequence 52, Appl	473	39	60.9	121	1	US-08-053-451B-29	Sequence 29, Appl
401	40	62.5	253	2	US-09-234-340A-55	Sequence 55, Appl	474	39	60.9	122	2	US-08-983-607-70	Sequence 30, Appl
402	40	62.5	253	2	US-09-443-213-17	Sequence 17, Appl	475	39	60.9	125	2	US-09-357-710A-20	Sequence 20, Appl
403	40	62.5	253	2	US-09-355-014-44	Sequence 44, Appl	476	39	60.9	125	2	US-09-357-707-20	Sequence 20, Appl
404	40	62.5	253	2	US-09-355-014-52	Sequence 52, Appl	477	39	60.9	125	2	US-09-357-708-20	Sequence 20, Appl
405	40	62.5	253	2	US-09-355-014-55	Sequence 55, Appl	478	39	60.9	126	1	US-08-480-434-18	Sequence 18, Appl
406	40	62.5	256	2	US-09-027-449-70	Sequence 70, Appl	479	39	60.9	126	1	US-08-480-434-19	Sequence 19, Appl
407	40	62.5	256	2	US-09-026-985-70	Sequence 70, Appl	480	39	60.9	126	1	US-08-053-451B-18	Sequence 18, Appl
408	40	62.5	256	2	US-09-121-952A-70	Sequence 70, Appl	481	39	60.9	126	1	US-08-053-451B-19	Sequence 19, Appl
409	40	62.5	256	2	US-09-234-340A-70	Sequence 70, Appl	482	39	60.9	128	1	US-08-202-047-21	Sequence 21, Appl
410	40	62.5	256	2	US-09-355-014-70	Sequence 70, Appl	483	39	60.9	128	2	US-08-964-690-21	Sequence 21, Appl
411	40	62.5	274	2	US-09-813-659-30	Sequence 30, Appl	484	39	60.9	132	2	US-09-386-658A-2	Sequence 2, Appl
412	40	62.5	274	2	US-09-549-067A-30	Sequence 30, Appl	485	39	60.9	134	1	US-08-137-117D-39	Sequence 39, Appl
413	40	62.5	298	2	US-09-027-449-60	Sequence 60, Appl	486	39	60.9	134	1	US-08-436-717-39	Sequence 39, Appl
414	40	62.5	298	2	US-08-804-444A-60	Sequence 60, Appl	487	39	60.9	135	1	US-08-621-751A-12	Sequence 12, Appl
415	40	62.5	298	2	US-09-026-985-60	Sequence 60, Appl	488	39	60.9	135	1	US-08-621-751A-16	Sequence 16, Appl
416	40	62.5	298	2	US-09-121-952A-60	Sequence 60, Appl	489	39	60.9	136	2	US-09-450-520A-4	Sequence 4, Appl
417	40	62.5	298	2	US-09-234-340A-60	Sequence 60, Appl	490	39	60.9	136	2	US-09-450-520A-8	Sequence 8, Appl
418	40	62.5	298	2	US-09-355-014-60	Sequence 60, Appl	491	39	60.9	138	1	US-07-634-278-85	Sequence 85, Appl
419	40	62.5	302	1	US-08-121-054C-18	Sequence 18, Appl	492	39	60.9	138	1	US-08-477-728-85	Sequence 85, Appl
420	40	62.5	302	1	US-08-121-054C-30	Sequence 30, Appl	493	39	60.9	138	1	US-08-474-040-85	Sequence 85, Appl
421	40	62.5	302	2	US-08-539-436-18	Sequence 18, Appl	494	39	60.9	138	1	US-08-487-200-85	Sequence 85, Appl
422	40	62.5	302	2	US-08-539-436-30	Sequence 30, Appl	495	39	60.9	138	2	US-08-484-537-85	Sequence 85, Appl
423	40	62.5	302	2	US-09-813-659-18	Sequence 18, Appl	496	39	60.9	138	2	US-09-254-180C-143	Sequence 143, Appl
424	40	62.5	302	2	US-09-813-659-32	Sequence 32, Appl	497	39	60.9	140	2	US-09-069-628-28	Sequence 28, Appl
425	40	62.5	302	2	US-09-549-067A-18	Sequence 18, Appl	498	39	60.9	152	1	US-07-634-278-101	Sequence 101, Appl
426	40	62.5	302	2	US-09-549-067A-32	Sequence 32, Appl	499	39	60.9	152	1	US-08-477-728-101	Sequence 101, Appl
427	40	62.5	355	2	US-08-875-811-41	Sequence 41, Appl	500	39	60.9	152	1	US-08-474-040-101	Sequence 101, Appl
428	40	62.5	355	2	US-08-875-811-49	Sequence 49, Appl	501	39	60.9	152	1	US-08-487-200-101	Sequence 101, Appl
429	40	62.5	355	2	US-08-875-811-64	Sequence 64, Appl	502	39	60.9	152	2	US-08-484-537-101	Sequence 101, Appl
430	40	62.5	358	2	US-08-875-811-45	Sequence 45, Appl	503	39	60.9	160	2	US-09-318-786-35	Sequence 35, Appl
431	40	62.5	358	2	US-08-875-811-51	Sequence 51, Appl	504	39	60.9	219	2	US-09-254-180C-180	Sequence 180, Appl
432	40	62.5	379	2	US-08-875-811-47	Sequence 47, Appl	505	39	60.9	337	2	US-09-543-681A-4829	Sequence 4829, Ap
433	40	62.5	379	2	US-08-875-811-43	Sequence 43, Appl	506	39	60.9	355	2	US-08-875-811-57	Sequence 57, Appl
434	40	62.5	452	2	US-09-027-449-71	Sequence 71, Appl	507	39	60.9	417	2	US-10-104-047-2563	Sequence 2563, Ap
435	40	62.5	452	2	US-09-026-985-71	Sequence 71, Appl	508	38	59.4	111	2	US-09-726-219A-171	Sequence 171, Appl
436	40	62.5	452	2	US-09-121-952A-71	Sequence 71, Appl	509	38	59.4	111	2	US-09-196-522-171	Sequence 171, Appl
437	40	62.5	452	2	US-09-234-340A-71	Sequence 71, Appl	510	38	59.4	118	2	US-08-983-607-74	Sequence 74, Appl
438	40	62.5	452	2	US-09-355-014-71	Sequence 71, Appl	511	38	59.4	119	1	US-08-553-497A-4	Sequence 4, Appl
439	39	60.9	14	1	US-08-204-656B-11	Sequence 11, Appl	512	38	59.4	121	2	US-08-983-607-20	Sequence 20, Appl
440	39	60.9	14	1	US-08-470-702-11	Sequence 11, Appl	513	38	59.4	139	1	US-08-894-607-20	Sequence 20, Appl
441	39	60.9	14	1	US-08-467-831-11	Sequence 11, Appl	514	38	59.4	219	2	US-08-924-180C-131	Sequence 131, Appl
442	39	60.9	20	1	US-08-053-451B-114	Sequence 114, App	515	38	59.4	219	2	US-09-254-180C-181	Sequence 181, Appl
443	39	60.9	104	2	US-10-014-012-216	Sequence 216, App	516	38	59.4	252	1	US-08-894-922A-14	Sequence 14, Appl
444	39	60.9	114	2	US-09-450-520A-9	Sequence 9, Appl	517	38	59.4	265	1	US-08-403-653-16	Sequence 16, Appl
445	39	60.9	114	2	US-09-450-520A-10	Sequence 10, Appl	518	38	59.4	271	1	US-08-894-922A-10	Sequence 10, Appl
446	39	60.9	114	2	US-09-450-520A-11	Sequence 11, Appl	519	38	59.4	468	1	US-08-204-656B-8	Sequence 8, Appl
447	39	60.9	114	2	US-09-726-219A-215	Sequence 215, App	520	38	59.4	468	1	US-08-470-702-9	Sequence 9, Appl
448	39	60.9	114	2	US-09-726-219A-224	Sequence 224, App	521	38	59.4	468	1	US-08-467-831-9	Sequence 9, Appl
449	39	60.9	114	2	US-09-726-219A-235	Sequence 235, App	522	38	59.4	545	2	US-09-248-796A-18865	Sequence 18865, A
450	39	60.9	114	2	US-09-196-522-215	Sequence 215, App	523	38	59.4	580	2	US-09-949-016-10834	Sequence 10834, A
451	39	60.9	114	2	US-09-196-522-224	Sequence 224, App	524	38	59.4	600	2	US-09-538-092-2117	Sequence 2117, App
452	39	60.9	114	2	US-09-196-522-235	Sequence 235, App	525	38	59.4	600	2	US-09-487-558B-158	Sequence 158, App
453	39	60.9	117	1	US-07-634-278-105	Sequence 105, App	526	38	59.4	1867	2	US-09-824-574-5	Sequence 5, Appl
454	39	60.9	117	1	US-08-477-728-105	Sequence 105, App	527	37	57.8	8	4	US-08-221-560-9	Sequence 9, Appl
455	39	60.9	117	1	US-08-474-040-105	Sequence 105, App	528	37	57.8	8	4	PCT-US95-04018-71	Sequence 71, Appl
456	39	60.9	117	1	US-08-487-200-105	Sequence 105, App	529	37	57.8	10	4	US-08-221-580-2	Sequence 2, Appl
457	39	60.9	117	2	US-08-484-537-105	Sequence 105, App	530	37	57.8	10	4	PCT-US95-04018-64	Sequence 64, Appl
458	39	60.9	118	2	US-09-065-059-5	Sequence 5, Appl	531	37	57.8	100	2	US-09-534-717-608	Sequence 608, App
459	39	60.9	118	2	US-08-913-555-5	Sequence 5, Appl	532	37	57.8	108	2	US-09-486-814A-4	Sequence 4, Appl
460	39	60.9	119	1	US-07-634-278-64	Sequence 64, Appl	533	37	57.8	114	2	US-09-726-219A-228	Sequence 228, App
461	39	60.9	119	1	US-08-477-728-64	Sequence 64, Appl	534	37	57.8	114	2	US-09-196-522-228	Sequence 228, Appl
462	39	60.9	119	1	US-08-474-040-64	Sequence 64, Appl	535	37	57.8	116	1	US-08-428-197-10	Sequence 10, Appl
463	39	60.9	119	1	US-08-487-200-64	Sequence 64, Appl	536	37	57.8	116	4	PCT-US93-10555-10	Sequence 10, Appl
464	39	60.9	119	1	US-08-053-451B-125	Sequence 125, App	537	37	57.8	119	1	US-08-318-157B-2	Sequence 2, Appl
465	39	60.9	119	2	US-08-484-537-64	Sequence 64, Appl	538	37	57.8	119	1	US-08-318-157B-8	Sequence 8, Appl

539	37	57.8	119	1	US-08-318-157B-9	Sequence 9, Appl1	612	36.5	57.0	575	2	US-09-399-886-8	Sequence 8, Appl1
540	37	57.8	119	1	US-08-318-157B-10	Sequence 10, Appl1	613	36.5	57.0	575	2	US-09-396-260-8	Sequence 8, Appl1
541	37	57.8	119	1	US-08-318-157B-11	Sequence 11, Appl1	614	36.5	57.0	575	2	US-09-576-281-8	Sequence 8, Appl1
542	37	57.8	119	1	US-08-318-157B-12	Sequence 12, Appl1	615	36.5	57.0	576	1	US-08-172-311B-2	Sequence 2, Appl1
543	37	57.8	119	1	US-08-318-157B-13	Sequence 13, Appl1	616	36.5	56.2	7	2	US-10-007-790-5	Sequence 5, Appl1
544	37	57.8	119	1	US-08-318-157B-14	Sequence 14, Appl1	617	36	56.2	7	2	US-10-007-790-5	Sequence 5, Appl1
545	37	57.8	119	1	US-08-318-157B-15	Sequence 15, Appl1	618	36	56.2	10	1	US-08-208-886C-83	Sequence 83, Appl1
546	37	57.8	119	1	US-08-318-157B-17	Sequence 17, Appl1	619	36	56.2	10	1	US-08-704-744-85	Sequence 85, Appl1
547	37	57.8	119	2	US-09-253-794-2	Sequence 2, Appl1	620	36	56.2	10	1	US-08-469-557-64	Sequence 64, Appl1
548	37	57.8	119	2	US-09-253-794-8	Sequence 8, Appl1	621	36	56.2	10	1	US-08-290-793B-64	Sequence 64, Appl1
549	37	57.8	119	2	US-09-253-794-9	Sequence 9, Appl1	622	36	56.2	10	2	US-08-908-469-1	Sequence 1, Appl1
550	37	57.8	119	2	US-09-253-794-10	Sequence 10, Appl1	623	36	56.2	17	2	US-09-513-968-40	Sequence 40, Appl1
551	37	57.8	119	2	US-09-253-794-11	Sequence 11, Appl1	624	36	56.2	77	2	US-09-205-658-218	Sequence 218, Appl1
552	37	57.8	119	2	US-09-253-794-12	Sequence 12, Appl1	625	36	56.2	88	2	US-09-726-219A-172	Sequence 172, Appl1
553	37	57.8	119	2	US-09-253-794-13	Sequence 13, Appl1	626	36	56.2	88	2	US-09-196-522-172	Sequence 172, Appl1
554	37	57.8	119	2	US-09-253-794-14	Sequence 14, Appl1	627	36	56.2	88	2	US-09-534-717-663	Sequence 663, Appl1
555	37	57.8	119	2	US-09-253-794-15	Sequence 15, Appl1	628	36	56.2	92	2	US-08-783-853A-84	Sequence 84, Appl1
556	37	57.8	119	2	US-09-253-794-17	Sequence 17, Appl1	629	36	56.2	92	2	US-09-344-050-94	Sequence 84, Appl1
557	37	57.8	137	1	US-08-574-699A-4	Sequence 4, Appl1	630	36	56.2	98	2	US-07-944-245-37	Sequence 37, Appl1
558	37	57.8	267	2	US-09-419-788B-30	Sequence 30, Appl1	631	36	56.2	98	2	US-10-194-975-15	Sequence 15, Appl1
559	37	57.8	297	2	US-09-486-814A-2	Sequence 2, Appl1	632	36	56.2	98	2	US-09-534-717-663	Sequence 663, Appl1
560	37	57.8	485	2	US-08-600-656-7	Sequence 7, Appl1	633	36	56.2	98	2	US-09-534-717-663	Sequence 664, Appl1
561	37	57.8	485	2	US-09-170-670-6	Sequence 6, Appl1	634	36	56.2	98	2	US-09-534-717-665	Sequence 665, Appl1
562	37	57.8	485	2	US-09-193-068-6	Sequence 6, Appl1	635	36	56.2	98	2	US-09-534-717-665	Sequence 666, Appl1
563	37	57.8	485	2	US-09-183-412-6	Sequence 6, Appl1	636	36	56.2	98	2	US-09-534-717-665	Sequence 667, Appl1
564	37	57.8	485	2	US-09-354-191A-7	Sequence 7, Appl1	637	36	56.2	100	2	US-09-905-243-47	Sequence 47, Appl1
565	37	57.8	485	2	US-09-391-023A-13	Sequence 13, Appl1	638	36	56.2	100	2	US-09-840-459-36	Sequence 36, Appl1
566	37	57.8	485	2	US-09-291-734-6	Sequence 6, Appl1	639	36	56.2	100	2	US-09-783-853A-20	Sequence 20, Appl1
567	37	57.8	485	2	US-09-290-734-24	Sequence 24, Appl1	640	36	56.2	112	2	US-08-425-336-124	Sequence 29, Appl1
568	37	57.8	485	2	US-09-290-734-26	Sequence 26, Appl1	641	36	56.2	112	2	US-08-425-336-124	Sequence 29, Appl1
569	37	57.8	485	2	US-09-417-359A-5	Sequence 5, Appl1	642	36	56.2	115	2	US-08-477-488B-124	Sequence 124, Appl1
570	37	57.8	485	2	US-09-381-687-5	Sequence 5, Appl1	643	36	56.2	115	2	US-09-513-999C-4117	Sequence 4117, Appl1
571	37	57.8	485	2	US-09-545-586-6	Sequence 6, Appl1	644	36	56.2	117	2	US-09-513-999C-4117	Sequence 4117, Appl1
572	37	57.8	485	2	US-09-545-586-24	Sequence 24, Appl1	645	36	56.2	117	2	US-09-513-999C-4117	Sequence 4117, Appl1
573	37	57.8	485	2	US-09-545-586-26	Sequence 26, Appl1	646	36	56.2	117	2	US-09-513-999C-4117	Sequence 4117, Appl1
574	37	57.8	485	2	US-09-540-715A-13	Sequence 13, Appl1	647	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
575	37	57.8	485	2	US-09-769-864-6	Sequence 6, Appl1	648	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
576	37	57.8	485	2	US-10-025-648-7	Sequence 7, Appl1	649	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
577	37	57.8	485	2	US-09-441-313-6	Sequence 6, Appl1	650	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
578	37	57.8	497	2	US-09-452-991A-22575	Sequence 22575, A	651	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
579	36.5	57.0	78	2	US-09-471-276-852	Sequence 852, App	652	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
580	36.5	57.0	116	4	US-08-561-521-41	Sequence 41, Appl1	653	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
581	36.5	57.0	116	4	PCT-US95-01219-41	Sequence 41, Appl1	654	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
582	36.5	57.0	119	2	US-10-194-975-122	Sequence 122, App	655	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
583	36.5	57.0	121	1	US-07-634-278-52	Sequence 52, Appl1	656	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
584	36.5	57.0	121	1	US-07-634-278-53	Sequence 53, Appl1	657	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
585	36.5	57.0	121	1	US-08-477-728-52	Sequence 52, Appl1	658	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
586	36.5	57.0	121	1	US-08-477-728-53	Sequence 53, Appl1	659	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
587	36.5	57.0	121	1	US-08-474-040-52	Sequence 52, Appl1	660	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
588	36.5	57.0	121	1	US-08-474-040-53	Sequence 53, Appl1	661	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
589	36.5	57.0	121	1	US-08-487-200-52	Sequence 52, Appl1	662	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
590	36.5	57.0	121	1	US-08-487-200-53	Sequence 53, Appl1	663	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
591	36.5	57.0	121	2	US-08-484-537-52	Sequence 52, Appl1	664	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
592	36.5	57.0	121	2	US-08-484-537-53	Sequence 53, Appl1	665	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
593	36.5	57.0	124	2	US-08-657-012-23	Sequence 23, Appl1	666	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
594	36.5	57.0	124	2	US-09-013-872-23	Sequence 23, Appl1	667	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
595	36.5	57.0	124	2	US-09-184-198-23	Sequence 23, Appl1	668	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
596	36.5	57.0	124	2	US-09-633-653-23	Sequence 23, Appl1	669	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
597	36.5	57.0	135	1	US-08-137-117D-27	Sequence 27, Appl1	670	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
598	36.5	57.0	135	1	US-08-137-117D-100	Sequence 100, App	671	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
599	36.5	57.0	135	1	US-08-137-117D-112	Sequence 112, App	672	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
600	36.5	57.0	135	1	US-08-137-117D-112	Sequence 112, App	673	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
601	36.5	57.0	135	1	US-08-436-717-27	Sequence 27, Appl1	674	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
602	36.5	57.0	135	1	US-08-436-717-100	Sequence 100, App	675	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
603	36.5	57.0	135	1	US-08-436-717-102	Sequence 102, App	676	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
604	36.5	57.0	135	1	US-08-436-717-112	Sequence 112, App	677	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
605	36.5	57.0	572	1	US-09-032-315-7	Sequence 7, Appl1	678	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
606	36.5	57.0	572	1	US-08-993-318A-7	Sequence 7, Appl1	679	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
607	36.5	57.0	572	2	US-09-399-886-7	Sequence 7, Appl1	680	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
608	36.5	57.0	572	2	US-09-396-260-7	Sequence 7, Appl1	681	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
609	36.5	57.0	572	2	US-09-576-281-7	Sequence 7, Appl1	682	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
610	36.5	57.0	575	1	US-09-032-315-8	Sequence 8, Appl1	683	36	56.2	118	1	US-08-472-788A-89	Sequence 89, Appl1
611	36.5	57.0	575	1	US-08-993-318A-8	Sequence 8, Appl1	684	36	56.2	118	2	US-08-908-469-108	Sequence 108, App

685	36	56.2	118	2	US-10-268-883-9	Sequence 9, Appl1	758	36	56.2	467	1	US-08-704-744-81	Sequence 81, Appl1
686	36	56.2	119	1	US-08-478-039-65	Sequence 65, Appl1	759	36	56.2	468	1	US-08-204-656B-2	Sequence 2, Appl1
687	36	56.2	119	1	US-08-476-349A-65	Sequence 65, Appl1	760	36	56.2	468	1	US-08-470-702-6	Sequence 6, Appl1
688	36	56.2	119	2	US-08-933-983-78	Sequence 78, Appl1	761	36	56.2	468	1	US-08-467-831-6	Sequence 6, Appl1
689	36	56.2	119	2	US-08-933-983-80	Sequence 80, Appl1	762	36	56.2	491	2	US-10-011-125A-2	Sequence 2, Appl1
690	36	56.2	120	2	US-09-233-290-48	Sequence 48, Appl1	763	36	56.2	618	2	US-10-104-047-3605	Sequence 3605, Ap
691	36	56.2	121	2	US-08-783-853A-7	Sequence 7, Appl1	764	36	56.2	622	1	US-08-356-786-16	Sequence 16, Appl1
692	36	56.2	121	2	US-08-783-853A-31	Sequence 31, Appl1	765	36	56.2	679	2	US-09-248-796A-18620	Sequence 18620, A
693	36	56.2	121	2	US-08-783-853A-52	Sequence 52, Appl1	766	36	56.2	3290	1	US-09-328-332-1486	Sequence 5486, Ap
694	36	56.2	121	2	US-08-783-853A-111	Sequence 111, App	767	35.5	55.5	124	1	US-07-934-373C-46	Sequence 46, Appl1
695	36	56.2	121	2	US-09-344-050-7	Sequence 7, Appl1	768	35.5	55.5	124	2	US-08-437-642B-46	Sequence 46, Appl1
696	36	56.2	121	2	US-09-344-050-31	Sequence 31, Appl1	769	35.5	55.5	232	1	US-08-425-763-2	Sequence 2, Appl1
697	36	56.2	121	2	US-09-344-050-52	Sequence 52, Appl1	770	35.5	55.5	232	1	US-07-934-373C-26	Sequence 26, Appl1
698	36	56.2	121	2	US-09-344-050-111	Sequence 111, App	771	35.5	55.5	232	1	US-07-934-373C-27	Sequence 27, Appl1
699	36	56.2	121	2	US-09-440-781-98	Sequence 98, Appl1	772	35.5	55.5	232	1	US-07-934-373C-28	Sequence 28, Appl1
700	36	56.2	123	2	US-08-783-853A-109	Sequence 109, App	773	35.5	55.5	232	1	US-07-934-373C-29	Sequence 29, Appl1
701	36	56.2	123	2	US-09-344-050-109	Sequence 109, App	774	35.5	55.5	232	1	US-07-934-373C-31	Sequence 31, Appl1
702	36	56.2	123	2	US-08-908-469-7	Sequence 7, Appl1	775	35.5	55.5	232	1	US-07-934-373C-32	Sequence 32, Appl1
703	36	56.2	123	2	US-08-908-469-9	Sequence 9, Appl1	776	35.5	55.5	232	1	US-07-934-373C-33	Sequence 33, Appl1
704	36	56.2	123	2	US-08-908-469-14	Sequence 14, Appl1	777	35.5	55.5	232	1	US-07-934-373C-34	Sequence 34, Appl1
705	36	56.2	123	2	US-08-908-469-16	Sequence 16, Appl1	778	35.5	55.5	232	1	US-07-934-373C-35	Sequence 35, Appl1
706	36	56.2	124	2	US-08-428-197-44	Sequence 44, Appl1	779	35.5	55.5	232	1	US-07-934-373C-36	Sequence 36, Appl1
707	36	56.2	124	2	US-09-543-681A-6834	Sequence 6834, Ap	780	35.5	55.5	232	1	US-07-934-373C-37	Sequence 37, Appl1
708	36	56.2	124	4	PCT-US93-1055-44	Sequence 44, Appl1	781	35.5	55.5	232	1	US-07-934-373C-38	Sequence 38, Appl1
709	36	56.2	125	1	US-08-665-202-45	Sequence 45, Appl1	782	35.5	55.5	232	1	US-08-788-800-10	Sequence 10, Appl1
710	36	56.2	125	1	US-08-665-202-46	Sequence 46, Appl1	783	35.5	55.5	232	2	US-08-437-642B-26	Sequence 26, Appl1
711	36	56.2	125	1	US-08-665-202-49	Sequence 49, Appl1	784	35.5	55.5	232	2	US-08-437-642B-27	Sequence 27, Appl1
712	36	56.2	125	1	US-08-665-202-51	Sequence 51, Appl1	785	35.5	55.5	232	2	US-08-437-642B-28	Sequence 28, Appl1
713	36	56.2	125	1	US-09-315-574-45	Sequence 45, Appl1	786	35.5	55.5	232	2	US-08-437-642B-29	Sequence 29, Appl1
714	36	56.2	125	2	US-09-315-574-46	Sequence 46, Appl1	787	35.5	55.5	232	2	US-08-437-642B-31	Sequence 31, Appl1
715	36	56.2	125	2	US-09-315-574-49	Sequence 49, Appl1	788	35.5	55.5	232	2	US-08-437-642B-32	Sequence 32, Appl1
716	36	56.2	125	2	US-09-315-574-51	Sequence 51, Appl1	789	35.5	55.5	232	2	US-08-437-642B-33	Sequence 33, Appl1
717	36	56.2	128	1	US-08-276-852-62	Sequence 62, Appl1	790	35.5	55.5	232	2	US-08-437-642B-34	Sequence 34, Appl1
718	36	56.2	128	1	US-08-899-575-62	Sequence 62, Appl1	791	35.5	55.5	232	2	US-08-437-642B-35	Sequence 35, Appl1
719	36	56.2	128	1	US-08-899-575-62	Sequence 62, Appl1	792	35.5	55.5	232	2	US-08-437-642B-36	Sequence 36, Appl1
720	36	56.2	128	1	US-09-134-000C-5776	Sequence 5776, Ap	793	35.5	55.5	232	2	US-08-437-642B-37	Sequence 37, Appl1
721	36	56.2	128	4	PCT-US95-08743-62	Sequence 62, Appl1	794	35.5	55.5	232	2	US-08-437-642B-38	Sequence 38, Appl1
722	36	56.2	137	2	US-10-268-883-8	Sequence 8, Appl1	795	35.5	55.5	232	2	US-08-811-757-2	Sequence 2, Appl1
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752	36	56.2	252	2	US-08-902-486-9	Sequence 9, Appl1	825	35.5	55.5	454	2	US-08-146-206C-22	Sequence 22, Appl1
753	36	56.2	254	2	US-08-908-469-101	Sequence 101, App	826	35.5	55.5	454	2	US-09-705-686-22	Sequence 22, Appl1
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755	36	56.2	365	2	US-08-875-811-53	Sequence 53, Appl1	828	35.5	55.5	454	2	US-09-705-398-22	Sequence 22, Appl1
756	36	56.2	366	2	US-08-875-811-55	Sequence 55, Appl1	829	35.5	55.5	454	4	PCT-US93-07832-22	Sequence 22, Appl1
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833	35.5	55.5	469	2	US-09-705-686-23	Sequence 23, Appl	906	35	54.7	128	4	PCT-US95-08743-60	Sequence 60, Appl
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977 34 53.1 106 1 US-07-942-245-15 Sequence 15, Appl
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983 34 53.1 123 2 US-08-908-469-127 Sequence 26, Appl
984 34 53.1 126 2 US-08-983-607-26 Sequence 13, Appl
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993 34 53.1 428 2 US-09-134-001C-4879 Sequence 4879, A
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ALIGNMENTS

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RESULT 1
US-08-974-899-10
; Sequence 10, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Prestea, Leonard G.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-10
Query Match 100.0%; Score 64; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00063;

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYSFTGHMMN 10
Db 1 GYSFTGHMMN 10

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RESULT 2
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; Sequence 10, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Prestea, Leonard G.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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Query Match 100.0%; Score 64; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GYSFTGHMMN 10
Db 1 GYSFTGHMMN 10

```

```

RESULT 3
US-08-974-899-4
; Sequence 4, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Prestea, Leonard G.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

```

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-4

Query Match 100.0%; Score 64; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
Db 26 GYSFTGHMNN 35

RESULT 4
US-08-974-899-5
Sequence 5, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-5

Query Match 100.0%; Score 64; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
Db 26 GYSFTGHMNN 35

RESULT 5
US-08-974-899-24
Sequence 24, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-24

Query Match 100.0%; Score 64; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
Db 26 GYSFTGHMNN 35

RESULT 6
US-09-795-798-4
Sequence 4, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-795-798-4
Query Match 100.0%; Score 64; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYSFTGHMNN 10
|||
Db 26 GYSFTGHMNN 35
RESULT 7
US-09-795-798-5
Sequence 5, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-795-798-5
Query Match 100.0%; Score 64; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYSFTGHMNN 10
|||
Db 26 GYSFTGHMNN 35
RESULT 8
US-09-795-798-24
Sequence 24, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-795-798-24
Query Match 100.0%; Score 64; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYSFTGHMNN 10
|||

Db 26 GVSFTGHMNN 35

RESULT 9
US-09-027-449-50

Sequence 50, Application US/09027449
Patent No. 6025158

GENERAL INFORMATION:

APPLICANT: Gonzalez, Tania R.

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and

TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/027,449

FILING DATE: 20-Feb-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/074,330

FILING DATE: 22-Jan-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/038,664

FILING DATE: 21-Feb-1997

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R3-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-027-449-50

Query Match 93.8%; Score 60; DB 2; Length 116;

Best Local Similarity 90.0%; Pred. No. 0.029;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSFTGHMNN 10

Db 26 GVSFTGHMNN 35

RESULT 10

US-08-804-444A-50

Sequence 50, Application US/0880444A

Patent No. 6117980

GENERAL INFORMATION:

APPLICANT: Gonzalez, Tania N

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/804,444A

FILING DATE: 21-Feb-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-804-444A-50

Query Match 93.8%; Score 60; DB 2; Length 116;

Best Local Similarity 90.0%; Pred. No. 0.029;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GVSFTGHMNN 10

Db 26 GVSFTGHMNN 35

RESULT 11

US-09-026-985-50

Sequence 50, Application US/09026985

Patent No. 6133426

GENERAL INFORMATION:

APPLICANT: Gonzalez, Tania R.

APPLICANT: Leong, Steven R.

APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and

TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/026,985

FILING DATE: 20-Feb-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R3-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: Amino Acid

```

:       TOPOLOGY:   Linear
US-09-026-985-50

Query Match          93.8%; Score 60; DB 2; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.029;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYSFTGHMWN 10
       |:|||||
Db      26 GFSFTGHMWN 35

RESULT 12
US-09-121-952A-50
: Sequence 50, Application US/09121952A
: Patent No. 6458355
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc., Hsei, Vanessa
: APPLICANT: Koumenis, Iphigenia
: APPLICANT: Leong, Steven R.
: APPLICANT: Presta, Leonard G.
: APPLICANT: Shahrokh, Zahra
: APPLICANT: Zapata, Gerardo A.
: TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
: TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/121,952A
: FILING DATE: 24-Jul-1998
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/074330
: FILING DATE: 22-Jan-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/075467
: FILING DATE: 20-FEB-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P1085R4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 116 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
US-09-121-952A-50

Query Match          93.8%; Score 60; DB 2; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.029;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYSFTGHMWN 10
       |:|||||
Db      26 GFSFTGHMWN 35

RESULT 13
US-09-234-340A-50

: Sequence 50, Application US/09234340A
: Patent No. 6468532
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc., Hsei, Vanessa
: APPLICANT: Koumenis, Iphigenia
: APPLICANT: Leong, Steven R.
: APPLICANT: Presta, Leonard G.
: APPLICANT: Shahrokh, Zahra
: APPLICANT: Zapata, Gerardo A.
: TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
: TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/234,340A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/121,952
: FILING DATE: 24-Jul-1998
: APPLICATION NUMBER: 60/074330
: FILING DATE: 22-Jan-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/075467
: FILING DATE: 20-FEB-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P1085R4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 116 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
US-09-234-340A-50

Query Match          93.8%; Score 60; DB 2; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.029;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYSFTGHMWN 10
       |:|||||
Db      26 GFSFTGHMWN 35

RESULT 14
US-09-355-014-50
: Sequence 50, Application US/09355014
: Patent No. 6670033
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc., Hsei, Vanessa
: APPLICANT: Koumenis, Iphigenia
: APPLICANT: Leong, Steven R.
: APPLICANT: Presta, Leonard G.
: APPLICANT: Shahrokh, Zahra
: APPLICANT: Zapata, Gerardo A.
: TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
: Humanized Anti-IL-8 Monoclonal Antibodies
: NUMBER OF SEQUENCES: 72
```

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/355,014
;; FILING DATE: 21-Jul-1999
;;
;; CLASSIFICATION: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P1085R3PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-5530
;; TELEFAX: 650/952-9881
;;
;; INFORMATION FOR SEQ ID NO: 50:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 116 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-355-014-50

Query Match 93.8%; Score 60; DB 2; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.029;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
||:|||||
Db 26 GYSFTGHMWN 35

RESULT 15
US-09-948-004-16
; Sequence 16, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 BP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-16

Query Match 81.2%; Score 52; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.51;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||:|
Db 36 GYSFTSYMWN 45

RESULT 16
US-08-767-128-2
; Sequence 2, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:

;; APPLICANT: WYLIE, DWANE E.
;; APPLICANT: LOPEZ, OSVALDO
;; APPLICANT: MURRAY, PETER JOSEPH
;; APPLICANT: GOEBEL, PETER
;; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
;; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
;; NUMBER OF SEQUENCES: 46
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: Merchant, Gould, Smith, Edell, Welter & Schmidt
;; STREET: 3100 No. 6111079west Center, 90 South Seventh St
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/767,128
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/09258
;; FILING DATE: 05-JUN-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/541,373
;; FILING DATE: 10-OCT-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/462,798
;; FILING DATE: 05-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Carter, Charles G.
;; REGISTRATION NUMBER: 35,093
;; REFERENCE/DOCKET NUMBER: 8648.49USF1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612/371-5278
;; TELEFAX: 612/332-9081
;;
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 118 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
US-08-767-128-2

Query Match 81.2%; Score 52; DB 2; Length 118;
Best Local Similarity 80.0%; Pred. No. 0.52;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||:|
Db 26 GYSFTSYMWN 35

RESULT 17
US-08-767-128-8
; Sequence 8, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO

```

; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 611079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-767-128-8

Query Match      81.2%; Score 52; DB 2; Length 118;
Best Local Similarity 80.0%; Pred. No. 0.52;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMWN 10
      |||||:||||
Db      26 GYSFTSYMWN 35

RESULT 18
US-09-948-004-14
; Sequence 14, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Mathias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; TITLE OF INVENTION: Immunological disorders
; FILE REFERENCE: E 2411 EP
```

```

; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-948-004-14

Query Match      81.2%; Score 52; DB 2; Length 138;
Best Local Similarity 80.0%; Pred. No. 0.61;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMWN 10
      |||||:||||
Db      45 GYSFTSYMWN 54

RESULT 19
US-09-948-004-18
; Sequence 18, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Mathias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-948-004-18

Query Match      81.2%; Score 52; DB 2; Length 495;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMWN 10
      |||||:||||
Db      148 GYSFTSYMWN 157

RESULT 20
US-08-468-252-5
; Sequence 5, Application US/08468252
; Patent No. 5910486
; GENERAL INFORMATION:
; APPLICANT: Curiel, David T.
; APPLICANT: Deshane, Jessy
; APPLICANT: King, C. Richter
; TITLE OF INVENTION: Methods for Modulating Protein Function in
; TITLE OF INVENTION: Cells Using Intracellular Antibody Homologues
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,252
; FILING DATE: 06-SEP-1994
```

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Geary, William C. III
REGISTRATION NUMBER: 31,359
REFERENCE/DOCKET NUMBER: UAG-009
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-252-5

Query Match 79.7%; Score 51; DB 1; Length 237;
Best Local Similarity 90.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
Db 146 GYSFTGHMNN 155

RESULT 21
US-08-668-706B-5
Sequence 5, Application US/08668706B
Patent No. 6028059
GENERAL INFORMATION:
APPLICANT: Curiel, David T.
APPLICANT: Deshane, Jessy
APPLICANT: King, C. Richter
TITLE OF INVENTION: Methods for Modulating Protein Function in
TITLE OF INVENTION: Cells Using Intracellular Antibody Homologues
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D., J.D.
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,706B
FILING DATE: June 24, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Benjamin Aaron
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5874C1P
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE:
US-08-668-706B-5

Query Match 79.7%; Score 51; DB 2; Length 237;

Best Local Similarity 90.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
Db 146 GYSFTGHMNN 155

RESULT 22
PCT-US95-10740-5
Sequence 5, Application PC/TUS9510740
GENERAL INFORMATION:
APPLICANT: Curiel, David T.
APPLICANT: Deshane, Jessy
APPLICANT: King, C. Richter
TITLE OF INVENTION: Methods for Modulating Protein Function in Cells Using Intra
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10740
FILING DATE: 06-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Geary, William C. III
REGISTRATION NUMBER: 31,359
REFERENCE/DOCKET NUMBER: UAG-009
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-10740-5

Query Match 79.7%; Score 51; DB 4; Length 237;
Best Local Similarity 90.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
Db 146 GYSFTGHMNN 155

RESULT 23
US-09-543-681A-6475
Sequence 6475, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709,1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6475
LENGTH: 269

```
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6475

Query Match      79.7%; Score 51; DB 2; Length 269;
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYSFTGHMNN 10
Db      177 GYDFIGHMNN 186

RESULT 24
US-07-946-421-24
; Sequence 24, Application US/07946421
; Patent No. 5558864
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettleborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,421
; FILING DATE: 06-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00480
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 911933892
; FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: Merck 1430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-07-946-421-24

Query Match      78.1%; Score 50; DB 1; Length 140;
Best Local Similarity 70.0%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMNN 10
Db      45 GYFTSHMMH 54

RESULT 25
US-08-553-497A-26
; Sequence 26, Application US/08553497A
```

```
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESC
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIUTATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-553-497A-26

Query Match      78.1%; Score 50; DB 1; Length 242;
Best Local Similarity 70.0%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMNN 10
Db      26 GYFTSHMMH 35

RESULT 26
US-08-553-497A-20
; Sequence 20, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
```

```
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-20

Query Match          78.1%; Score 50; DB 1; Length 244;
Best Local Similarity 70.0%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMNN 10
DB      26 GYFTSHMWH 35

RESULT 27
US-08-553-497A-22
Sequence 22, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSLOW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF SEQUENCES: 30
```

```
CORRESPONDENCE ADDRESS:
ADDRESS: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-22

Query Match          78.1%; Score 50; DB 1; Length 244;
Best Local Similarity 70.0%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMNN 10
DB      26 GYFTSHMWH 35

RESULT 28
US-08-553-497A-24
Sequence 24, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSLOW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-497A-24
```

```
Query Match          78.1%; Score 50; DB 1; Length 246;
Best Local Similarity 70.0%; Pred. No. 2.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GYSFTGHMMN 10
        ||:|||||:
Db      26 GYFTSHMMH 35
```

```
RESULT 29
US-09-214-095D-118
; Sequence 118, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landt, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 118
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
; US-09-214-095D-118
```

```
Query Match          76.6%; Score 49; DB 2; Length 113;
Best Local Similarity 70.0%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GYSFTGHMMN 10
        ||:|||||:
Db      25 GYFTDMMH 34
```

```
RESULT 30
US-09-940-727B-118
; Sequence 118, Application US/09940727B
; Patent No. 6913917
```

```
; GENERAL INFORMATION:
; APPLICANT: Landt, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 118
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
; US-09-940-727B-118
```

```
Query Match          76.6%; Score 49; DB 2; Length 113;
Best Local Similarity 70.0%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GYSFTGHMMN 10
        ||:|||||:
Db      25 GYFTDMMH 34
```

```
RESULT 31
US-09-698-705-4
; Sequence 4, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P1777R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 4
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 46-48, 50-52
; OTHER INFORMATION: unknown amino acid
; US-09-698-705-4
```

```
Query Match          76.6%; Score 49; DB 2; Length 115;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
Qy      1 GYSFTGHMMN 10
        ||:|||||:
Db      17 GYFTNMMN 26
```

```
RESULT 32
US-08-672-345C-17
; Sequence 17, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landt, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
```


NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-17

Query Match 76.6%; Score 49; DB 1; Length 116;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNM 10
||:|||||:
DB 25 GYFTDHWMH 34

RESULT 33
US-09-214-095D-17
Sequence 17, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
LENGTH: 116
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-214-095D-17

Query Match 76.6%; Score 49; DB 2; Length 116;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNM 10
||:|||||:
DB 25 GYFTDHWMH 34

RESULT 34
US-09-940-727B-17
Sequence 17, Application US/09940727B
Patent No. 6913917

GENERAL INFORMATION:
APPLICANT: Landry, Donald W
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B
CURRENT APPLICATION NUMBER: US/09/940,727B
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 09/214,095
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: PCT/US97/10965
PRIOR FILING DATE: 1997-06-25
PRIOR APPLICATION NUMBER: 08/672,345
PRIOR FILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 116
TYPE: PRT
ORGANISM: mouse
US-09-940-727B-17

Query Match 76.6%; Score 49; DB 2; Length 116;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNM 10
||:|||||:
DB 25 GYFTDHWMH 34

RESULT 35
US-09-698-705-9
Sequence 9, Application US/09698705
Patent No. 6824780
GENERAL INFORMATION:
APPLICANT: Devaux, B.
APPLICANT: Keller, G.
APPLICANT: Koepfen, H.
APPLICANT: Lasky, L.
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
FILE REFERENCE: P1777R1
CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/162,558
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/182,872
PRIOR FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 9
LENGTH: 118
TYPE: PRT
ORGANISM: Mus musculus
US-09-698-705-9

Query Match 76.6%; Score 49; DB 2; Length 118;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNM 10
||:|||||:
DB 20 GYFTDHWMH 29

RESULT 36
US-08-767-128-6
Sequence 6, Application US/08767128
Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYLIB, DWANE B.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOBBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
NUCLEOTIDES CODING THEREFORE

NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 611079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-6

Query Match 76.6%; Score 49; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
||:|:|:|
Db 26 GYFTSYMWN 35

RESULT 37
US-09-526-738A-2
Sequence 2, Application US/09526738A
Patent No. 6630584
GENERAL INFORMATION:
APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
APPLICANT: LTD.
TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
FILE REFERENCE: 1196336
CURRENT APPLICATION NUMBER: US/09/526,738A
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1

SEQ ID NO 2
LENGTH: 256
TYPE: PRT
ORGANISM: Humanus
US-09-526-738A-2

Query Match 76.6%; Score 49; DB 2; Length 256;
Best Local Similarity 70.0%; Pred. No. 3.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
||:|:|:|
Db 26 GYFTSYMWN 35

RESULT 38
US-09-526-738A-4
Sequence 4, Application US/09526738A
Patent No. 6630584
GENERAL INFORMATION:
APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
APPLICANT: LTD.
TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
FILE REFERENCE: 1196336
CURRENT APPLICATION NUMBER: US/09/526,738A
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 258
TYPE: PRT
ORGANISM: Humanus
US-09-526-738A-4

Query Match 76.6%; Score 49; DB 2; Length 258;
Best Local Similarity 70.0%; Pred. No. 3.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
||:|:|:|
Db 28 GYFTSYMWN 37

RESULT 39
US-09-513-999C-4119
Sequence 4119, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4119
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -19...-1
OTHER INFORMATION: score 12.7
FEATURE:
NAME/KEY: UNSURE
LOCATION: 60
OTHER INFORMATION: Xaa= * or Tyr

US-09-513-999C-4119

Query Match 75.0%; Score 48; DB 2; Length 95;
Best Local Similarity 77.8%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMN 9
|||||
DB 45 GYSFTSHWI 53

RESULT 40

US-09-497-997C-29

Sequence 29, Application US/09497997C
Patent No. 6635248
GENERAL INFORMATION:
APPLICANT: TERNYNCK, THERESA
APPLICANT: AVRAMEAS, ALEXANDRE
APPLICANT: BUTTIN, GERARD
APPLICANT: AVRAMEAS, STRAITIS
APPLICANT: SARON, MARIE-FRANCOISE
APPLICANT: BLONDEL, BRUNO
APPLICANT: COUDERC, THERESA
APPLICANT: MICHELSON, SUSAN
APPLICANT: ZIPETO, DONATO
TITLE OF INVENTION: VECTOR DERIVED FROM ANTIBODIES FOR TRANSFERRING SUBSTANCES INTO C
FILE REFERENCE: 0660-0166-0XCONT
CURRENT APPLICATION NUMBER: US/09/497,997C
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: PCT/FR98/01740
PRIOR FILING DATE: 1998-08-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-497-997C-29

Query Match 75.0%; Score 48; DB 2; Length 109;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMN 10
|||||
DB 17 GYSFTGYFMN 26

RESULT 41

US-08-672-345C-107
Sequence 107, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-391-0525
TELEFAX: 212-278-0400
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-107

Query Match 75.0%; Score 48; DB 1; Length 112;
Best Local Similarity 77.8%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMN 9
|||||
DB 25 GYFTDMM 33

RESULT 42

US-09-726-219A-217

Sequence 217, Application US/09726219A
Patent No. 6806079
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McAferly, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 217
LENGTH: 116
TYPE: PRT

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-217

Query Match      75.0%; Score 48; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMMN 10
   |||||:|
Db 26 GYSFTGYFMN 35

RESULT 43
US-09-196-522-217
; Sequence 217, Application US/09196522
; Patent No. 6916605
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Jackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00004
; CURRENT APPLICATION NUMBER: US/09/196,522
; CURRENT FILING DATE: 1998-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-217

Query Match      75.0%; Score 48; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMMN 10
   |||||:|
Db 26 GYSFTGYFMN 35
```

```

RESULT 44
US-08-793-490-9
; Sequence 9, Application US/08793490
; Patent No. 5968824
; GENERAL INFORMATION:
; APPLICANT: Spruce, Barbara A
; APPLICANT: Prescott, Alan
; APPLICANT: Botzger, Angelika
; APPLICANT: Dewar, Deborah A
; TITLE OF INVENTION: Agents for Inducing Apoptosis and Applications of Said
; TITLE OF INVENTION: Agents in Therapy
; FILE REFERENCE: ME A9701
; CURRENT APPLICATION NUMBER: US/08/793,490
; CURRENT FILING DATE: 1997-04-28
; EARLIER APPLICATION NUMBER: GB 9419285.3
; EARLIER FILING DATE: 1994-09-23
; EARLIER APPLICATION NUMBER: GB 9417444.8
; EARLIER FILING DATE: 1994-08-30
; EARLIER APPLICATION NUMBER: PCT/GB95/02037
; EARLIER FILING DATE: 1995-08-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoded by anti-pirenkephalin immunoglobulin heavy
; OTHER INFORMATION: chain variable domain genes
US-08-793-490-9

Query Match      73.4%; Score 47; DB 1; Length 106;
Best Local Similarity 70.0%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMMN 10
   |||||:|
Db 25 GYSFTSYMNH 34

RESULT 45
US-08-300-386A-65
; Sequence 65, Application US/08300386A
; Patent No. 5667988
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F,III
; APPLICANT: Burton, Dennis R
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
; TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESS: The Scripps Research Institute
; STREET: 10666 No. 5667988th Torrey Pines Road, TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/300,386A
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/174,674
; FILING DATE: 28-DEC-1993
```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 409.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-300-386A-65

Query Match 73.4%; Score 47; DB 1; Length 119;
Best Local Similarity 70.0%; Pred. No. 3.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
||:||||:|
Db 26 GYFTGHYVMH 35

RESULT 46
US-08-931-645-65
Sequence 65, Application US/08931645
Patent No. 6096551
GENERAL INFORMATION:
APPLICANT: Bardas, Carlos F, III
APPLICANT: Burton, Dennis R
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10666 No. 6096551th Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,645
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/300,386
FILING DATE: 02-SEP-1994
APPLICATION NUMBER: US 08/174,674
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566

FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 409.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-931-645-65

Query Match 73.4%; Score 47; DB 2; Length 119;
Best Local Similarity 70.0%; Pred. No. 3.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
||:||||:|
Db 26 GYFTGHYVMH 35

RESULT 47
PCT-US95-11235-65
Sequence 65, Application PC/TUS9511235
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10666 North Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11235
FILING DATE: 01-SEP-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,386
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,674
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 409.1 (PC)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-11235-65

Query Match 73.4%; Score 47; DB 4; Length 119;
Best Local Similarity 70.0%; Pred. No. 3.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
||:||||:|
Db 26 GYTFGTGHMM 35

RESULT 48
US-09-905-243-15
Sequence 15, Application US/09905243
Patent No. 6936698
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 96
TYPE: PRT
ORGANISM: Pan troglodytes
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (31)...(35)
OTHER INFORMATION: CDRI
NAME/KEY: DOMAIN
LOCATION: (50)...(66)
OTHER INFORMATION: CDRII
US-09-905-243-15

Query Match 71.9%; Score 46; DB 2; Length 96;
Best Local Similarity 77.8%; Pred. No. 3.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMM 9
|||||:
Db 26 GYSFTNYMM 34

RESULT 49
US-09-254-180C-7
Sequence 7, Application US/09254180C
Patent No. 6777540
GENERAL INFORMATION:
APPLICANT: OKUMURA, KO
APPLICANT: EDA, Yasuyuki
APPLICANT: MAEDA, Hiroaki
APPLICANT: USHIO, Yoshitaka
APPLICANT: HIGUCHI, Hirofumi
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
TITLE OF INVENTION: Fragments thereof, and Apoptosis-Induced Site from Fas Ligand
FILE REFERENCE: 050006-0055
CURRENT APPLICATION NUMBER: US/09/254,180C
CURRENT FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: PCT/JP97/02983
PRIOR FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 271546/1996
PRIOR FILING DATE: 1996-09-20
PRIOR APPLICATION NUMBER: 231472/1996

PRIOR FILING DATE: 1996-09-02
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-180C-7

Query Match 71.9%; Score 46; DB 2; Length 121;
Best Local Similarity 60.0%; Pred. No. 4.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
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Db 26 GYTFSSHMM 35

RESULT 50
US-09-698-705-6
Sequence 6, Application US/09698705
Patent No. 6824780
GENERAL INFORMATION:
APPLICANT: Devaux, B.
APPLICANT: Keller, G.
APPLICANT: Koepfen, H.
APPLICANT: Laaky, L.
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
FILE REFERENCE: P1777RI
CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/162,558
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/182,872
PRIOR FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 6
LENGTH: 124
TYPE: PRT
ORGANISM: Mus musculus
US-09-698-705-6

Query Match 71.9%; Score 46; DB 2; Length 124;
Best Local Similarity 60.0%; Pred. No. 4.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 26 GYTFNYWLN 35

Search completed: January 17, 2006, 12:07:29
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:50:44 ; Search time 48.6364 Seconds
(without alignments)
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Title: US-10-665-658-10
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Sequence: 1 GVSFTGHMMN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database : Published Applications AA Main:*

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- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	64	100.0	121	3	US-09-795-798-4
4	64	100.0	121	3	US-09-795-798-5
5	64	100.0	121	3	US-09-795-798-24
6	64	100.0	121	4	US-10-727-737-4
7	64	100.0	121	4	US-10-727-737-5
8	64	100.0	121	4	US-10-727-737-17
9	64	100.0	121	5	US-10-877-532-6
10	64	100.0	451	4	US-10-423-299-4
11	61	95.3	10	4	US-10-727-737-21
12	60	92.8	116	3	US-09-726-258-50
13	59	92.2	10	4	US-10-727-737-22
14	58	90.6	10	4	US-10-727-737-23
15	54	84.4	10	4	US-10-727-737-24
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18	52	81.2	118	4	US-10-435-614-13
19	52	81.2	121	3	US-09-144-886-54
20	52	81.2	121	4	US-10-632-706-51
21	52	81.2	125	3	US-09-144-886-51
22	52	81.2	125	3	US-09-144-886-52
23	52	81.2	125	3	US-09-144-886-53
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25	52	81.2	125	4	US-10-632-706-49
26	52	81.2	125	4	US-10-632-706-50
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34	51	79.7	506	4	US-10-964-195-11	Sequence 25, Appl
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62	49	76.6	258	4	US-10-247-488-4	Sequence 4, Appl
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69	48	75.0	117	5	US-10-726-332-9	Sequence 17, Appl
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77	47	73.4	119	4	US-10-308-817-195	Sequence 192, App
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79	47	73.4	119	4	US-10-453-698-193	Sequence 195, App
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96	46	71.9	96	6	US-11-099-331-15	Sequence 183, App
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101	46	71.9	120	3	US-09-144-886-55	Sequence 55, Appl	174	45	70.3	521	5	US-10-627-556-398	Sequence 398, App
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103	46	71.9	120	4	US-10-338-627-7	Sequence 7, Appl1	176	45	70.3	637	4	US-10-296-085A-16	Sequence 16, Appl1
104	46	71.9	120	4	US-10-633-706-52	Sequence 52, Appl	177	45	70.3	638	4	US-10-296-085A-21	Sequence 21, Appl
105	46	71.9	124	5	US-10-937-046-6	Sequence 6, Appl1	178	45	70.3	642	4	US-10-296-085A-38	Sequence 38, Appl
106	46	71.9	128	4	US-10-364-743-112	Sequence 112, App	179	45	70.3	642	5	US-10-436-179-6	Sequence 6, Appl1
107	46	71.9	128	5	US-10-452-593-112	Sequence 112, App	180	45	70.3	643	4	US-10-296-085A-69	Sequence 69, Appl
108	46	71.9	128	5	US-10-937-046-11	Sequence 11, Appl	181	45	70.3	643	5	US-10-436-179-1	Sequence 1, Appl1
109	45	70.3	10	4	US-10-338-552-39	Sequence 39, Appl	182	45	70.3	652	4	US-10-296-085A-120	Sequence 120, App
110	45	70.3	10	4	US-10-338-627-39	Sequence 39, Appl	183	45	70.3	656	4	US-10-296-085A-17	Sequence 39, Appl
111	45	70.3	10	5	US-10-823-253-1	Sequence 1, Appl1	184	45	70.3	657	4	US-10-296-085A-68	Sequence 68, Appl
112	45	70.3	10	5	US-10-823-810-1	Sequence 1, Appl1	185	45	70.3	895	4	US-10-296-085A-19	Sequence 19, Appl
113	45	70.3	110	4	US-10-471-475A-4	Sequence 4, Appl1	186	45	70.3	895	4	US-10-296-085A-20	Sequence 20, Appl
114	45	70.3	111	4	US-10-297-371A-2	Sequence 2, Appl1	187	45	70.3	895	4	US-10-296-085A-27	Sequence 27, Appl
115	45	70.3	113	4	US-10-745-102-14	Sequence 14, Appl1	188	45	70.3	895	5	US-10-436-179-4	Sequence 4, Appl1
116	45	70.3	114	4	US-10-251-215-57	Sequence 57, Appl	189	45	70.3	896	4	US-10-296-085A-18	Sequence 18, Appl
117	45	70.3	114	5	US-10-700-632-80	Sequence 80, Appl	190	45	70.3	896	4	US-10-296-085A-17	Sequence 17, Appl
118	45	70.3	115	5	US-10-488-673-4	Sequence 4, Appl1	191	45	70.3	896	4	US-10-296-085A-26	Sequence 26, Appl
119	45	70.3	118	5	US-10-823-253-7	Sequence 7, Appl1	192	45	70.3	896	5	US-10-436-179-2	Sequence 2, Appl1
120	45	70.3	118	5	US-10-823-810-7	Sequence 7, Appl1	193	45	70.3	896	5	US-10-436-179-3	Sequence 3, Appl1
121	45	70.3	119	4	US-10-389-155-24	Sequence 24, Appl	194	45	70.3	896	5	US-10-436-179-7	Sequence 7, Appl1
122	45	70.3	119	4	US-10-389-417-24	Sequence 24, Appl	195	45	70.3	899	4	US-10-296-085A-28	Sequence 28, Appl
123	45	70.3	119	4	US-10-452-357-65	Sequence 65, Appl	196	45	70.3	899	5	US-10-436-179-5	Sequence 5, Appl1
124	45	70.3	119	4	US-10-452-357-89	Sequence 89, Appl	197	45	68.8	10	4	US-10-436-782-6	Sequence 6, Appl1
125	45	70.3	120	5	US-10-823-253-17	Sequence 17, Appl	198	44	68.8	10	5	US-10-729-441-53	Sequence 53, Appl
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136	45	70.3	122	5	US-10-835-641-14	Sequence 14, Appl	209	44	68.8	98	5	US-10-897-406-57	Sequence 57, Appl
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140	45	70.3	123	4	US-10-251-215-54	Sequence 54, Appl	213	44	68.8	114	4	US-10-453-698-194	Sequence 194, App
141	45	70.3	123	4	US-10-251-215-55	Sequence 55, Appl	214	44	68.8	114	4	US-10-803-622-226	Sequence 226, App
142	45	70.3	123	4	US-10-251-215-56	Sequence 56, Appl	215	44	68.8	114	4	US-10-803-622-229	Sequence 229, App
143	45	70.3	124	5	US-10-823-253-9	Sequence 9, Appl1	216	44	68.8	114	4	US-10-803-653-226	Sequence 226, App
144	45	70.3	124	5	US-10-903-858-4	Sequence 4, Appl1	217	44	68.8	114	4	US-10-803-653-229	Sequence 229, App
145	45	70.3	124	5	US-10-903-858-9	Sequence 9, Appl1	218	44	68.8	115	5	US-10-994-129-21	Sequence 21, Appl
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147	45	70.3	124	5	US-10-903-858-15	Sequence 15, Appl	220	44	68.8	115	6	US-11-004-794A-53	Sequence 53, Appl
148	45	70.3	124	5	US-10-823-810-9	Sequence 9, Appl1	221	44	68.8	117	3	US-09-982-992A-6	Sequence 6, Appl1
149	45	70.3	129	5	US-10-627-556-390	Sequence 390, App	222	44	68.8	117	4	US-10-194-975-117	Sequence 117, App
150	45	70.3	129	5	US-10-627-556-394	Sequence 394, App	223	44	68.8	118	4	US-10-436-782-5	Sequence 5, Appl1
151	45	70.3	136	5	US-10-240-353B-8	Sequence 8, Appl1	224	44	68.8	118	5	US-10-816-938-23	Sequence 23, Appl
152	45	70.3	164	4	US-10-471-475A-23	Sequence 23, Appl	225	44	68.8	118	5	US-10-700-632-79	Sequence 79, Appl
153	45	70.3	209	5	US-10-488-074-65	Sequence 65, Appl	226	44	68.8	118	6	US-11-004-795A-5	Sequence 5, Appl1
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156	45	70.3	243	5	US-10-935-299-41	Sequence 41, Appl1	229	44	68.8	119	3	US-09-927-703-5	Sequence 5, Appl1
157	45	70.3	246	3	US-10-251-215-53	Sequence 53, Appl	230	44	68.8	119	3	US-09-766-535A-5	Sequence 5, Appl1
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163	45	70.3	271	6	US-11-089-190-12	Sequence 12, Appl	236	44	68.8	119	4	US-10-044-534-5	Sequence 5, Appl1
164	45	70.3	271	6	US-11-088-570-12	Sequence 12, Appl	237	44	68.8	119	4	US-10-043-432-5	Sequence 5, Appl1
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173	45	70.3	505	5	US-10-627-556-402	Sequence 402, App	246	44	68.8	119	4	US-10-319-011-5	Sequence 5, Appl1

247	44	68.8	119	4	US-10-371-443-5	Sequence 5, Appl1	320	43	67.2	98	4	US-10-032-037B-110	Sequence 110, App
248	44	68.8	119	4	US-10-379-866-5	Sequence 5, Appl1	321	43	67.2	98	4	US-10-032-037B-111	Sequence 111, App
249	44	68.8	119	4	US-10-371-966-5	Sequence 5, Appl1	322	43	67.2	98	4	US-10-029-988B-109	Sequence 109, App
250	44	68.8	119	4	US-10-384-060-29	Sequence 29, Appl1	323	43	67.2	98	4	US-10-029-988B-110	Sequence 110, App
251	44	68.8	119	4	US-10-665-971-5	Sequence 5, Appl1	324	43	67.2	98	4	US-10-029-988B-111	Sequence 109, App
252	44	68.8	119	4	US-10-637-759-5	Sequence 5, Appl1	325	43	67.2	98	4	US-10-032-423A-109	Sequence 110, App
253	44	68.8	119	4	US-10-774-118-5	Sequence 5, Appl1	326	43	67.2	98	4	US-10-032-423A-110	Sequence 111, App
254	44	68.8	119	5	US-10-957-134-5	Sequence 5, Appl1	327	43	67.2	98	4	US-10-032-423A-111	Sequence 109, App
255	44	68.8	119	5	US-10-957-549-5	Sequence 5, Appl1	328	43	67.2	98	4	US-10-453-698-89	Sequence 89, Appl
256	44	68.8	119	5	US-10-877-467A-2	Sequence 2, Appl1	329	43	67.2	98	4	US-10-029-926B-109	Sequence 110, App
257	44	68.8	120	5	US-10-096-246-12	Sequence 12, Appl1	330	43	67.2	98	4	US-10-029-926B-110	Sequence 111, App
258	44	68.8	120	4	US-10-351-748-24	Sequence 24, Appl1	331	43	67.2	98	4	US-10-379-332-54	Sequence 54, Appl
259	44	68.8	120	4	US-10-351-748-24	Sequence 24, Appl1	332	43	67.2	98	4	US-10-453-698-186	Sequence 186, App
260	44	68.8	120	5	US-10-729-441-71	Sequence 71, Appl1	333	43	67.2	117	4	US-10-453-698-186	Sequence 186, App
261	44	68.8	120	5	US-10-729-441-72	Sequence 72, Appl1	334	43	67.2	117	5	US-10-816-938-10	Sequence 10, Appl
262	44	68.8	120	5	US-10-895-135-57	Sequence 57, Appl1	335	43	67.2	117	5	US-10-627-556-310	Sequence 310, App
263	44	68.8	120	5	US-10-897-406-71	Sequence 71, Appl1	336	43	67.2	118	5	US-10-627-556-316	Sequence 316, App
264	44	68.8	120	5	US-10-897-406-72	Sequence 72, Appl1	337	43	67.2	118	5	US-10-981-738-44	Sequence 44, Appl
265	44	68.8	121	5	US-10-879-994-82	Sequence 82, Appl1	338	43	67.2	119	5	US-10-981-738-52	Sequence 52, Appl
266	44	68.8	122	2	US-08-779-784-28	Sequence 28, Appl1	339	43	67.2	119	5	US-10-981-738-52	Sequence 7, Appl1
267	44	68.8	122	2	US-10-096-246-10	Sequence 10, Appl1	340	43	67.2	121	5	US-10-842-011-7	Sequence 3, Appl1
268	44	68.8	122	4	US-10-096-246-11	Sequence 11, Appl1	341	43	67.2	130	3	US-09-839-447A-3	Sequence 3, Appl1
269	44	68.8	122	4	US-10-729-441-73	Sequence 73, Appl1	342	43	67.2	130	4	US-10-153-271-3	Sequence 3, Appl1
270	44	68.8	122	5	US-10-897-406-73	Sequence 73, Appl1	343	43	67.2	130	4	US-10-384-933-75	Sequence 75, Appl1
271	44	68.8	123	5	US-10-729-441-87	Sequence 87, Appl1	344	43	67.2	145	4	US-10-642-120-2	Sequence 2, Appl1
272	44	68.8	123	5	US-10-729-441-88	Sequence 88, Appl1	345	43	67.2	152	4	US-10-642-120-2	Sequence 2, Appl1
273	44	68.8	123	5	US-10-729-441-92	Sequence 92, Appl1	346	43	67.2	152	4	US-10-642-120-2	Sequence 2, Appl1
274	44	68.8	123	5	US-10-897-406-87	Sequence 87, Appl1	347	43	67.2	152	4	US-10-642-122-2	Sequence 2, Appl1
275	44	68.8	123	5	US-10-897-406-88	Sequence 88, Appl1	348	43	67.2	152	4	US-10-642-122-2	Sequence 2, Appl1
276	44	68.8	123	5	US-10-897-406-92	Sequence 92, Appl1	349	43	67.2	152	4	US-10-642-124-2	Sequence 2, Appl1
277	44	68.8	124	4	US-10-007-790-2	Sequence 2, Appl1	350	43	67.2	152	4	US-10-642-124-2	Sequence 2, Appl1
278	44	68.8	124	5	US-10-729-441-7	Sequence 7, Appl1	351	43	67.2	152	4	US-10-620-850-2	Sequence 2, Appl1
279	44	68.8	124	5	US-10-729-441-13	Sequence 13, Appl1	352	43	67.2	152	4	US-10-642-118-2	Sequence 2, Appl1
280	44	68.8	124	5	US-10-729-441-70	Sequence 70, Appl1	353	43	67.2	152	4	US-10-642-119-2	Sequence 2, Appl1
281	44	68.8	124	5	US-10-957-163-2	Sequence 2, Appl1	354	43	67.2	152	4	US-10-642-117-2	Sequence 2, Appl1
282	44	68.8	124	5	US-10-897-406-7	Sequence 7, Appl1	355	43	67.2	152	5	US-10-642-099-2	Sequence 2, Appl1
283	44	68.8	124	5	US-10-897-406-13	Sequence 13, Appl1	356	43	67.2	152	5	US-10-642-064-2	Sequence 2, Appl1
284	44	68.8	124	5	US-10-897-406-70	Sequence 70, Appl1	357	43	67.2	152	5	US-10-642-064-2	Sequence 2, Appl1
285	44	68.8	126	4	US-10-312-316-44	Sequence 44, Appl1	358	43	67.2	152	5	US-10-642-116-2	Sequence 2, Appl1
286	44	68.8	136	4	US-10-768-193-7	Sequence 7, Appl1	359	43	67.2	152	5	US-10-642-100-2	Sequence 2, Appl1
287	44	68.8	140	3	US-09-748-960-4	Sequence 4, Appl1	360	43	67.2	152	5	US-10-642-058-2	Sequence 2, Appl1
288	44	68.8	143	4	US-08-779-784-26	Sequence 26, Appl1	361	43	67.2	152	5	US-10-642-121-2	Sequence 2, Appl1
289	44	68.8	143	4	US-10-010-729-66	Sequence 66, Appl1	362	43	67.2	152	5	US-10-642-065-2	Sequence 2, Appl1
290	44	68.8	143	5	US-10-729-441-52	Sequence 52, Appl1	363	43	67.2	152	5	US-10-642-071-2	Sequence 2, Appl1
291	44	68.8	143	5	US-10-897-406-52	Sequence 52, Appl1	364	43	67.2	152	5	US-10-259-087A-18	Sequence 18, Appl1
292	44	68.8	180	3	US-09-748-960-6	Sequence 6, Appl1	365	43	67.2	242	4	US-10-689-006-18	Sequence 18, Appl1
293	44	68.8	226	4	US-10-411-037-42	Sequence 42, Appl1	366	43	67.2	248	3	US-09-880-748-2088	Sequence 2088, App
294	44	68.8	226	4	US-10-411-026-42	Sequence 42, Appl1	367	43	67.2	248	4	US-10-293-418-2088	Sequence 2088, App
295	44	68.8	226	4	US-10-410-962-42	Sequence 42, Appl1	368	43	67.2	259	4	US-10-207-655-13	Sequence 13, Appl1
296	44	68.8	226	4	US-10-411-049-42	Sequence 42, Appl1	369	43	67.2	259	6	US-10-053-530-13	Sequence 13, Appl1
297	44	68.8	226	4	US-10-410-930-42	Sequence 42, Appl1	370	43	67.2	259	6	US-11-089-511-13	Sequence 13, Appl1
298	44	68.8	226	4	US-10-410-997-42	Sequence 42, Appl1	371	43	67.2	259	6	US-11-089-190-13	Sequence 13, Appl1
299	44	68.8	226	4	US-10-411-012-42	Sequence 42, Appl1	372	43	67.2	259	6	US-11-088-570-13	Sequence 13, Appl1
300	44	68.8	226	4	US-10-287-994-42	Sequence 42, Appl1	373	43	67.2	259	6	US-11-088-737-13	Sequence 13, Appl1
301	44	68.8	226	4	US-10-410-913-42	Sequence 42, Appl1	374	43	67.2	259	6	US-11-088-569-13	Sequence 13, Appl1
302	44	68.8	226	5	US-10-410-980-42	Sequence 42, Appl1	375	43	67.2	259	6	US-11-088-693-13	Sequence 13, Appl1
303	44	68.8	226	5	US-10-410-897-42	Sequence 42, Appl1	376	43	67.2	259	6	US-11-089-367-13	Sequence 13, Appl1
304	44	68.8	226	5	US-10-492-861-42	Sequence 42, Appl1	377	43	67.2	259	6	US-11-089-368-13	Sequence 13, Appl1
305	44	68.8	226	5	US-10-384-060-27	Sequence 27, Appl1	378	43	67.2	260	4	US-10-767-701-3809	Sequence 3809, A
306	44	68.8	243	4	US-10-334-235-37	Sequence 37, Appl1	379	43	67.2	261	5	US-10-627-556-314	Sequence 314, App
307	44	68.8	248	5	US-10-879-994-14	Sequence 14, Appl1	380	43	67.2	272	6	US-10-207-655-14	Sequence 14, Appl1
308	44	68.8	248	5	US-10-610-452-14	Sequence 14, Appl1	381	43	67.2	272	4	US-10-053-530-14	Sequence 14, Appl1
309	44	68.8	488	4	US-10-534-235-39	Sequence 39, Appl1	382	43	67.2	272	4	US-11-089-511-14	Sequence 14, Appl1
310	44	68.8	488	5	US-10-473-127-1954	Sequence 1954, Ap	383	43	67.2	272	6	US-11-089-570-14	Sequence 14, Appl1
311	44	68.8	488	5	US-10-473-127-1963	Sequence 1963, Ap	384	43	67.2	272	6	US-11-088-570-14	Sequence 14, Appl1
312	44	68.8	600	4	US-10-334-235-38	Sequence 38, Appl1	385	43	67.2	272	6	US-11-088-569-14	Sequence 14, Appl1
313	44	68.8	672	3	US-09-900-766-1	Sequence 1, Appl1	386	43	67.2	272	6	US-11-088-569-14	Sequence 14, Appl1
314	44	68.8	10	5	US-10-996-316-147	Sequence 147, App	387	43	67.2	272	6	US-11-089-367-14	Sequence 14, Appl1
315	43	67.2	20	3	US-09-839-47A-29	Sequence 29, Appl	388	43	67.2	272	6	US-11-089-367-14	Sequence 14, Appl1
316	43	67.2	20	4	US-10-153-271-29	Sequence 29, Appl	389	43	67.2	272	6	US-11-089-368-14	Sequence 14, Appl1
317	43	67.2	20	4	US-10-369-060A-29	Sequence 29, Appl	390	43	67.2	272	6	US-11-089-368-14	Sequence 14, Appl1
318	43	67.2	98	4	US-10-308-817-89	Sequence 89, Appl	391	43	67.2	296	5	US-10-627-556-336	Sequence 386, App
319	43	67.2	98	4	US-10-032-037B-109	Sequence 109, App	392	43	67.2	450	4	US-10-425-115-332466	Sequence 332466,

393	43	67.2	464	4	US-10-216-484-9	Sequence 9, Appl1	466	42	65.6	98	4	US-10-029-9888-106	Sequence 106, App
394	43	67.2	464	5	US-10-384-933-9	Sequence 9, Appl1	467	42	65.6	98	4	US-10-029-9888-107	Sequence 107, App
395	43	67.2	467	4	US-10-500-696-2	Sequence 2, Appl1	468	42	65.6	98	4	US-10-029-9888-108	Sequence 108, App
396	43	67.2	469	4	US-10-425-114-57241	Sequence 57241, A	469	42	65.6	98	4	US-10-032-423A-106	Sequence 106, App
397	43	67.2	470	4	US-10-216-484-89	Sequence 89, Appl1	470	42	65.6	98	4	US-10-032-423A-107	Sequence 107, App
398	43	67.2	470	4	US-10-216-484-117	Sequence 117, App	471	42	65.6	98	4	US-10-032-423A-108	Sequence 108, App
399	43	67.2	470	4	US-10-216-484-143	Sequence 143, App	472	42	65.6	98	4	US-10-453-698-88	Sequence 88, Appl1
400	43	67.2	470	4	US-10-216-484-145	Sequence 145, App	473	42	65.6	98	4	US-10-029-9268-106	Sequence 106, App
401	43	67.2	470	4	US-10-216-484-147	Sequence 147, App	474	42	65.6	98	4	US-10-029-9268-107	Sequence 107, App
402	43	67.2	470	4	US-10-216-484-157	Sequence 157, App	475	42	65.6	98	4	US-10-029-9268-108	Sequence 108, App
403	43	67.2	470	4	US-10-384-933-89	Sequence 89, Appl1	476	42	65.6	98	5	US-10-379-392-53	Sequence 53, Appl1
404	43	67.2	470	4	US-10-384-933-117	Sequence 117, App	477	42	65.6	98	5	US-10-769-144-30	Sequence 30, Appl1
405	43	67.2	470	4	US-10-384-933-143	Sequence 143, App	478	42	65.6	98	5	US-10-936-191-16	Sequence 16, Appl1
406	43	67.2	470	4	US-10-384-933-145	Sequence 145, App	479	42	65.6	98	5	US-10-903-191-30	Sequence 30, Appl1
407	43	67.2	470	4	US-10-384-933-147	Sequence 147, App	480	42	65.6	98	6	US-11-009-731-49	Sequence 49, Appl1
408	43	67.2	470	4	US-10-384-933-157	Sequence 157, App	481	42	65.6	104	6	US-10-032-482-1	Sequence 1, Appl1
409	43	67.2	470	5	US-10-627-556-326	Sequence 326, App	482	42	65.6	104	6	US-11-129-359-1	Sequence 144, App
410	43	67.2	493	5	US-10-627-556-328	Sequence 328, App	483	42	65.6	109	4	US-10-800-197-144	Sequence 145, App
411	43	67.2	493	5	US-10-627-556-330	Sequence 330, App	484	42	65.6	109	4	US-10-800-197-145	Sequence 146, App
412	43	67.2	493	5	US-10-627-556-376	Sequence 376, App	485	42	65.6	109	5	US-10-800-197-146	Sequence 283, App
413	43	67.2	493	5	US-10-627-556-378	Sequence 378, App	486	42	65.6	109	5	US-10-727-155-283	Sequence 293, App
414	43	67.2	493	5	US-10-627-556-378	Sequence 378, App	487	42	65.6	109	5	US-10-727-155-291	Sequence 217, App
415	43	67.2	493	5	US-10-627-556-378	Sequence 378, App	488	42	65.6	110	5	US-10-726-332-217	Sequence 217, App
416	43	67.2	495	5	US-10-627-556-324	Sequence 324, App	489	42	65.6	117	5	US-10-684-957-10	Sequence 10, Appl1
417	43	67.2	495	5	US-10-627-556-322	Sequence 322, App	490	42	65.6	117	5	US-10-684-957-10	Sequence 10, Appl1
418	43	67.2	500	5	US-10-627-556-382	Sequence 382, App	491	42	65.6	117	5	US-10-726-332-138	Sequence 138, App
419	43	67.2	500	5	US-10-627-556-384	Sequence 384, App	492	42	65.6	117	5	US-10-726-332-144	Sequence 144, App
420	43	67.2	592	5	US-10-627-556-380	Sequence 380, App	493	42	65.6	117	5	US-10-450-763-57248	Sequence 57248, A
421	42.5	66.4	114	5	US-10-846-981-7	Sequence 7, Appl1	494	42	65.6	118	4	US-10-181-324-2	Sequence 2, Appl1
422	42.5	66.4	114	5	US-10-919-923-7	Sequence 7, Appl1	495	42	65.6	118	4	US-10-460-595-8	Sequence 8, Appl1
423	42.5	66.4	117	3	US-09-956-206A-76	Sequence 76, Appl1	496	42	65.6	118	5	US-10-726-332-15	Sequence 15, Appl1
424	42.5	66.4	117	3	US-09-956-206A-78	Sequence 78, Appl1	497	42	65.6	118	5	US-10-726-332-15	Sequence 15, Appl1
425	42.5	66.4	117	5	US-10-965-616-76	Sequence 76, Appl1	498	42	65.6	118	5	US-10-726-332-30	Sequence 30, Appl1
426	42.5	66.4	117	5	US-10-965-616-78	Sequence 78, Appl1	499	42	65.6	118	5	US-10-726-332-134	Sequence 134, App
427	42.5	66.4	136	3	US-09-956-206A-47	Sequence 47, Appl1	500	42	65.6	118	5	US-10-726-332-135	Sequence 135, App
428	42.5	66.4	136	3	US-09-956-206A-63	Sequence 63, Appl1	501	42	65.6	118	5	US-10-726-332-139	Sequence 139, App
429	42.5	66.4	136	5	US-10-965-616-47	Sequence 47, Appl1	502	42	65.6	118	5	US-10-726-332-140	Sequence 140, App
430	42.5	66.4	136	5	US-10-965-616-63	Sequence 63, Appl1	503	42	65.6	118	5	US-10-726-332-141	Sequence 141, App
431	42.5	66.4	137	5	US-10-687-035-30	Sequence 30, Appl1	504	42	65.6	118	5	US-10-726-332-143	Sequence 143, App
432	42.5	66.4	214	5	US-10-488-074-67	Sequence 67, Appl1	505	42	65.6	118	5	US-10-726-332-145	Sequence 145, App
433	42.5	66.4	214	5	US-10-488-074-71	Sequence 71, Appl1	506	42	65.6	118	5	US-10-693-576-185	Sequence 185, App
434	42.5	66.4	214	3	US-09-880-748-1948	Sequence 1948, Ap	507	42	65.6	119	4	US-10-153-024-2	Sequence 2, Appl1
435	42.5	66.4	241	4	US-10-293-418-1948	Sequence 1948, Ap	508	42	65.6	120	4	US-10-125-687-6	Sequence 6, Appl1
436	42.5	66.4	245	3	US-09-880-748-1900	Sequence 1900, Ap	509	42	65.6	120	4	US-10-412-703A-128	Sequence 128, App
437	42.5	66.4	245	4	US-10-293-418-1900	Sequence 1900, Ap	510	42	65.6	120	5	US-10-638-265-2	Sequence 2, Appl1
438	42.5	66.4	248	3	US-09-880-748-950	Sequence 950, App	511	42	65.6	120	5	US-10-879-994-98	Sequence 98, Appl1
439	42.5	66.4	248	4	US-10-293-418-950	Sequence 950, App	512	42	65.6	120	5	US-10-923-068-508	Sequence 508, App
440	42	65.6	10	4	US-10-128-520-367	Sequence 367, App	513	42	65.6	120	5	US-10-996-191-6	Sequence 6, Appl1
441	42	65.6	10	5	US-10-327-558-450	Sequence 450, App	514	42	65.6	121	4	US-10-078-958-6	Sequence 6, Appl1
442	42	65.6	10	5	US-10-638-265-89	Sequence 89, Appl1	515	42	65.6	123	3	US-09-850-165-90	Sequence 90, Appl1
443	42	65.6	10	5	US-10-726-332-54	Sequence 54, Appl1	516	42	65.6	123	4	US-10-173-551-4	Sequence 4, Appl1
444	42	65.6	10	5	US-10-726-332-72	Sequence 72, Appl1	517	42	65.6	126	4	US-10-041-860-23	Sequence 23, Appl1
445	42	65.6	10	5	US-10-726-332-87	Sequence 87, Appl1	518	42	65.6	126	4	US-10-041-860-46	Sequence 46, Appl1
446	42	65.6	10	5	US-10-726-332-90	Sequence 90, Appl1	519	42	65.6	126	4	US-10-041-860-217	Sequence 217, App
447	42	65.6	10	5	US-10-726-332-98	Sequence 98, Appl1	520	42	65.6	126	4	US-10-041-860-248	Sequence 248, App
448	42	65.6	11	5	US-10-879-994-128	Sequence 128, App	521	42	65.6	126	4	US-10-041-860-300	Sequence 300, App
449	42	65.6	11	5	US-10-078-958-5	Sequence 5, Appl1	522	42	65.6	126	4	US-10-041-860-313	Sequence 313, App
450	42	65.6	98	3	US-09-850-156-89	Sequence 89, Appl1	523	42	65.6	126	4	US-10-041-860-366	Sequence 366, App
451	42	65.6	98	4	US-10-194-975-45	Sequence 45, Appl1	524	42	65.6	126	4	US-10-665-383-26	Sequence 26, Appl1
452	42	65.6	98	4	US-10-125-687-16	Sequence 16, Appl1	525	42	65.6	126	4	US-10-665-383-70	Sequence 70, Appl1
453	42	65.6	98	4	US-10-041-860-6	Sequence 6, Appl1	526	42	65.6	127	4	US-10-041-860-252	Sequence 252, App
454	42	65.6	98	4	US-10-041-860-310	Sequence 310, App	527	42	65.6	127	4	US-10-320-231A-38	Sequence 38, Appl1
455	42	65.6	98	4	US-10-041-860-312	Sequence 312, App	528	42	65.6	127	5	US-10-867-506-18	Sequence 18, Appl1
456	42	65.6	98	4	US-10-041-860-332	Sequence 332, App	529	42	65.6	127	5	US-10-505-313-237	Sequence 237, App
457	42	65.6	98	4	US-10-041-860-332	Sequence 332, App	530	42	65.6	129	4	US-10-041-860-29	Sequence 29, Appl1
458	42	65.6	98	4	US-10-041-860-318	Sequence 318, App	531	42	65.6	129	4	US-10-041-860-215	Sequence 215, App
459	42	65.6	98	4	US-10-041-860-330	Sequence 330, App	532	42	65.6	129	4	US-10-041-860-250	Sequence 250, App
460	42	65.6	98	4	US-10-041-860-336	Sequence 336, App	533	42	65.6	129	4	US-10-041-860-319	Sequence 319, App
461	42	65.6	98	4	US-10-041-860-367	Sequence 367, App	534	42	65.6	129	4	US-10-665-383-38	Sequence 38, Appl1
462	42	65.6	98	4	US-10-308-817-88	Sequence 88, Appl1	535	42	65.6	130	4	US-10-041-860-213	Sequence 213, App
463	42	65.6	98	4	US-10-032-037B-106	Sequence 106, App	536	42	65.6	132	5	US-10-783-311-279	Sequence 279, App
464	42	65.6	98	4	US-10-032-037B-107	Sequence 107, App	537	42	65.6	132	5	US-10-783-311-311	Sequence 311, App
465	42	65.6	98	4	US-10-032-037B-108	Sequence 108, App	538	42	65.6	138	4	US-10-395-894-27	Sequence 27, Appl1

539	-42	65.6	138	4	US-10-695-667-27	Sequence 27, Appl	612	41	64.1	54	4	US-10-029-386-33621	Sequence 33621, A
540	-42	65.6	139	5	US-10-976-352-27	Sequence 27, Appl	613	41	64.1	76	4	US-10-424-539-161621	Sequence 161621, A
541	-42	65.6	138	5	US-10-893-576-29	Sequence 29, Appl	614	41	64.1	98	4	US-10-194-975-1	Sequence 1, Appl
542	-42	65.6	151	4	US-10-106-698-6771	Sequence 6771, Ap	615	41	64.1	98	4	US-10-125-667-17	Sequence 17, Appl
543	-42	65.6	222	4	US-10-128-520-169	Sequence 169, App	616	41	64.1	98	4	US-10-308-817-41	Sequence 41, Appl
544	-42	65.6	224	4	US-10-128-520-164	Sequence 164, App	617	41	64.1	98	4	US-10-032-037B-33	Sequence 33, Appl
545	-42	65.6	224	4	US-10-128-520-165	Sequence 165, App	618	41	64.1	98	4	US-10-032-037B-34	Sequence 34, Appl
546	-42	65.6	224	4	US-10-128-520-167	Sequence 167, App	619	41	64.1	98	4	US-10-032-037B-35	Sequence 35, Appl
547	-42	65.6	224	4	US-10-128-520-170	Sequence 170, App	620	41	64.1	98	4	US-10-029-968B-36	Sequence 36, Appl
548	-42	65.6	224	4	US-10-128-520-176	Sequence 176, App	621	41	64.1	98	4	US-10-029-968B-33	Sequence 33, Appl
549	-42	65.6	224	4	US-10-128-520-180	Sequence 180, App	622	41	64.1	98	4	US-10-029-968B-35	Sequence 35, Appl
550	-42	65.6	224	4	US-10-128-520-181	Sequence 181, App	623	41	64.1	98	4	US-10-029-968B-36	Sequence 36, Appl
551	-42	65.6	224	4	US-10-128-520-182	Sequence 182, App	624	41	64.1	98	4	US-10-032-423A-33	Sequence 33, Appl
552	-42	65.6	225	4	US-10-128-520-157	Sequence 157, App	625	41	64.1	98	4	US-10-032-423A-34	Sequence 34, Appl
553	-42	65.6	225	4	US-10-128-520-158	Sequence 158, App	626	41	64.1	98	4	US-10-032-423A-35	Sequence 35, Appl
554	-42	65.6	225	4	US-10-128-520-162	Sequence 162, App	627	41	64.1	98	4	US-10-032-423A-36	Sequence 36, Appl
555	-42	65.6	225	4	US-10-128-520-166	Sequence 166, App	628	41	64.1	98	4	US-10-453-658-41	Sequence 41, Appl
556	-42	65.6	225	4	US-10-128-520-173	Sequence 173, App	629	41	64.1	98	4	US-10-029-926B-33	Sequence 33, Appl
557	-42	65.6	225	4	US-10-128-520-178	Sequence 178, App	630	41	64.1	98	4	US-10-029-926B-35	Sequence 35, Appl
558	-42	65.6	226	4	US-10-128-520-159	Sequence 159, App	631	41	64.1	98	4	US-10-029-926B-36	Sequence 36, Appl
559	-42	65.6	226	4	US-10-128-520-179	Sequence 179, App	632	41	64.1	98	4	US-10-029-926B-36	Sequence 36, Appl
560	-42	65.6	243	5	US-10-879-994-10	Sequence 10, Appl	633	41	64.1	98	4	US-10-379-392-1	Sequence 1, Appl
561	-42	65.6	243	5	US-10-610-452-10	Sequence 10, Appl	634	41	64.1	106	5	US-10-996-131-17	Sequence 17, Appl
562	-42	65.6	247	5	US-10-620-278-21	Sequence 21, Appl	635	41	64.1	106	5	US-10-010-729-29	Sequence 29, Appl
563	-42	65.6	247	5	US-10-620-049-21	Sequence 21, Appl	636	41	64.1	109	5	US-10-779-461-156	Sequence 156, App
564	-42	65.6	250	3	US-09-880-748-1319	Sequence 1319, Ap	637	41	64.1	109	5	US-10-727-155-298	Sequence 298, App
565	-42	65.6	250	3	US-10-293-418-1319	Sequence 1319, Ap	638	41	64.1	114	4	US-10-422-049-11	Sequence 11, Appl
566	-42	65.6	252	3	US-09-880-748-1537	Sequence 1537, Ap	639	41	64.1	114	4	US-10-422-049-12	Sequence 12, Appl
567	-42	65.6	252	4	US-10-293-418-1537	Sequence 1537, Ap	640	41	64.1	114	4	US-10-309-762-141	Sequence 141, App
568	-42	65.6	254	6	US-11-090-847-130	Sequence 1307, App	641	41	64.1	115	5	US-10-938-992-11	Sequence 11, Appl
569	-42	65.6	255	3	US-09-888-721-34	Sequence 34, Appl	642	41	64.1	116	3	US-09-741-843-4	Sequence 4, Appl
570	-42	65.6	262	3	US-09-956-086-4	Sequence 4, Appl	643	41	64.1	116	3	US-09-741-843-8	Sequence 8, Appl
571	-42	65.6	262	3	US-09-956-087-4	Sequence 4, Appl	644	41	64.1	116	3	US-09-741-843-9	Sequence 9, Appl
572	-42	65.6	262	3	US-09-888-721-36	Sequence 36, Appl	645	41	64.1	116	3	US-09-894-839-4	Sequence 4, Appl
573	-42	65.6	269	3	US-09-888-721-38	Sequence 38, Appl	646	41	64.1	116	3	US-09-894-839-8	Sequence 8, Appl
574	-42	65.6	282	3	US-09-983-580-7	Sequence 7, Appl	647	41	64.1	116	3	US-09-894-839-21	Sequence 21, Appl
575	-42	65.6	282	3	US-09-985-442-7	Sequence 7, Appl	648	41	64.1	116	3	US-09-988-013A-4	Sequence 4, Appl
576	-42	65.6	287	3	US-09-888-721-40	Sequence 40, Appl	649	41	64.1	116	3	US-09-988-013A-8	Sequence 8, Appl
577	-42	65.6	291	3	US-09-888-721-44	Sequence 44, Appl	650	41	64.1	116	3	US-09-988-013A-9	Sequence 9, Appl
578	-42	65.6	291	6	US-11-093-103-102	Sequence 102, App	651	41	64.1	116	3	US-10-169-351-105	Sequence 105, App
579	-42	65.6	296	3	US-09-888-721-42	Sequence 42, Appl	652	41	64.1	116	4	US-10-160-506-47	Sequence 47, Appl
580	-42	65.6	322	6	US-11-093-103-96	Sequence 96, Appl	653	41	64.1	116	4	US-10-160-506-49	Sequence 49, Appl
581	-42	65.6	447	5	US-10-684-957-19	Sequence 19, Appl	654	41	64.1	116	4	US-10-160-506-55	Sequence 55, Appl
582	-42	65.6	447	5	US-10-684-957-32	Sequence 32, Appl	655	41	64.1	116	4	US-10-160-506-59	Sequence 59, Appl
583	-42	65.6	729	6	US-11-093-103-94	Sequence 94, Appl	656	41	64.1	116	4	US-10-160-506-60	Sequence 60, Appl
584	-41	64.1	10	4	US-10-160-506-29	Sequence 29, Appl	657	41	64.1	116	4	US-10-160-506-61	Sequence 61, Appl
585	-41	64.1	10	4	US-10-449-379-29	Sequence 29, Appl	658	41	64.1	116	4	US-10-446-688-4	Sequence 4, Appl
586	-41	64.1	10	4	US-10-688-015-29	Sequence 29, Appl	659	41	64.1	116	4	US-10-446-688-8	Sequence 8, Appl
587	-41	64.1	10	5	US-10-160-505-29	Sequence 29, Appl	660	41	64.1	116	4	US-10-446-689-9	Sequence 9, Appl
588	-41	64.1	10	5	US-10-879-994-67	Sequence 67, Appl	661	41	64.1	116	4	US-10-449-379-47	Sequence 47, Appl
589	-41	64.1	10	5	US-10-726-332-81	Sequence 81, Appl	662	41	64.1	116	4	US-10-449-379-49	Sequence 49, Appl
590	-41	64.1	10	5	US-10-687-035-9	Sequence 9, Appl	663	41	64.1	116	4	US-10-449-379-59	Sequence 59, Appl
591	-41	64.1	11	4	US-10-327-598-466	Sequence 466, App	664	41	64.1	116	4	US-10-449-379-60	Sequence 60, Appl
592	-41	64.1	49	3	US-09-509-098-135	Sequence 135, App	665	41	64.1	116	4	US-10-449-379-61	Sequence 61, Appl
593	-41	64.1	49	3	US-09-509-098-138	Sequence 138, App	666	41	64.1	116	4	US-10-688-015-47	Sequence 47, Appl
594	-41	64.1	49	3	US-09-509-098-139	Sequence 139, App	667	41	64.1	116	4	US-10-688-015-49	Sequence 49, Appl
595	-41	64.1	49	3	US-09-509-098-140	Sequence 140, App	668	41	64.1	116	4	US-10-688-015-59	Sequence 59, Appl
596	-41	64.1	49	3	US-09-509-098-141	Sequence 141, App	669	41	64.1	116	4	US-10-688-015-60	Sequence 60, Appl
597	-41	64.1	49	3	US-09-509-098-142	Sequence 142, App	670	41	64.1	116	4	US-10-688-015-61	Sequence 61, Appl
598	-41	64.1	49	3	US-09-509-098-143	Sequence 143, App	671	41	64.1	116	4	US-10-160-505-47	Sequence 47, Appl
599	-41	64.1	49	3	US-09-509-098-144	Sequence 144, App	672	41	64.1	116	4	US-10-160-505-49	Sequence 49, Appl
600	-41	64.1	49	3	US-09-509-098-145	Sequence 145, App	673	41	64.1	116	4	US-10-160-505-59	Sequence 59, Appl
601	-41	64.1	49	3	US-09-509-098-146	Sequence 146, App	674	41	64.1	116	4	US-10-160-505-60	Sequence 60, Appl
602	-41	64.1	49	3	US-09-509-098-147	Sequence 147, App	675	41	64.1	116	4	US-10-160-505-61	Sequence 61, Appl
603	-41	64.1	49	3	US-09-509-098-148	Sequence 148, App	676	41	64.1	116	5	US-10-787-378-4	Sequence 4, Appl
604	-41	64.1	49	3	US-09-509-098-149	Sequence 149, App	677	41	64.1	116	5	US-10-787-378-21	Sequence 21, Appl
605	-41	64.1	49	3	US-09-509-098-150	Sequence 150, App	678	41	64.1	116	5	US-10-974-678-4	Sequence 4, Appl
606	-41	64.1	49	3	US-09-509-098-151	Sequence 151, App	679	41	64.1	116	5	US-10-974-678-8	Sequence 8, Appl
607	-41	64.1	49	3	US-09-509-098-152	Sequence 152, App	680	41	64.1	116	5	US-10-974-678-9	Sequence 9, Appl
608	-41	64.1	49	3	US-09-509-098-153	Sequence 153, App	681	41	64.1	117	4	US-10-194-975-118	Sequence 118, App
609	-41	64.1	49	3	US-09-509-098-154	Sequence 154, App	682	41	64.1	117	4	US-10-309-762-142	Sequence 142, App
610	-41	64.1	49	3	US-09-509-098-155	Sequence 155, App	683	41	64.1	117	4	US-10-309-762-142	Sequence 142, App
611	-41	64.1	52	4	US-10-425-115-249279	Sequence 249279,	684	41	64.1	118	4	US-10-309-762-124	Sequence 124, App

685	41	64.1	118	4	US-10-327-598-802	Sequence 802, App	758	41	64.1	139	3	US-09-269-921-123	Sequence 123, App
686	41	64.1	118	4	US-10-327-598-803	Sequence 803, App	759	41	64.1	139	3	US-09-269-921-124	Sequence 124, App
687	41	64.1	118	4	US-10-327-598-804	Sequence 804, App	760	41	64.1	139	3	US-09-269-921-125	Sequence 125, App
688	41	64.1	118	4	US-10-327-598-805	Sequence 805, App	761	41	64.1	139	3	US-09-269-921-126	Sequence 126, App
689	41	64.1	118	4	US-10-327-598-806	Sequence 806, App	762	41	64.1	139	3	US-09-269-921-127	Sequence 127, App
690	41	64.1	118	4	US-10-327-598-807	Sequence 807, App	763	41	64.1	139	3	US-09-269-921-128	Sequence 128, App
691	41	64.1	118	4	US-10-327-598-808	Sequence 808, App	764	41	64.1	139	3	US-09-509-098-4	Sequence 4, Appli
692	41	64.1	119	3	US-09-144-886-73	Sequence 73, Appl	765	41	64.1	139	3	US-09-509-098-16	Sequence 16, Appl
693	41	64.1	119	3	US-09-144-886-74	Sequence 74, Appl	766	41	64.1	139	3	US-09-509-098-18	Sequence 18, Appl
694	41	64.1	119	3	US-09-920-262A-7	Sequence 7, Appli	767	41	64.1	139	3	US-09-509-098-20	Sequence 20, Appl
695	41	64.1	119	3	US-10-632-706-70	Sequence 70, Appl	768	41	64.1	139	3	US-09-509-098-22	Sequence 22, Appl
696	41	64.1	119	3	US-10-632-706-71	Sequence 71, Appl	769	41	64.1	139	3	US-09-509-098-24	Sequence 24, Appl
697	41	64.1	119	5	US-10-912-994-7	Sequence 7, Appli	770	41	64.1	139	3	US-09-509-098-26	Sequence 26, Appl
698	41	64.1	119	5	US-10-975-883-7	Sequence 7, Appli	771	41	64.1	139	3	US-09-509-098-28	Sequence 28, Appl
699	41	64.1	119	5	US-10-975-740A-7	Sequence 7, Appli	772	41	64.1	139	3	US-09-509-098-30	Sequence 30, Appl
700	41	64.1	119	5	US-10-975-708-7	Sequence 7, Appli	773	41	64.1	139	3	US-09-509-098-32	Sequence 32, Appl
701	41	64.1	119	6	US-11-015-558-7	Sequence 7, Appli	774	41	64.1	139	3	US-09-509-098-34	Sequence 34, Appl
702	41	64.1	120	3	US-09-509-098-138	Sequence 138, App	775	41	64.1	139	3	US-09-509-098-36	Sequence 36, Appl
703	41	64.1	120	3	US-09-509-098-201	Sequence 201, App	776	41	64.1	139	3	US-09-509-098-38	Sequence 38, Appl
704	41	64.1	120	3	US-09-509-098-202	Sequence 202, App	777	41	64.1	139	3	US-09-509-098-40	Sequence 40, Appl
705	41	64.1	122	4	US-10-292-088-110	Sequence 110, App	778	41	64.1	139	3	US-09-509-098-42	Sequence 42, Appl
706	41	64.1	122	5	US-10-879-994-66	Sequence 66, Appl	779	41	64.1	139	3	US-09-509-098-44	Sequence 44, Appl
707	41	64.1	123	3	US-09-753-436-86	Sequence 86, Appl	780	41	64.1	139	3	US-09-509-098-46	Sequence 46, Appl
708	41	64.1	123	4	US-10-160-506-69	Sequence 69, Appl	781	41	64.1	139	3	US-09-509-098-48	Sequence 48, Appl
709	41	64.1	123	4	US-10-160-506-70	Sequence 70, Appl	782	41	64.1	139	3	US-09-509-098-50	Sequence 50, Appl
710	41	64.1	123	4	US-10-163-942-86	Sequence 86, Appl	783	41	64.1	139	3	US-09-509-098-58	Sequence 58, Appl
711	41	64.1	123	4	US-10-449-379-69	Sequence 69, Appl	784	41	64.1	139	3	US-09-509-098-100	Sequence 100, App
712	41	64.1	123	4	US-10-449-379-70	Sequence 70, Appl	785	41	64.1	139	3	US-09-509-098-127	Sequence 127, App
713	41	64.1	123	4	US-10-688-015-69	Sequence 69, Appl	786	41	64.1	139	4	US-10-315-125-7	Sequence 7, Appli
714	41	64.1	123	4	US-10-688-015-70	Sequence 70, Appl	787	41	64.1	139	4	US-10-315-125-8	Sequence 8, Appli
715	41	64.1	123	4	US-10-160-505-69	Sequence 69, Appl	788	41	64.1	139	4	US-10-218-253-105	Sequence 105, App
716	41	64.1	123	4	US-10-160-505-70	Sequence 70, Appl	789	41	64.1	139	4	US-10-218-253-108	Sequence 108, App
717	41	64.1	123	5	US-10-745-115-86	Sequence 86, Appl	790	41	64.1	139	4	US-10-218-253-110	Sequence 110, App
718	41	64.1	124	4	US-10-309-762-125	Sequence 125, App	791	41	64.1	139	4	US-10-218-253-119	Sequence 119, App
719	41	64.1	125	4	US-10-160-506-80	Sequence 80, Appl	792	41	64.1	139	4	US-10-218-253-111	Sequence 111, App
720	41	64.1	125	4	US-10-449-379-80	Sequence 80, Appl	793	41	64.1	139	4	US-10-218-253-112	Sequence 112, App
721	41	64.1	125	4	US-10-688-015-80	Sequence 80, Appl	794	41	64.1	139	4	US-10-218-253-113	Sequence 113, App
722	41	64.1	125	4	US-10-160-505-80	Sequence 80, Appl	795	41	64.1	139	4	US-10-218-253-114	Sequence 114, App
723	41	64.1	125	5	US-10-727-155-162	Sequence 162, App	796	41	64.1	139	4	US-10-218-253-115	Sequence 115, App
724	41	64.1	126	4	US-10-292-088-42	Sequence 42, Appl	797	41	64.1	139	4	US-10-218-253-121	Sequence 121, App
725	41	64.1	126	6	US-11-001-980-5	Sequence 5, Appli	798	41	64.1	139	4	US-10-218-253-117	Sequence 117, App
726	41	64.1	129	5	US-10-926-683-864	Sequence 864, App	799	41	64.1	139	4	US-10-218-253-118	Sequence 118, App
727	41	64.1	130	4	US-10-466-242-17	Sequence 17, Appl	800	41	64.1	139	4	US-10-218-253-119	Sequence 119, App
728	41	64.1	133	4	US-10-160-506-54	Sequence 54, Appl	801	41	64.1	139	4	US-10-218-253-120	Sequence 120, App
729	41	64.1	133	4	US-10-449-379-54	Sequence 54, Appl	802	41	64.1	139	4	US-10-218-253-121	Sequence 121, App
730	41	64.1	133	4	US-10-688-015-54	Sequence 54, Appl	803	41	64.1	139	4	US-10-218-253-122	Sequence 122, App
731	41	64.1	133	4	US-10-160-505-54	Sequence 54, Appl	804	41	64.1	139	4	US-10-218-253-123	Sequence 123, App
732	41	64.1	136	4	US-10-364-743-108	Sequence 108, App	805	41	64.1	139	4	US-10-218-253-124	Sequence 124, App
733	41	64.1	136	5	US-10-452-593-108	Sequence 108, App	806	41	64.1	139	4	US-10-218-253-125	Sequence 125, App
734	41	64.1	137	4	US-10-656-769-16	Sequence 16, Appl	807	41	64.1	139	4	US-10-218-253-126	Sequence 126, App
735	41	64.1	138	3	US-09-753-436-78	Sequence 78, Appl	808	41	64.1	139	4	US-10-218-253-127	Sequence 127, App
736	41	64.1	138	4	US-10-163-942-78	Sequence 78, Appl	809	41	64.1	139	4	US-10-218-253-128	Sequence 128, App
737	41	64.1	138	5	US-10-745-115-78	Sequence 78, Appl	810	41	64.1	139	4	US-10-428-085-7	Sequence 7, Appli
738	41	64.1	139	3	US-09-760-723-7	Sequence 7, Appli	811	41	64.1	139	4	US-10-428-085-8	Sequence 8, Appli
739	41	64.1	139	3	US-09-760-723-8	Sequence 8, Appli	812	41	64.1	139	4	US-10-474-714-6	Sequence 6, Appli
740	41	64.1	139	3	US-09-355-925-7	Sequence 7, Appli	813	41	64.1	139	5	US-10-488-074-85	Sequence 85, Appl
741	41	64.1	139	3	US-09-355-925-8	Sequence 8, Appli	814	41	64.1	222	4	US-10-379-392-160	Sequence 160, App
742	41	64.1	139	3	US-09-269-921-105	Sequence 105, App	815	41	64.1	222	4	US-10-379-392-162	Sequence 162, App
743	41	64.1	139	3	US-09-269-921-108	Sequence 108, App	816	41	64.1	230	3	US-09-995-693-2	Sequence 2, Appli
744	41	64.1	139	3	US-09-269-921-109	Sequence 109, App	817	41	64.1	230	3	US-10-232-408-2	Sequence 2, Appli
745	41	64.1	139	3	US-09-269-921-110	Sequence 110, App	818	41	64.1	241	3	US-09-880-748-2008	Sequence 2008, App
746	41	64.1	139	3	US-09-269-921-111	Sequence 111, App	819	41	64.1	241	3	US-09-880-748-2031	Sequence 2031, App
747	41	64.1	139	3	US-09-269-921-112	Sequence 112, App	820	41	64.1	241	3	US-09-880-748-2032	Sequence 2032, App
748	41	64.1	139	3	US-09-269-921-113	Sequence 113, App	821	41	64.1	241	4	US-10-293-418-2008	Sequence 2008, App
749	41	64.1	139	3	US-09-269-921-114	Sequence 114, App	822	41	64.1	241	4	US-10-293-418-2031	Sequence 2031, App
750	41	64.1	139	3	US-09-269-921-115	Sequence 115, App	823	41	64.1	241	4	US-10-293-418-2032	Sequence 2032, App
751	41	64.1	139	3	US-09-269-921-116	Sequence 116, App	824	41	64.1	242	5	US-10-887-231-13	Sequence 13, Appl
752	41	64.1	139	3	US-09-269-921-117	Sequence 117, App	825	41	64.1	242	3	US-09-880-748-2021	Sequence 2021, App
753	41	64.1	139	3	US-09-269-921-118	Sequence 118, App	826	41	64.1	242	3	US-09-880-748-2046	Sequence 2046, App
754	41	64.1	139	3	US-09-269-921-119	Sequence 119, App	827	41	64.1	242	3	US-09-880-748-2106	Sequence 2106, App
755	41	64.1	139	3	US-09-269-921-120	Sequence 120, App	828	41	64.1	242	4	US-10-293-418-2021	Sequence 2021, App
756	41	64.1	139	3	US-09-269-921-121	Sequence 121, App	829	41	64.1	242	4	US-10-293-418-2046	Sequence 2046, App
757	41	64.1	139	3	US-09-269-921-122	Sequence 122, App	830	41	64.1	242	4	US-10-293-418-2106	Sequence 2106, App

831	41	64.1	243	3	US-09-880-748-2009	Sequence 2009, Ap	904	40	62.5	108	4	US-10-632-929-7	Sequence 7, Appl
832	41	64.1	243	3	US-09-880-748-2012	Sequence 2012, Ap	905	40	62.5	113	5	US-10-805-177-6	Sequence 6, Appl
833	41	64.1	243	3	US-09-880-748-2014	Sequence 2014, Ap	906	40	62.5	117	3	US-09-726-258-48	Sequence 48, Appl
834	41	64.1	243	3	US-09-880-748-2063	Sequence 2063, Ap	907	40	62.5	117	3	US-09-726-258-49	Sequence 49, Appl
835	41	64.1	243	3	US-09-880-748-2107	Sequence 2107, Ap	908	40	62.5	118	4	US-10-698-041-3	Sequence 3, Appl
836	41	64.1	243	3	US-09-880-748-2109	Sequence 2109, Ap	909	40	62.5	119	4	US-10-233-996-2	Sequence 2, Appl
837	41	64.1	243	4	US-10-293-418-2009	Sequence 2009, Ap	910	40	62.5	119	4	US-10-233-996-4	Sequence 4, Appl
838	41	64.1	243	4	US-10-293-418-2012	Sequence 2012, Ap	911	40	62.5	119	4	US-10-233-996-6	Sequence 3, Appl
839	41	64.1	243	4	US-10-293-418-2014	Sequence 2014, Ap	912	40	62.5	119	4	US-10-233-996-39	Sequence 5, Appl
840	41	64.1	243	4	US-10-293-418-2063	Sequence 2063, Ap	913	40	62.5	123	3	US-09-842-776A-60	Sequence 60, Appl
841	41	64.1	243	4	US-10-293-418-2107	Sequence 2107, Ap	914	40	62.5	123	3	US-09-726-258-37	Sequence 37, Appl
842	41	64.1	243	4	US-10-293-418-2109	Sequence 2109, Ap	915	40	62.5	123	3	US-09-855-153-13	Sequence 13, Appl
843	41	64.1	244	3	US-09-880-748-1908	Sequence 1908, Ap	916	40	62.5	122	3	US-09-854-811-13	Sequence 13, Appl
844	41	64.1	244	3	US-09-880-748-2011	Sequence 2011, Ap	917	40	62.5	142	3	US-09-334-773-13	Sequence 13, Appl
845	41	64.1	244	3	US-09-880-748-2026	Sequence 2026, Ap	918	40	62.5	142	3	US-09-663-620-13	Sequence 13, Appl
846	41	64.1	244	3	US-09-880-748-2037	Sequence 2037, Ap	919	40	62.5	142	3	US-09-655-632-13	Sequence 13, Appl
847	41	64.1	244	3	US-10-293-418-1908	Sequence 1908, Ap	920	40	62.5	142	4	US-10-225-784-13	Sequence 13, Appl
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849	41	64.1	244	4	US-10-293-418-2026	Sequence 2026, Ap	922	40	62.5	142	4	US-10-225-779-13	Sequence 13, Appl
850	41	64.1	244	4	US-10-293-418-2037	Sequence 2037, Ap	923	40	62.5	142	4	US-10-374-381-13	Sequence 13, Appl
851	41	64.1	244	6	US-11-090-847-86	Sequence 86, Appl	924	40	62.5	142	4	US-10-446-542-13	Sequence 13, Appl
852	41	64.1	245	3	US-09-880-748-1946	Sequence 1946, Ap	925	40	62.5	142	5	US-10-769-308-25	Sequence 25, Appl
853	41	64.1	245	3	US-09-880-748-2004	Sequence 2004, Ap	926	40	62.5	142	5	US-10-769-074-25	Sequence 25, Appl
854	41	64.1	245	3	US-09-880-748-2042	Sequence 2042, Ap	927	40	62.5	142	5	US-10-997-735-13	Sequence 13, Appl
855	41	64.1	245	3	US-09-880-748-2116	Sequence 2116, Ap	928	40	62.5	142	6	US-11-021-950-13	Sequence 13, Appl
856	41	64.1	245	4	US-10-293-418-1946	Sequence 1946, Ap	929	40	62.5	156	5	US-10-805-177-116	Sequence 10, Appl
857	41	64.1	245	4	US-10-293-418-2004	Sequence 2004, Ap	930	40	62.5	249	5	US-10-516-429-10	Sequence 48, Appl
858	41	64.1	245	4	US-10-293-418-2042	Sequence 2042, Ap	931	40	62.5	249	2	US-08-779-457-48	Sequence 18, Appl
859	41	64.1	245	4	US-10-293-418-2116	Sequence 2116, Ap	932	40	62.5	249	3	US-09-964-186-18	Sequence 18, Appl
860	41	64.1	245	6	US-11-017-030-41	Sequence 41, Appl	933	40	62.5	249	3	US-09-880-748-1312	Sequence 18, Appl
861	41	64.1	246	5	US-10-935-290-78	Sequence 78, Appl	934	40	62.5	249	4	US-10-237-667-18	Sequence 18, Appl
862	41	64.1	247	4	US-10-620-278-23	Sequence 23, Appl	935	40	62.5	249	4	US-10-237-708-18	Sequence 18, Appl
863	41	64.1	247	4	US-10-620-278-25	Sequence 25, Appl	936	40	62.5	249	4	US-10-237-866-18	Sequence 18, Appl
864	41	64.1	247	5	US-10-620-049-23	Sequence 23, Appl	937	40	62.5	249	4	US-10-237-871-18	Sequence 18, Appl
865	41	64.1	247	5	US-10-620-049-25	Sequence 25, Appl	938	40	62.5	249	4	US-10-237-871-18	Sequence 18, Appl
866	41	64.1	247	5	US-10-981-692-37	Sequence 37, Appl	939	40	62.5	249	4	US-10-237-871-18	Sequence 18, Appl
867	41	64.1	249	3	US-09-880-748-1635	Sequence 1635, Ap	940	40	62.5	249	4	US-10-233-418-1312	Sequence 18, Appl
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869	41	64.1	250	3	US-09-880-748-1722	Sequence 1722, Ap	942	40	62.5	249	4	US-10-702-636-18	Sequence 18, Appl
870	41	64.1	250	3	US-09-880-748-1723	Sequence 1723, Ap	943	40	62.5	249	5	US-10-921-710-48	Sequence 48, Appl
871	41	64.1	250	4	US-10-293-418-1722	Sequence 1723, Ap	944	40	62.5	249	5	US-11-146-077-18	Sequence 44, Appl
872	41	64.1	250	4	US-10-293-418-1723	Sequence 1723, Ap	945	40	62.5	253	3	US-09-726-258-14	Sequence 52, Appl
873	41	64.1	251	3	US-09-880-748-1688	Sequence 1688, Ap	946	40	62.5	253	3	US-09-726-258-52	Sequence 52, Appl
874	41	64.1	251	3	US-09-880-748-1806	Sequence 1806, Ap	947	40	62.5	253	3	US-09-726-258-55	Sequence 55, Appl
875	41	64.1	251	3	US-10-293-418-1888	Sequence 1806, Ap	948	40	62.5	256	3	US-09-726-258-70	Sequence 70, Appl
876	41	64.1	251	4	US-10-293-418-1806	Sequence 1806, Ap	949	40	62.5	256	6	US-11-090-847-114	Sequence 114, Appl
877	41	64.1	251	3	US-09-880-748-1818	Sequence 1818, Ap	950	40	62.5	274	3	US-09-813-659-10	Sequence 30, Appl
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879	41	64.1	253	4	US-10-293-418-1418	Sequence 1418, Ap	952	40	62.5	299	3	US-09-726-258-60	Sequence 38, Appl
880	41	64.1	253	4	US-10-293-418-1672	Sequence 1672, Ap	953	40	62.5	299	4	US-10-425-115-338758	Sequence 38, Appl
881	41	64.1	253	5	US-10-935-290-68	Sequence 68, Appl	954	40	62.5	302	3	US-09-813-659-18	Sequence 18, Appl
882	41	64.1	255	6	US-11-090-847-79	Sequence 79, Appl	955	40	62.5	302	3	US-09-813-659-12	Sequence 32, Appl
883	41	64.1	256	3	US-09-880-748-1640	Sequence 1640, Ap	956	40	62.5	302	4	US-10-283-610A-18	Sequence 18, Appl
884	41	64.1	256	4	US-10-293-418-1640	Sequence 1640, Ap	957	40	62.5	302	4	US-10-283-610A-32	Sequence 32, Appl
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886	41	64.1	256	4	US-10-437-965-123655	Sequence 123655, A	959	40	62.5	365	5	US-10-880-320-14	Sequence 44, Appl
887	41	64.1	259	4	US-10-425-114-70055	Sequence 70055, A	960	40	62.5	378	5	US-10-743-697-11	Sequence 11, Appl
888	41	64.1	255	6	US-10-656-769-34	Sequence 34, Appl	961	40	62.5	443	4	US-10-424-599-184995	Sequence 184995, A
889	41	64.1	255	6	US-10-656-769-36	Sequence 36, Appl	962	40	62.5	446	5	US-10-450-763-38849	Sequence 38849, A
890	41	64.1	256	4	US-10-656-769-32	Sequence 32, Appl	963	40	62.5	452	3	US-09-726-258-71	Sequence 71, Appl
891	41	64.1	256	4	US-09-859-053-28	Sequence 28, Appl	964	40	62.5	458	4	US-10-052-456-196	Sequence 456, Appl
892	41	64.1	256	4	US-10-800-250-28	Sequence 28, Appl	965	40	62.5	458	4	US-10-174-590-196	Sequence 496, Appl
893	41	64.1	256	4	US-10-625-105-28	Sequence 28, Appl	966	40	62.5	458	4	US-10-176-758-196	Sequence 496, Appl
894	41	64.1	256	4	US-10-292-088-46	Sequence 46, Appl	967	40	62.5	458	4	US-10-175-737-196	Sequence 496, Appl
895	41	64.1	256	4	US-10-239-656-77	Sequence 27643, A	968	40	62.5	458	4	US-10-174-551-196	Sequence 496, Appl
896	41	64.1	256	4	US-10-097-143-27843	Sequence 27843, A	969	40	62.5	458	4	US-10-176-463-196	Sequence 496, Appl
897	41	64.1	256	4	US-10-425-114-48923	Sequence 48923, A	970	40	62.5	458	4	US-10-176-914-196	Sequence 496, Appl
898	41	64.1	256	4	US-10-425-115-195566	Sequence 195566, A	971	40	62.5	458	4	US-10-176-914-196	Sequence 496, Appl
899	41	64.1	256	4	US-09-842-776A-28	Sequence 28, Appl	972	40	62.5	458	4	US-10-176-914-196	Sequence 496, Appl
900	41	64.1	256	4	US-10-769-308-30	Sequence 30, Appl	973	40	62.5	458	4	US-10-173-706-196	Sequence 496, Appl
901	41	64.1	256	4	US-10-769-074-30	Sequence 30, Appl	974	40	62.5	458	4	US-10-175-728-196	Sequence 496, Appl
902	41	64.1	256	4	US-10-996-316-138	Sequence 138, Appl	975	40	62.5	458	4	US-10-175-728-196	Sequence 496, Appl
903	41	64.1	256	4	US-09-800-908-7	Sequence 7, Appl	976	40	62.5	458	4	US-10-176-482-496	Sequence 496, Appl

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ALIGNMENTS

RESULT 1

US-09-795-798-10
Sequence 10, Application US/09795798
Publication No. US20030207336A1

GENERAL INFORMATION:

APPLICANT: Prestea, Leonard G.

Jardieu, Paula M.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/795,798

FILING DATE: 28-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/974,899

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P1014R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-795-798-10

Query Match 100.0%; Score 64; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSTGHMN 10
DB 1 GYSTGHMN 10

RESULT 2

US-10-727-737-19

Sequence 19, Application US/10727737

Publication No. US20040146507A1

GENERAL INFORMATION:

APPLICANT: Prestea, Leonard G.

Jardieu, Paula M.

TITLE OF INVENTION: Antibody Mutants

NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/727,737

FILING DATE: 03-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/975,329B

FILING DATE: 20-Nov-1997

APPLICATION NUMBER: 60/031945

FILING DATE: 27-Nov-1996

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P1064R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-727-737-19

Query Match 100.0%; Score 64; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSTGHMN 10

DB 1 GYSTGHMN 10

RESULT 3

US-09-795-798-4

Sequence 4, Application US/09795798

Publication No. US20030207336A1

GENERAL INFORMATION:

APPLICANT: Prestea, Leonard G.

Jardieu, Paula M.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPattn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-795-798-4
Query Match 100.0%; Score 64; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYSFTGHMWN 10
|||
Db 26 GYSFTGHMWN 35
RESULT 4
US-09-795-798-5
Sequence 5, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPattn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-795-798-5
Query Match 100.0%; Score 64; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYSFTGHMWN 10
|||
Db 26 GYSFTGHMWN 35
RESULT 5
US-09-795-798-24
Sequence 24, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPattn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-795-798-24
Query Match 100.0%; Score 64; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYSFTGHMWN 10
|||
Db 26 GYSFTGHMWN 35
RESULT 6

US-10-727-737-4
; Sequence 4, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-727-737-4
Query Match 100.0%; Score 64; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYSFTGHMNN 10
|||
Db 26 GYSFTGHMNN 35
RESULT 7
US-10-727-737-5
; Sequence 5, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-727-737-5
Query Match 100.0%; Score 64; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GYSFTGHMNN 10
|||
Db 26 GYSFTGHMNN 35
RESULT 8
US-10-727-737-17
; Sequence 17, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-727-737-17

Query Match 100.0%; Score 64; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
26 GYSFTGHMNN 35

RESULT 9
US-10-877-532-6
; Sequence 6, Application US/10877532
; Publication No. US20050038231A1
; GENERAL INFORMATION:
; APPLICANT: FAHRNER, ROBERT L.
; APPLICANT: LAVERDIERE, AMY
; APPLICANT: MCDONALD, PAUL J.
; APPLICANT: O'LEARY, RHONA M.
; TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAPHY
; FILE REFERENCE: P2015R1
; CURRENT APPLICATION NUMBER: US/10/877,532
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US 60/490,500
; PRIOR FILING DATE: 2003-07-28
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 6
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-877-532-6

Query Match 100.0%; Score 64; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
26 GYSFTGHMNN 35

RESULT 10
US-10-423-299-4
; Sequence 4, Application US/10423289
; Publication No. US20030229212A1
; GENERAL INFORMATION:
; APPLICANT: FAHRNER, ROBERT
; APPLICANT: FOLLMAN, DEBORAH
; APPLICANT: LEBRETON, BENEDICTE
; APPLICANT: VAN REIS, ROBERT
; TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
; FILE REFERENCE: 39766-0121A
; CURRENT APPLICATION NUMBER: US/10/423,299
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/375,953
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-423-299-4

Query Match 100.0%; Score 64; DB 4; Length 451;

Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
26 GYSFTGHMNN 35

RESULT 11
US-10-727-737-21
; Sequence 21, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Prestea, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-727-737-21

Query Match 95.3%; Score 61; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0039;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||
26 GYSFTGHMNN 35

RESULT 12
US-09-726-258-50
; Sequence 50, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., HseI, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Prestea, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.

TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/225-5530
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-09-726-258-50

Query Match 93.8%; Score 60; DB 3; Length 116;
Best Local Similarity 90.0%; Pred. No. 0.056;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
|:|||||
Db 26 GFSFTGHMNN 35

RESULT 13
US-10-727-737-22
Sequence 22, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-727-737-22

Query Match 92.2%; Score 59; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0082;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
|:|||||
Db 1 GYSFAGHMNN 10

RESULT 14
US-10-727-737-23
Sequence 23, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-727-737-23

Query Match 90.6%; Score 58; DB 4; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||
 DB 1 GYSFTAHMNN 10

RESULT 15

US-10-727-737-24
 ; Sequence 24, Application US/10727737
 ; Publication No. US20040146507A1

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.

Jardieu, Paula M.

TITLE OF INVENTION: Antibody Mutants

NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/727,737

FILING DATE: 03-Dec-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/975,329B

FILING DATE: 20-Nov-1997

APPLICATION NUMBER: 60/031945

FILING DATE: 27-Nov-1996

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P1064R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-10-727-737-24

Query Match 84.4%; Score 54; DB 4; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.052;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||
 DB 1 GYSFTAHMNN 10

RESULT 16

US-09-948-004-16
 ; Sequence 16, Application US/09948004
 ; Publication No. US20030017979A1

GENERAL INFORMATION:

APPLICANT: MACK, Mathias

TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in

TITLE OF INVENTION: Immunological disorders

FILE REFERENCE: E 2411 EP

;; CURRENT APPLICATION NUMBER: US/09/948,004
 ;; CURRENT FILING DATE: 2001-09-05
 ;; NUMBER OF SEQ ID NOS: 34
 ;; SOFTWARE: PatentIn Ver. 2.1
 ;; SEQ ID NO 16

LENGTH: 117

TYPE: PRT

ORGANISM: Mus sp.

US-09-948-004-16

Query Match 81.2%; Score 52; DB 3; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||
 DB 36 GYSFTSYMNN 45

RESULT 17

US-10-672-932-16

; Sequence 16, Application US/10672932

; Publication No. US20050191702A1

GENERAL INFORMATION:

APPLICANT: MACK, Mathias

TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in

TITLE OF INVENTION: Immunological disorders

FILE REFERENCE: E 2411 EP

CURRENT APPLICATION NUMBER: US/10/672,932

CURRENT FILING DATE: 2003-09-26

PRIOR APPLICATION NUMBER: US/09/948,004

PRIOR FILING DATE: 2001-09-05

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 117

TYPE: PRT

ORGANISM: Mus sp.

US-10-672-932-16

Query Match 81.2%; Score 52; DB 5; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
 |||||
 DB 36 GYSFTSYMNN 45

RESULT 18

US-10-435-614-13

; Sequence 13, Application US/10435614

; Publication No. US20040005647A1

GENERAL INFORMATION:

APPLICANT: DENARDO, SALLY J.

APPLICANT: WINTROP, MICHELLE D.

APPLICANT: DENARDO, GERALD L.

TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING

FILE REFERENCE: 309T-000220US

CURRENT APPLICATION NUMBER: US/10/435,614

CURRENT FILING DATE: 2003-05-09

PRIOR APPLICATION NUMBER: 10/112,788

PRIOR FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: 60/280,721

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.2

SEQ ID NO 13

LENGTH: 118

TYPE: PRT

ORGANISM: Mus Musculus

US-10-435-614-13

Query Match 81.2%; Score 52; DB 4; Length 118;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||||:||||
Db 26 GYSFTSYMWN 35

RESULT 19
US-09-144-886-54
; Sequence 54, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C1 region VH epitope 1
US-09-144-886-54

Query Match 81.2%; Score 52; DB 3; Length 121;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||||:||||
Db 26 GYSFTSYMWN 35

RESULT 20
US-10-632-706-51
; Sequence 51, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 4077-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-51

Query Match 81.2%; Score 52; DB 4; Length 121;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||||:||||

Db 26 GYSFTSYMWN 35

RESULT 21
US-09-144-886-51
; Sequence 51, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C15 region VH epitope 1
US-09-144-886-51

Query Match 81.2%; Score 52; DB 3; Length 125;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||||:||||
Db 26 GYSFTSYMWN 35

RESULT 22
US-09-144-886-52
; Sequence 52, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; TITLE OF INVENTION: Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: C9 region VH epitope 1
US-09-144-886-52

Query Match 81.2%; Score 52; DB 3; Length 125;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||||:||||
Db 26 GYSFTSYMWN 35

RESULT 23
US-09-144-886-53
; Sequence 53, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D

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; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 53
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
; OTHER INFORMATION: IDS region VH epitope 1
US-09-144-886-53

Query Match
Best Local Similarity 81.2%; Score 52; DB 3; Length 125;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
Db 26 GYSFTSYMNN 35

RESULT 24
US-10-632-706-48
; Sequence 48, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 48
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-48

Query Match
Best Local Similarity 81.2%; Score 52; DB 4; Length 125;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
Db 26 GYSFTSYMNN 35

RESULT 25
US-10-632-706-49
; Sequence 49, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
```

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; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 49
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-49

Query Match
Best Local Similarity 81.2%; Score 52; DB 4; Length 125;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
Db 26 GYSFTSYMNN 35

RESULT 26
US-10-632-706-50
; Sequence 50, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 50
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-50

Query Match
Best Local Similarity 81.2%; Score 52; DB 4; Length 125;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
Db 26 GYSFTSYMNN 35

RESULT 27
US-09-948-004-14
; Sequence 14, Application US/09948004
; Publication No. US20030017979A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 138
```

TYPE: PRT
ORGANISM: Mus sp.
US-09-948-004-14

Query Match 81.2% Score 52; DB 3; Length 138;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMNN 10
|||||:||||
DB 45 GYSFTSYMMN 54

RESULT 28

US-10-672-932-14
Sequence 14, Application US/10672932
Publication No. US20050191702A1
GENERAL INFORMATION:
APPLICANT: MACK, Mathias
TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
FILE REFERENCE: E 2411 EP
CURRENT APPLICATION NUMBER: US/10/672,932
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US/09/948,004
PRIOR FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 138
TYPE: PRT
ORGANISM: Mus sp.
US-10-672-932-14

Query Match 81.2% Score 52; DB 5; Length 138;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMNN 10
|||||:||||
DB 45 GYSFTSYMMN 54

RESULT 29

US-10-435-614-21
Sequence 21, Application US/10435614
Publication No. US20040005647A1
GENERAL INFORMATION:
APPLICANT: DENARDO, SALLY J.
APPLICANT: WINTHROP, MICHELLE D.
APPLICANT: DENARDO, GERALD L.
TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING
FILE REFERENCE: 309T-000220US
CURRENT APPLICATION NUMBER: US/10/435,614
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: 10/112,788
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,721
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 177
TYPE: PRT
ORGANISM: Mus Musculus
US-10-435-614-21

Query Match 81.2% Score 52; DB 4; Length 177;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMNN 10
|||||:||||

DB 28 GYSFTSYMMN 37

RESULT 30

US-09-948-004-18
Sequence 18, Application US/09948004
Publication No. US2003001979A1
GENERAL INFORMATION:
APPLICANT: MACK, Mathias
TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
FILE REFERENCE: E 2411 EP
CURRENT APPLICATION NUMBER: US/09/948,004
CURRENT FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 495
TYPE: PRT
ORGANISM: Mus sp.
US-09-948-004-18

Query Match 81.2% Score 52; DB 3; Length 495;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMNN 10
|||||:||||
DB 148 GYSFTSYMMN 157

RESULT 31

US-10-672-932-18
Sequence 18, Application US/10672932
Publication No. US20050191702A1
GENERAL INFORMATION:
APPLICANT: MACK, Mathias
TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
FILE REFERENCE: E 2411 EP
CURRENT APPLICATION NUMBER: US/10/672,932
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: US/09/948,004
PRIOR FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 495
TYPE: PRT
ORGANISM: Mus sp.
US-10-672-932-18

Query Match 81.2% Score 52; DB 5; Length 495;
Best Local Similarity 80.0%; Pred. No. 4.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYSFTGHMNN 10
|||||:||||
DB 148 GYSFTSYMMN 157

RESULT 32

US-10-812-366-3
Sequence 3, Application US/10812366
Publication No. US20040234519A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs
TITLE OF INVENTION: METHOD OF TREATING CANCER WITH ANTI-PLEIOTROPHIN ANTIBODIES
FILE REFERENCE: 05882, 014, NUS01
CURRENT APPLICATION NUMBER: US/10/812,366
CURRENT FILING DATE: 2004-03-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.2

SEQ ID NO 3
LENGTH: 120
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-812-366-3

Query Match 79.7%; Score 51; DB 5; Length 120;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||:|||||
DB 26 GYAFSSHMMN 35

RESULT 33
US-10-964-195-13
Sequence 13, Application US/10964195
Publication No. US20050163774A1
GENERAL INFORMATION:
APPLICANT: Rosenblum et al.
TITLE OF INVENTION: Immunotoxins Directed Against C-erbB-2 (HER-2/Neu)
FILE REFERENCE: D5425CIP2
CURRENT APPLICATION NUMBER: US/10/964,195
PRIORITY FILING DATE: 2004-10-13
PRIOR APPLICATION NUMBER: US/09/320,156
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: 08/404,499
PRIOR FILING DATE: 1995-03-17
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 13
LENGTH: 498
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Polypeptide encoded by the scFv23-gelolin immunotoxin
US-10-964-195-13

Query Match 79.7%; Score 51; DB 5; Length 498;
Best Local Similarity 90.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||||||
DB 147 GYSFTGHMNN 156

RESULT 34
US-10-964-195-11
Sequence 11, Application US/10964195
Publication No. US20050163774A1
GENERAL INFORMATION:
APPLICANT: Rosenblum et al.
TITLE OF INVENTION: Immunotoxins Directed Against C-erbB-2 (HER-2/Neu)
FILE REFERENCE: D5425CIP2
CURRENT APPLICATION NUMBER: US/10/964,195
PRIORITY FILING DATE: 2004-10-13
PRIOR APPLICATION NUMBER: US/09/320,156
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: 08/404,499
PRIOR FILING DATE: 1995-03-17
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 11
LENGTH: 506
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Polypeptide encoded by the scFv23-gelolin immunotoxin
US-10-964-195-11

Query Match 79.7%; Score 51; DB 5; Length 506;

Best Local Similarity 90.0%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||||||
DB 150 GYSFTGHMNN 159

RESULT 35
US-10-727-737-25
Sequence 25, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-727-737-25

Query Match 78.1%; Score 50; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||||||
DB 1 GYSFTGHMNN 10

RESULT 36
US-10-842-011-3
Sequence 3, Application US/10842011
Publication No. US20050025763A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs
TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
FILE REFERENCE: 05882, 0110, NPU504
CURRENT APPLICATION NUMBER: US/10/842,011
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 93

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-842-011-3

Query Match      78.1%; Score 50; DB 5; Length 120;
Best Local Similarity 80.0%; Pred. No. 2.3;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHWMN 10
        |||:|||||
Db      26 GYFTSHWMH 35

RESULT 37
US-10-468-370-642
; Sequence 642, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: May, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-468-370-642

Query Match      78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHWMN 10
        |||:|||||
Db      26 GYFTSHWMH 35

RESULT 38
US-10-468-370-644
; Sequence 644, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
```

```
; APPLICANT: May, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 644
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-644

Query Match      78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHWMN 10
        |||:|||||
Db      26 GYFTSHWMH 35

RESULT 39
US-10-468-370-646
; Sequence 646, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: May, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 646
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-646

Query Match      78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHWMN 10
        |||:|||||
```


Db 26 GYFTSHMMH 35

RESULT 40

US-10-468-370-648
; Sequence 648, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 648
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-648

Query Match 78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
||:|||||:
Db 26 GYFTSHMMH 35

RESULT 41

US-10-468-370-650
; Sequence 650, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690

; PRIOR FILING DATE: 2002-02-18

; NUMBER OF SEQ ID NOS: 689

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 650

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-650

Query Match 78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
||:|||||:
Db 26 GYFTSHMMH 35

RESULT 42

US-10-468-370-652
; Sequence 652, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 652
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-652

Query Match 78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMMN 10
||:|||||:
Db 26 GYFTSHMMH 35

RESULT 43

US-10-468-370-654
; Sequence 654, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim

```

; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: May, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 654
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-654
```

```
Query Match          78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 GYSFTGHMMN 10
        ||:|||||:
Db       26 GYFTSHMMH 35
```

```
RESULT 44
US-10-468-370-656
; Sequence 656, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: May, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 656
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-656
```

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Query Match          78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
OY      1 GYSFTGHMMN 10
        ||:|||||:
Db       26 GYFTSHMMH 35

RESULT 45
US-10-468-528-1
; Sequence 1, Application US/10468528
; Publication No. US20040096442A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED ANTI-EGFR ANTIBODIES WITH
; FILE REFERENCE: MER-116
; CURRENT APPLICATION NUMBER: US/10/468,528
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01687
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antibody fragment
US-10-468-528-1
```

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Query Match          78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 GYSFTGHMMN 10
        ||:|||||:
Db       26 GYFTSHMMH 35
```

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RESULT 46
US-10-468-528-3
; Sequence 3, Application US/10468528
; Publication No. US20040096442A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED ANTI-EGFR ANTIBODIES WITH
; FILE REFERENCE: MER-116
; CURRENT APPLICATION NUMBER: US/10/468,528
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01687
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Antibody fragment
US-10-468-528-3

Query Match 78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|||||:
Db 26 GYFTSHWMH 35

RESULT 47
US-10-468-528-5

Sequence 5, Application US/10468528
Publication No. US20040096442A1

GENERAL INFORMATION:

APPLICANT: Carr, Francis J.

APPLICANT: Carter, Graham

APPLICANT: Jones, Tim

APPLICANT: Williams, Stephen

APPLICANT: Hamilton, Anita

TITLE OF INVENTION: MODIFIED ANTI-EGFR ANTIBODIES WITH

TITLE OF INVENTION: REDUCED IMMUNOGENICITY

FILE REFERENCE: MER-116

CURRENT APPLICATION NUMBER: US/10/468,528

PRIOR FILING DATE: 2003-08-19

PRIOR APPLICATION NUMBER: EP 01103954.2

PRIOR FILING DATE: 2001-02-19

PRIOR APPLICATION NUMBER: PCT/EP02/01687

PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 121

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antibody fragment

US-10-468-528-5

Query Match 78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|||||:
Db 26 GYFTSHWMH 35

RESULT 48
US-10-468-528-7

Sequence 7, Application US/10468528
Publication No. US20040096442A1

GENERAL INFORMATION:

APPLICANT: Carr, Francis J.

APPLICANT: Carter, Graham

APPLICANT: Jones, Tim

APPLICANT: Williams, Stephen

APPLICANT: Hamilton, Anita

TITLE OF INVENTION: MODIFIED ANTI-EGFR ANTIBODIES WITH

TITLE OF INVENTION: REDUCED IMMUNOGENICITY

FILE REFERENCE: MER-116

CURRENT APPLICATION NUMBER: US/10/468,528

PRIOR FILING DATE: 2003-08-19

PRIOR APPLICATION NUMBER: EP 01103954.2

PRIOR FILING DATE: 2001-02-19

PRIOR APPLICATION NUMBER: PCT/EP02/01687

PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 121

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antibody fragment
US-10-468-528-7

Query Match 78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|||||:
Db 26 GYFTSHWMH 35

RESULT 49
US-10-468-528-9

Sequence 9, Application US/10468528
Publication No. US20040096442A1

GENERAL INFORMATION:

APPLICANT: Carr, Francis J.

APPLICANT: Carter, Graham

APPLICANT: Jones, Tim

APPLICANT: Williams, Stephen

APPLICANT: Hamilton, Anita

TITLE OF INVENTION: MODIFIED ANTI-EGFR ANTIBODIES WITH

TITLE OF INVENTION: REDUCED IMMUNOGENICITY

FILE REFERENCE: MER-116

CURRENT APPLICATION NUMBER: US/10/468,528

PRIOR FILING DATE: 2003-08-19

PRIOR APPLICATION NUMBER: EP 01103954.2

PRIOR FILING DATE: 2001-02-19

PRIOR APPLICATION NUMBER: PCT/EP02/01687

PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 121

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antibody fragment

US-10-468-528-9

Query Match 78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|||||:
Db 26 GYFTSHWMH 35

RESULT 50
US-10-468-528-11

Sequence 11, Application US/10468528
Publication No. US20040096442A1

GENERAL INFORMATION:

APPLICANT: Carr, Francis J.

APPLICANT: Carter, Graham

APPLICANT: Jones, Tim

APPLICANT: Williams, Stephen

APPLICANT: Hamilton, Anita

TITLE OF INVENTION: MODIFIED ANTI-EGFR ANTIBODIES WITH

TITLE OF INVENTION: REDUCED IMMUNOGENICITY

FILE REFERENCE: MER-116

CURRENT APPLICATION NUMBER: US/10/468,528

PRIOR FILING DATE: 2003-08-19

PRIOR APPLICATION NUMBER: EP 01103954.2

PRIOR FILING DATE: 2001-02-19

PRIOR APPLICATION NUMBER: PCT/EP02/01687

PRIOR FILING DATE: 2002-02-19

NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antibody fragment
US-10-468-528-11

Query Match 78.1%; Score 50; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 2.3;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GVSFTGHWMN 10
||:|||||:
Db 26 GYFTSHWMH 35

Search completed: January 17, 2006, 12:13:00
Job time : 52.6364 secs

GenCore version 5.1.6
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OM protein~~in~~ protein search, using sw model

Run on: January 17, 2006, 11:59:34 : Search time 3.3333 Seconds
(without alignments)
28.363 Million cell updates/sec

Title: US-10-665-658-10

Perfect score: 64

Sequence: 1 GYSTFGHMMN 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep:*
2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep:*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB pep:*
4: /cgn2_6/ptodata/2/pubppaa/FCI_NEW_PUB pep:*
5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB pep:*
6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB pep:*
7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB pep:*
8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	10	6	US-10-665-658-10
2	64	100.0	10	6	US-10-665-658-25
3	64	100.0	121	6	US-10-665-658-4
4	64	100.0	121	6	US-10-665-658-5
5	64	100.0	121	6	US-10-665-658-24
6	64	100.0	121	7	US-11-07-028-50
7	64	100.0	121	7	US-11-07-028-52
8	61	95.3	10	6	US-10-665-658-27
9	59	92.2	10	6	US-10-665-658-28
10	58	90.6	10	6	US-10-665-658-29
11	54	84.4	10	6	US-10-665-658-30
12	52	81.2	121	6	US-10-507-662-25
13	52	81.2	121	6	US-10-507-662-26
14	50	78.1	10	6	US-10-665-658-31
15	48	75.0	10	6	US-10-880-238-63
16	48	75.0	119	6	US-10-507-662-22
17	47	73.4	49	7	US-11-051-481-46
18	47	73.4	66	7	US-11-051-481-45
19	47	73.4	86	7	US-11-051-481-44
20	47	73.4	119	6	US-10-507-662-29
21	47	73.4	250	7	US-11-054-515-1161
22	46	71.9	10	6	US-10-665-658-26
23	46	71.9	108	7	US-11-097-812-27
24	45	70.3	10	7	US-11-105-268-1
25	45	70.3	118	7	US-11-105-268-7

26	45	70.3	120	7	US-11-105-268-17	Sequence 17, Appl
27	45	70.3	124	7	US-11-105-268-9	Sequence 9, Appl
28	45	70.3	133	7	US-11-069-834-2	Sequence 2, Appl
29	45	70.3	249	7	US-11-054-515-1957	Sequence 1957, Ap
30	44	68.8	10	6	US-10-932-334-53	Sequence 53, Appl
31	44	68.8	98	6	US-10-932-334-57	Sequence 57, Appl
32	44	68.8	111	7	US-11-097-812-17	Sequence 17, Appl
33	44	68.8	111	7	US-11-097-812-20	Sequence 20, Appl
34	44	68.8	111	7	US-11-097-812-21	Sequence 21, Appl
35	44	68.8	111	7	US-11-097-812-25	Sequence 25, Appl
36	44	68.8	111	7	US-11-097-812-32	Sequence 32, Appl
37	44	68.8	111	7	US-11-097-812-34	Sequence 34, Appl
38	44	68.8	111	7	US-11-097-812-36	Sequence 36, Appl
39	44	68.8	111	7	US-11-097-812-205	Sequence 205, App
40	44	68.8	117	7	US-11-054-669-119	Sequence 119, App
41	44	68.8	119	7	US-11-054-669-119	Sequence 5, Appl
42	44	68.8	119	7	US-11-053-750-5	Sequence 5, Appl
43	44	68.8	119	7	US-11-053-749-5	Sequence 5, Appl
44	44	68.8	119	7	US-10-932-334-71	Sequence 71, Appl
45	44	68.8	120	6	US-10-932-334-72	Sequence 72, Appl
46	44	68.8	122	6	US-10-932-334-73	Sequence 73, Appl
47	44	68.8	122	6	US-10-932-334-87	Sequence 87, Appl
48	44	68.8	123	6	US-10-932-334-88	Sequence 88, Appl
49	44	68.8	123	6	US-10-932-334-92	Sequence 92, Appl
50	44	68.8	123	6	US-10-932-334-7	Sequence 7, Appl
51	44	68.8	124	6	US-10-932-334-13	Sequence 13, Appl
52	44	68.8	124	6	US-10-932-334-70	Sequence 70, Appl
53	44	68.8	143	6	US-10-932-334-52	Sequence 52, Appl
54	44	68.8	143	6	US-10-512-184-36	Sequence 36, Appl
55	44	68.8	248	6	US-10-512-184-36	Sequence 50, Appl
56	44	68.8	615	6	US-11-051-164-50	Sequence 51, Appl
57	44	68.8	116	7	US-11-055-163-17	Sequence 27, Appl
58	43	67.2	119	6	US-10-507-662-27	Sequence 28, Appl
59	43	67.2	119	6	US-10-507-662-28	Sequence 63, Appl
60	43	67.2	119	7	US-11-097-812-63	Sequence 64, Appl
61	43	67.2	119	7	US-11-097-812-64	Sequence 65, Appl
62	43	67.2	119	7	US-11-097-812-65	Sequence 66, Appl
63	43	67.2	119	7	US-11-097-812-66	Sequence 67, Appl
64	43	67.2	119	7	US-11-097-812-67	Sequence 70, Appl
65	43	67.2	119	7	US-11-097-812-70	Sequence 71, Appl
66	43	67.2	119	7	US-11-097-812-71	Sequence 72, Appl
67	43	67.2	119	7	US-11-097-812-72	Sequence 73, Appl
68	43	67.2	119	7	US-11-097-812-73	Sequence 74, Appl
69	43	67.2	119	7	US-11-097-812-74	Sequence 75, Appl
70	43	67.2	119	7	US-11-097-812-75	Sequence 76, Appl
71	43	67.2	119	7	US-11-097-812-76	Sequence 77, Appl
72	43	67.2	119	7	US-11-097-812-77	Sequence 78, Appl
73	43	67.2	119	7	US-11-097-812-78	Sequence 80, Appl
74	43	67.2	119	7	US-11-097-812-80	Sequence 81, Appl
75	43	67.2	119	7	US-11-097-812-81	Sequence 86, App
76	43	67.2	119	7	US-11-097-812-135	Sequence 135, App
77	43	67.2	120	7	US-11-097-812-136	Sequence 136, App
78	43	67.2	120	7	US-11-097-812-138	Sequence 138, App
79	43	67.2	120	7	US-11-097-812-143	Sequence 143, App
80	43	67.2	120	7	US-11-097-812-144	Sequence 144, App
81	43	67.2	120	7	US-11-097-812-145	Sequence 145, App
82	43	67.2	120	7	US-11-054-515-2088	Sequence 2088, Ap
83	43	67.2	248	7	US-11-102-743-7	Sequence 7, Appl
84	42.5	66.4	114	7	US-11-054-515-1948	Sequence 1948, Ap
85	42.5	66.4	241	7	US-11-054-515-1900	Sequence 1900, Ap
86	42.5	66.4	245	7	US-11-054-515-1900	Sequence 950, App
87	42.5	66.4	248	7	US-11-054-669-45	Sequence 45, Appl
88	42	65.6	98	7	US-11-084-554-56	Sequence 56, Appl
89	42	65.6	98	7	US-11-051-453-81	Sequence 81, Appl
90	42	65.6	98	7	US-11-061-848-24	Sequence 24, Appl
91	42	65.6	119	6	US-10-834-397-26	Sequence 26, Appl
92	42	65.6	119	6	US-11-051-453-54	Sequence 54, Appl
93	42	65.6	120	6	US-10-834-397-40	Sequence 40, Appl
94	42	65.6	120	6	US-10-834-397-67	Sequence 67, Appl
95	42	65.6	121	6	US-10-502-145-21	Sequence 21, Appl
96	42	65.6	138	7	US-11-051-453-56	Sequence 56, Appl
97	42	65.6	247	7	US-11-084-717-21	Sequence 21, Appl
98	42	65.6	247	7	US-11-084-717-21	Sequence 21, Appl

99	42	65.6	247	7	US-11-179-244-21	Sequence 21, Appl	172	37	57.8	242	7	US-11-054-515-2084	Sequence 2084, Ap
100	42	65.6	250	7	US-11-054-515-1319	Sequence 1319, Ap	173	37	57.8	250	7	US-11-054-515-1486	Sequence 1486, Ap
101	42	65.6	252	7	US-11-054-515-1537	Sequence 1537, Ap	174	37	57.8	474	7	US-11-000-463-284	Sequence 284, Ap
102	41	64.1	10	6	US-10-880-238-45	Sequence 45, Appl	175	37	57.8	483	7	US-11-113-775A-1	Sequence 1, Appl
103	41	64.1	10	6	US-10-880-238-48	Sequence 48, Appl	176	37	57.8	483	7	US-11-113-775A-2	Sequence 2, Appl
104	41	64.1	10	6	US-10-880-238-51	Sequence 51, Appl	177	37	57.8	483	7	US-11-113-799-1	Sequence 1, Appl
105	41	64.1	10	6	US-10-880-238-54	Sequence 54, Appl	178	37	57.8	483	7	US-11-113-799-2	Sequence 2, Appl
106	41	64.1	10	6	US-10-880-238-57	Sequence 57, Appl	179	37	57.8	485	6	US-10-630-203-12	Sequence 12, Appl
107	41	64.1	98	7	US-11-054-669-1	Sequence 1, Appl	180	37	57.8	485	7	US-11-103-037-7	Sequence 7, Appl
108	41	64.1	98	7	US-11-084-554-16	Sequence 16, Appl	181	37	57.8	485	7	US-11-113-775A-3	Sequence 3, Appl
109	41	64.1	116	7	US-11-097-812-19	Sequence 19, Appl	182	37	57.8	485	7	US-11-113-799-3	Sequence 3, Appl
110	41	64.1	117	7	US-11-054-669-120	Sequence 120, App	183	36.5	57.0	116	7	US-11-096-074-50	Sequence 50, Appl
111	41	64.1	124	7	US-11-040-159-8	Sequence 8, Appl	184	36.5	57.0	116	7	US-11-095-822-50	Sequence 50, Appl
112	41	64.1	241	7	US-11-054-515-2008	Sequence 2008, Ap	185	36.5	57.0	119	7	US-11-054-669-124	Sequence 124, App
113	41	64.1	241	7	US-11-054-515-2031	Sequence 2031, Ap	186	36.5	57.0	118	7	US-11-125-837-22	Sequence 22, Appl
114	41	64.1	241	7	US-11-054-515-2032	Sequence 2032, Ap	187	36.5	57.0	248	7	US-11-054-515-1700	Sequence 1700, Ap
115	41	64.1	242	7	US-11-054-515-2021	Sequence 2021, Ap	188	36.5	57.0	248	7	US-11-054-515-1790	Sequence 1790, Ap
116	41	64.1	242	7	US-11-054-515-2046	Sequence 2046, Ap	189	36.5	57.0	251	7	US-11-054-515-1496	Sequence 1496, Ap
117	41	64.1	242	7	US-11-054-515-2046	Sequence 2106, Ap	190	36.5	57.0	251	7	US-11-054-515-1802	Sequence 1802, Ap
118	41	64.1	243	7	US-11-054-515-2009	Sequence 2009, Ap	191	36	56.2	10	6	US-10-880-238-60	Sequence 60, Appl
119	41	64.1	243	7	US-11-054-515-2012	Sequence 2012, Ap	192	36	56.2	10	7	US-11-105-268-11	Sequence 11, Appl
120	41	64.1	243	7	US-11-054-515-2014	Sequence 2014, Ap	193	36	56.2	97	7	US-11-093-274-35	Sequence 35, Appl
121	41	64.1	243	7	US-11-054-515-2063	Sequence 2063, Ap	194	36	56.2	98	7	US-11-054-669-15	Sequence 15, Appl
122	41	64.1	243	7	US-11-054-515-2107	Sequence 2107, Ap	195	36	56.2	98	7	US-11-054-669-33	Sequence 33, Appl
123	41	64.1	243	7	US-11-054-515-2109	Sequence 2109, Ap	196	36	56.2	98	7	US-11-084-554-44	Sequence 44, Appl
124	41	64.1	244	7	US-11-054-515-1908	Sequence 1908, Ap	197	36	56.2	98	7	US-11-084-554-47	Sequence 47, Appl
125	41	64.1	244	7	US-11-054-515-2011	Sequence 2011, Ap	198	36	56.2	116	7	US-11-174-186-2	Sequence 2, Appl
126	41	64.1	244	7	US-11-054-515-2026	Sequence 2026, Ap	199	36	56.2	116	7	US-11-174-186-6	Sequence 6, Appl
127	41	64.1	244	7	US-11-054-515-2037	Sequence 2037, Ap	200	36	56.2	116	7	US-11-174-186-6	Sequence 6, Appl
128	41	64.1	245	7	US-11-054-515-1946	Sequence 1946, Ap	201	36	56.2	116	7	US-11-174-186-17	Sequence 17, Appl
129	41	64.1	245	7	US-11-054-515-1946	Sequence 2042, Ap	202	36	56.2	116	7	US-11-174-186-18	Sequence 18, Appl
130	41	64.1	245	7	US-11-054-515-2004	Sequence 2004, Ap	203	36	56.2	116	7	US-11-174-186-19	Sequence 19, Appl
131	41	64.1	245	7	US-11-054-515-2042	Sequence 2042, Ap	204	36	56.2	116	7	US-11-174-186-20	Sequence 20, Appl
132	41	64.1	245	7	US-11-054-515-2116	Sequence 2116, Ap	205	36	56.2	116	7	US-11-174-186-21	Sequence 21, Appl
133	41	64.1	247	7	US-11-084-717-23	Sequence 23, Appl	206	36	56.2	116	7	US-11-174-186-22	Sequence 22, Appl
134	41	64.1	247	7	US-11-179-244-23	Sequence 25, Appl	207	36	56.2	116	7	US-11-174-186-23	Sequence 23, Appl
135	41	64.1	247	7	US-11-179-244-23	Sequence 23, Appl	208	36	56.2	116	7	US-11-174-186-24	Sequence 24, Appl
136	41	64.1	249	7	US-11-054-515-1635	Sequence 1635, Ap	209	36	56.2	116	7	US-11-174-186-25	Sequence 25, Appl
137	41	64.1	250	7	US-11-054-515-1722	Sequence 1722, Ap	210	36	56.2	116	7	US-11-174-186-26	Sequence 26, Appl
138	41	64.1	250	7	US-11-054-515-1723	Sequence 1723, Ap	211	36	56.2	117	7	US-11-174-186-35	Sequence 35, Appl
139	41	64.1	251	7	US-11-054-515-1688	Sequence 1688, Ap	212	36	56.2	118	6	US-10-648-816-9	Sequence 9, Appl
140	41	64.1	251	7	US-11-054-515-1806	Sequence 1806, Ap	213	36	56.2	118	6	US-10-648-816-14	Sequence 14, Appl
141	41	64.1	253	7	US-11-054-515-1618	Sequence 1618, Ap	214	36	56.2	118	7	US-11-109-939-22	Sequence 22, Appl
142	41	64.1	253	7	US-11-054-515-1618	Sequence 1418, Ap	215	36	56.2	120	7	US-11-005-268-15	Sequence 15, Appl
143	41	64.1	256	7	US-11-054-515-1672	Sequence 1672, Ap	216	36	56.2	121	6	US-10-648-816-15	Sequence 15, Appl
144	40	62.5	114	7	US-11-055-163-18	Sequence 1640, Ap	217	36	56.2	129	6	US-10-648-816-15	Sequence 12, Appl
145	40	62.5	121	6	US-10-502-145-17	Sequence 17, Appl	218	36	56.2	241	7	US-11-054-515-1889	Sequence 1889, Ap
146	40	62.5	121	6	US-11-108-135-24	Sequence 24, Appl	219	36	56.2	245	7	US-11-054-515-1826	Sequence 1826, Ap
147	40	62.5	249	7	US-11-054-515-1112	Sequence 1312, Ap	220	36	56.2	247	7	US-11-054-515-1470	Sequence 1470, Ap
148	40	62.5	543	6	US-10-495-664-3	Sequence 3, Appl	221	36	56.2	251	7	US-11-054-515-1584	Sequence 1584, Ap
149	39.5	61.7	49	7	US-11-051-481-28	Sequence 28, Appl	222	36	56.2	251	7	US-11-054-515-1592	Sequence 1592, Ap
150	39.5	61.7	7	7	US-11-051-481-27	Sequence 27, Appl	223	36	56.2	251	7	US-11-054-515-1594	Sequence 1594, Ap
151	39.5	61.7	87	7	US-11-051-481-26	Sequence 26, Appl	224	36	56.2	251	7	US-11-054-515-1245	Sequence 3245, Ap
152	39.5	61.7	125	7	US-11-112-240-18	Sequence 18, Appl	225	36	56.2	257	7	US-11-056-825-10	Sequence 10, Appl
153	39.5	61.7	126	7	US-11-112-304A-18	Sequence 18, Appl	226	36	56.2	579	7	US-11-174-186-61	Sequence 41, Appl
154	39.5	61.7	245	7	US-11-054-515-2079	Sequence 2079, Ap	227	35.5	55.5	232	7	US-11-025-712-10	Sequence 12, Appl
155	39.5	61.7	248	7	US-11-054-515-1386	Sequence 1386, Ap	228	35.5	55.5	232	7	US-11-173-564-2	Sequence 2, Appl
156	39.5	61.7	248	7	US-11-054-515-1388	Sequence 1388, Ap	229	35.5	55.5	241	7	US-11-054-515-1303	Sequence 1303, Ap
157	39.5	61.7	251	7	US-11-054-515-1146	Sequence 1146, Ap	230	35.5	55.5	242	7	US-11-054-515-1985	Sequence 1985, Ap
158	39	60.9	114	7	US-11-065-943-47	Sequence 47, Appl	231	35.5	55.5	242	7	US-11-054-515-2099	Sequence 2099, Ap
159	39	60.9	257	7	US-11-054-515-1514	Sequence 1514, Ap	232	35.5	55.5	251	7	US-11-054-515-1769	Sequence 1769, Ap
160	39	60.9	447	7	US-11-102-621-130	Sequence 130, App	233	35.5	55.5	253	7	US-11-054-515-1526	Sequence 1526, Ap
161	39	60.9	447	7	US-11-102-621-131	Sequence 131, App	234	35.5	55.5	450	7	US-11-025-712-12	Sequence 12, Appl
162	39	60.9	447	7	US-11-102-621-132	Sequence 132, App	235	35	54.7	98	7	US-11-054-669-7	Sequence 7, Appl
163	39	60.9	447	7	US-11-102-621-133	Sequence 133, App	236	35	54.7	98	7	US-11-054-669-47	Sequence 47, Appl
164	39	60.9	447	7	US-11-102-621-134	Sequence 134, App	237	35	54.7	98	7	US-11-084-554-20	Sequence 20, Appl
165	38	59.4	120	7	US-11-097-812-68	Sequence 68, Appl	238	35	54.7	98	7	US-11-061-848-25	Sequence 25, Appl
166	38	59.4	121	6	US-10-932-334-81	Sequence 81, Appl	239	35	54.7	117	6	US-10-834-397-22	Sequence 22, Appl
167	38	59.4	246	7	US-11-054-515-1996	Sequence 1996, Ap	240	35	54.7	118	7	US-11-112-240A-10	Sequence 10, Appl
168	38	59.4	247	7	US-11-054-515-2092	Sequence 2092, Ap	241	35	54.7	118	7	US-11-112-304A-10	Sequence 10, Appl
169	38	59.4	254	7	US-11-054-515-1350	Sequence 1350, Ap	242	35	54.7	120	6	US-10-932-334-78	Sequence 78, Appl
170	37	57.8	98	7	US-11-084-554-58	Sequence 58, Appl	243	35	54.7	120	6	US-10-834-397-26	Sequence 26, Appl
171	37	57.8	120	6	US-10-932-334-74	Sequence 74, Appl	244	35	54.7	120	6	US-10-834-397-59	Sequence 59, Appl

245	35	54.7	120	7	US-11-173-071-2	Sequence 2, Appl1	318	33.5	52.3	140	7	US-11-193-512-78	Sequence 78, Appl1
246	35	54.7	123	7	US-11-112-240-14	Sequence 14, Appl1	319	33.5	52.3	140	7	US-11-193-512-83	Sequence 83, Appl1
247	35	54.7	123	7	US-11-112-304A-14	Sequence 14, Appl1	320	33.5	52.3	245	7	US-11-054-515-1896	Sequence 1896, Ap
248	35	54.7	128	7	US-11-173-071-12	Sequence 12, Appl1	321	33.5	52.3	247	7	US-11-054-515-1240	Sequence 1240, Ap
249	35	54.7	128	7	US-11-173-071-14	Sequence 14, Appl1	322	33.5	52.3	248	7	US-11-054-515-1675	Sequence 1675, Ap
250	35	54.7	142	7	US-11-158-505-36	Sequence 36, Appl1	323	33.5	52.3	250	7	US-11-054-515-932	Sequence 932, App
251	35	54.7	192	6	US-10-980-388-85	Sequence 85, Appl1	324	33.5	52.3	250	7	US-11-054-515-2093	Sequence 2093, Ap
252	35	54.7	192	6	US-10-980-388-85	Sequence 85, Appl1	325	33.5	52.3	250	7	US-11-054-515-2093	Sequence 2093, Ap
253	35	54.7	243	7	US-11-054-515-1947	Sequence 1451, Ap	326	33.5	52.3	251	7	US-11-054-515-1071	Sequence 1071, Ap
254	35	54.7	245	7	US-11-054-515-1451	Sequence 1902, Ap	327	33.5	52.3	251	7	US-11-054-515-1077	Sequence 1077, Ap
255	35	54.7	245	7	US-11-054-515-1902	Sequence 1919, Ap	328	33.5	52.3	251	7	US-11-054-515-1355	Sequence 1355, Ap
256	35	54.7	245	7	US-11-054-515-1919	Sequence 1919, Ap	329	33.5	52.3	251	7	US-11-054-515-1396	Sequence 1396, Ap
257	35	54.7	247	7	US-11-054-515-1729	Sequence 1729, Ap	330	33.5	52.3	251	7	US-11-054-515-1706	Sequence 1706, Ap
258	35	54.7	248	7	US-11-054-515-1178	Sequence 1178, Ap	331	33.5	52.3	251	7	US-11-054-515-1776	Sequence 1807, Ap
259	35	54.7	248	7	US-11-054-515-2094	Sequence 2094, Ap	332	33.5	52.3	251	7	US-11-054-515-1807	Sequence 1812, Ap
260	35	54.7	249	7	US-11-054-515-974	Sequence 974, App	333	33.5	52.3	251	7	US-11-054-515-2001	Sequence 2001, Ap
261	35	54.7	249	7	US-11-054-515-1280	Sequence 1290, Ap	334	33.5	52.3	251	7	US-11-054-515-1881	Sequence 1698, Ap
262	35	54.7	249	7	US-11-054-515-1289	Sequence 1299, Ap	335	33.5	52.3	252	7	US-11-054-515-1698	Sequence 1954, Ap
263	35	54.7	250	7	US-11-054-515-1851	Sequence 1851, Ap	336	33.5	52.3	252	7	US-11-054-515-1954	Sequence 1950, Ap
264	35	54.7	251	7	US-11-054-515-1336	Sequence 1336, Ap	337	33.5	52.3	253	7	US-11-054-515-1530	Sequence 1850, Ap
265	35	54.7	253	7	US-11-054-515-1003	Sequence 1003, Ap	338	33.5	52.3	253	7	US-11-054-515-1850	Sequence 1859, Ap
266	35	54.7	253	7	US-11-054-515-1007	Sequence 1007, Ap	339	33.5	52.3	253	7	US-11-054-515-1859	Sequence 20, Appl1
267	35	54.7	253	7	US-11-054-515-1936	Sequence 1936, Ap	340	33.5	52.3	253	7	US-11-106-820-20	Sequence 1846, Ap
268	35	54.7	253	7	US-11-054-515-1987	Sequence 1987, Ap	341	33.5	52.3	254	7	US-11-054-515-1846	Sequence 1849, Ap
269	35	54.7	254	7	US-11-054-515-873	Sequence 873, App	342	33.5	52.3	255	7	US-11-054-515-1849	Sequence 124, App
270	35	54.7	254	7	US-11-054-515-888	Sequence 888, App	343	33.5	52.3	442	7	US-11-102-621-124	Sequence 125, App
271	35	54.7	254	7	US-11-054-515-1087	Sequence 1087, Ap	344	33.5	52.3	442	7	US-11-102-621-125	Sequence 126, App
272	35	54.7	254	7	US-11-054-515-1088	Sequence 1088, Ap	345	33.5	52.3	442	7	US-11-102-621-126	Sequence 127, App
273	35	54.7	254	7	US-11-054-515-1893	Sequence 1893, Ap	346	33.5	52.3	442	7	US-11-102-621-127	Sequence 128, App
274	35	54.7	254	7	US-11-054-515-1961	Sequence 1961, Ap	347	33.5	52.3	446	7	US-11-102-621-128	Sequence 119, App
275	35	54.7	254	7	US-11-054-515-1983	Sequence 1983, Ap	348	33.5	52.3	446	7	US-11-102-621-119	Sequence 120, App
276	35	54.7	255	7	US-11-054-515-857	Sequence 857, App	349	33.5	52.3	446	7	US-11-102-621-120	Sequence 121, App
277	35	54.7	255	7	US-11-054-515-1156	Sequence 1156, Ap	350	33.5	52.3	446	7	US-11-102-621-121	Sequence 122, App
278	34.5	53.9	259	7	US-11-054-515-1567	Sequence 1567, Ap	351	33.5	52.3	446	7	US-11-102-621-122	Sequence 123, App
279	34.5	53.9	243	7	US-11-054-515-1959	Sequence 1959, Ap	352	33.5	52.3	451	7	US-11-120-338-22	Sequence 22, Appl1
280	34.5	53.9	245	7	US-11-054-515-1979	Sequence 1979, Ap	353	33.5	52.3	451	7	US-11-120-338-25	Sequence 25, Appl1
281	34	53.1	251	7	US-11-054-515-1059	Sequence 1059, Ap	354	33.5	52.3	452	7	US-11-120-338-14	Sequence 14, Appl1
282	34	53.1	98	7	US-11-054-669-11	Sequence 11, Appl1	355	33.5	52.3	452	7	US-11-120-338-15	Sequence 15, Appl1
283	34	53.1	115	6	US-10-932-334-80	Sequence 80, Appl1	356	33.5	52.3	452	7	US-11-120-338-17	Sequence 17, Appl1
284	34	53.1	126	7	US-11-089-872-3	Sequence 3, Appl1	357	33.5	52.3	452	7	US-11-107-028-32	Sequence 32, Appl1
285	34	53.1	148	7	US-11-054-515-1638	Sequence 1638, Ap	358	33.5	52.3	452	7	US-11-107-028-33	Sequence 33, Appl1
286	34	53.1	247	7	US-11-054-515-2103	Sequence 2103, Ap	359	33.5	52.3	452	7	US-11-107-028-32	Sequence 33, Appl1
287	34	53.1	248	7	US-11-054-515-1995	Sequence 1995, Ap	360	33.5	52.3	452	7	US-11-107-028-43	Sequence 43, Appl1
288	34	53.1	249	7	US-11-054-515-2091	Sequence 2091, Ap	361	33.5	52.3	452	7	US-11-107-028-45	Sequence 45, Appl1
289	34	53.1	254	7	US-11-054-515-1970	Sequence 1970, Ap	362	33.5	52.3	452	7	US-11-107-028-46	Sequence 46, Appl1
290	34	53.1	254	7	US-11-054-515-2082	Sequence 2082, Ap	363	33.5	52.3	452	7	US-11-107-028-47	Sequence 47, Appl1
291	34	53.1	259	6	US-10-512-184-31	Sequence 2087, Ap	364	33.5	52.3	452	7	US-11-106-820-26	Sequence 26, Appl1
292	34	53.1	259	6	US-10-512-184-31	Sequence 31, Appl1	365	33.5	52.3	452	7	US-11-106-820-28	Sequence 28, Appl1
293	34	53.1	329	6	US-10-512-184-33	Sequence 33, Appl1	366	33.5	52.3	452	7	US-11-106-820-30	Sequence 30, Appl1
294	34	53.1	329	6	US-10-512-184-68	Sequence 68, Appl1	367	33.5	52.3	452	7	US-11-106-820-33	Sequence 33, Appl1
295	34	53.1	329	6	US-10-512-184-70	Sequence 70, Appl1	368	33.5	52.3	471	7	US-11-106-820-25	Sequence 25, Appl1
296	34	53.1	658	6	US-10-873-528-17	Sequence 17, Appl1	369	33.5	52.3	471	7	US-11-106-820-27	Sequence 27, Appl1
297	34	53.1	677	6	US-10-873-528-155	Sequence 155, App	370	33.5	52.3	471	7	US-10-648-816-10	Sequence 10, Appl1
298	34	53.1	726	6	US-10-873-528-155	Sequence 155, App	371	33.5	52.3	471	7	US-10-648-816-12	Sequence 12, Appl1
299	33.5	52.3	98	7	US-11-054-669-2	Sequence 217, App	372	33.5	52.3	471	7	US-10-648-816-13	Sequence 13, Appl1
300	33.5	52.3	98	7	US-11-084-554-18	Sequence 18, Appl1	373	33.5	52.3	471	7	US-11-009-939-12	Sequence 6, Appl1
301	33.5	52.3	118	6	US-10-932-334-75	Sequence 75, Appl1	374	33.5	52.3	471	7	US-11-061-848-6	Sequence 6, Appl1
302	33.5	52.3	120	7	US-10-507-662-36	Sequence 36, Appl1	375	33.5	52.3	471	7	US-11-061-848-7	Sequence 7, Appl1
303	33.5	52.3	120	7	US-11-096-074-59	Sequence 59, Appl1	376	33.5	52.3	471	7	US-11-061-848-8	Sequence 8, Appl1
304	33.5	52.3	121	7	US-11-095-822-59	Sequence 59, Appl1	377	33.5	52.3	471	7	US-11-061-848-9	Sequence 9, Appl1
305	33.5	52.3	121	7	US-11-107-028-27	Sequence 27, Appl1	378	33.5	52.3	471	7	US-11-061-848-9	Sequence 16, Appl1
306	33.5	52.3	121	7	US-11-107-028-35	Sequence 35, Appl1	379	33.5	52.3	471	7	US-10-648-816-16	Sequence 16, Appl1
307	33.5	52.3	121	7	US-11-107-028-37	Sequence 37, Appl1	380	33.5	52.3	471	6	US-10-527-500-31	Sequence 31, Appl1
308	33.5	52.3	122	7	US-11-120-338-7	Sequence 37, Appl1	381	33.5	52.3	471	6	US-11-054-515-1932	Sequence 1933, Ap
309	33.5	52.3	122	7	US-11-120-338-8	Sequence 8, Appl1	382	33.5	52.3	471	6	US-11-054-515-2054	Sequence 2054, Ap
310	33.5	52.3	122	7	US-11-120-338-24	Sequence 24, Appl1	383	33.5	52.3	471	6	US-11-054-515-1909	Sequence 1916, Ap
311	33.5	52.3	122	7	US-11-107-028-39	Sequence 39, Appl1	384	33.5	52.3	243	7	US-11-054-515-1916	Sequence 2051
312	33.5	52.3	122	7	US-11-107-028-41	Sequence 41, Appl1	385	33.5	52.3	243	7	US-11-054-515-2051	Sequence 1, Appl1
313	33.5	52.3	122	7	US-11-106-820-7	Sequence 7, Appl1	386	33.5	52.3	249	7	US-11-054-515-2065	Sequence 2065, Ap
314	33.5	52.3	122	7	US-11-106-820-8	Sequence 8, Appl1	387	33.5	52.3	251	7	US-11-054-515-1459	Sequence 1459, Ap
315	33.5	52.3	140	7	US-11-193-512-27	Sequence 27, Appl1	388	33.5	52.3	258	7	US-11-054-515-1409	Sequence 1209, Ap
316	33.5	52.3	140	7	US-11-193-512-63	Sequence 63, Appl1	389	33.5	52.3	258	7	US-11-054-515-1841	Sequence 1841, Ap
317	33.5	52.3	140	7	US-11-193-512-74	Sequence 74, Appl1	390	33.5	52.3	645	6	US-10-793-626-2984	Sequence 2984, Ap

391	33	51.6	1179	7	US-11-097-125-1	Sequence 1, Appl1	464	32	50.0	3104	6	US-10-453-372-34	Sequence 34, Appl1
392	33	51.6	1196	6	US-10-995-561-921	Sequence 921, App	465	32	50.0	3104	6	US-10-453-372-62	Sequence 62, Appl1
393	33	51.6	1501	6	US-10-793-626-2850	Sequence 2850, App	466	32	50.0	3104	6	US-10-453-372-64	Sequence 64, Appl1
394	32.5	50.8	116	6	US-10-489-866-19	Sequence 19, Appl1	467	32	50.0	3130	6	US-10-453-372-42	Sequence 42, Appl1
395	32.5	50.8	116	6	US-11-097-812-31	Sequence 31, Appl1	468	32	50.0	3483	6	US-10-453-372-40	Sequence 40, Appl1
396	32.5	50.8	117	6	US-10-932-334-76	Sequence 76, Appl1	469	32	50.0	3546	6	US-10-453-372-60	Sequence 32, Appl1
397	32.5	50.8	120	7	US-11-097-812-153	Sequence 153, App	470	31.5	49.2	100	7	US-11-084-554-46	Sequence 46, Appl1
398	32.5	50.8	1249	7	US-11-054-515-1730	Sequence 1730, Ap	471	31.5	49.2	116	6	US-11-127-677-51	Sequence 51, Appl1
399	32.5	50.8	249	7	US-11-054-515-2033	Sequence 2033, Ap	472	31.5	49.2	117	6	US-10-771-257-53	Sequence 53, Appl1
400	32.5	50.8	251	7	US-11-054-515-992	Sequence 992, App	473	31.5	49.2	119	7	US-11-221-900-10	Sequence 10, Appl1
401	32.5	50.8	251	7	US-11-054-515-1068	Sequence 1068, App	474	31.5	49.2	119	7	US-11-221-900-12	Sequence 12, Appl1
402	32.5	50.8	251	7	US-11-054-515-1079	Sequence 1079, Ap	475	31.5	49.2	119	7	US-11-221-900-13	Sequence 13, Appl1
403	32.5	50.8	251	7	US-11-054-515-1238	Sequence 1238, Ap	476	31.5	49.2	119	7	US-11-221-900-14	Sequence 14, Appl1
404	32.5	50.8	251	7	US-11-054-515-1292	Sequence 1292, Ap	477	31.5	49.2	236	7	US-11-221-900-2	Sequence 2, Appl1
405	32.5	50.8	251	7	US-11-054-515-1342	Sequence 1342, Ap	478	31.5	49.2	239	7	US-11-054-515-1023	Sequence 2023, App
406	32.5	50.8	251	7	US-11-054-515-1389	Sequence 1389, Ap	479	31.5	49.2	247	7	US-11-054-515-999	Sequence 999, App
407	32.5	50.8	252	7	US-11-054-515-1534	Sequence 1534, Ap	480	31.5	49.2	247	7	US-11-054-515-1307	Sequence 1307, App
408	32.5	50.8	255	7	US-11-054-515-1407	Sequence 1407, Ap	481	31.5	49.2	248	7	US-11-054-515-877	Sequence 877, App
409	32.5	50.8	293	7	US-11-116-939-10	Sequence 10, Appl1	482	31.5	49.2	248	7	US-11-054-515-953	Sequence 953, App
410	32.5	50.8	412	7	US-11-116-939-12	Sequence 12, Appl1	483	31.5	49.2	248	7	US-11-054-515-965	Sequence 965, App
411	32.5	50.8	824	7	US-11-116-939-11	Sequence 11, Appl1	484	31.5	49.2	248	7	US-11-054-515-980	Sequence 980, App
412	32	50.0	40	6	US-10-467-657-9217	Sequence 9217, Ap	485	31.5	49.2	248	7	US-11-054-515-984	Sequence 984, App
413	32	50.0	100	7	US-11-054-669-19	Sequence 19, Appl1	486	31.5	49.2	248	7	US-11-054-515-987	Sequence 987, App
414	32	50.0	100	7	US-11-054-669-32	Sequence 32, Appl1	487	31.5	49.2	248	7	US-11-054-515-1181	Sequence 1181, Ap
415	32	50.0	100	7	US-11-084-554-29	Sequence 29, Appl1	488	31.5	49.2	248	7	US-11-054-515-1182	Sequence 1182, Ap
416	32	50.0	100	7	US-11-084-554-45	Sequence 45, Appl1	489	31.5	49.2	248	7	US-11-054-515-1293	Sequence 1293, Ap
417	32	50.0	118	6	US-10-648-816-11	Sequence 11, Appl1	490	31.5	49.2	248	7	US-11-054-515-1306	Sequence 1306, Ap
418	32	50.0	118	6	US-10-995-561-676	Sequence 676, App	491	31.5	49.2	248	7	US-11-054-515-1417	Sequence 1417, Ap
419	32	50.0	120	6	US-10-932-334-77	Sequence 77, Appl1	492	31.5	49.2	248	7	US-11-054-515-1588	Sequence 1588, Ap
420	32	50.0	120	6	US-10-932-334-79	Sequence 79, Appl1	493	31.5	49.2	248	7	US-11-054-515-1609	Sequence 1609, Ap
421	32	50.0	121	7	US-11-108-135-28	Sequence 28, Appl1	494	31.5	49.2	248	7	US-11-054-515-1622	Sequence 1622, Ap
422	32	50.0	190	7	US-11-170-653-31	Sequence 31, Appl1	495	31.5	49.2	248	7	US-11-054-515-1633	Sequence 1633, Ap
423	32	50.0	241	6	US-10-793-626-1894	Sequence 1894, Ap	496	31.5	49.2	248	7	US-11-054-515-1643	Sequence 1643, Ap
424	32	50.0	247	7	US-11-054-515-1382	Sequence 1382, Ap	497	31.5	49.2	248	7	US-11-054-515-1643	Sequence 1643, Ap
425	32	50.0	248	7	US-11-054-515-1008	Sequence 1008, Ap	498	31.5	49.2	248	7	US-11-054-515-1657	Sequence 1657, Ap
426	32	50.0	250	7	US-11-054-515-1191	Sequence 1191, Ap	499	31.5	49.2	248	7	US-11-054-515-1660	Sequence 1660, Ap
427	32	50.0	250	7	US-11-054-515-1325	Sequence 1325, Ap	500	31.5	49.2	248	7	US-11-054-515-1667	Sequence 1667, Ap
428	32	50.0	250	7	US-11-054-515-1471	Sequence 1471, Ap	501	31.5	49.2	248	7	US-11-054-515-1668	Sequence 1668, Ap
429	32	50.0	251	7	US-11-054-515-997	Sequence 997, App	502	31.5	49.2	248	7	US-11-054-515-1670	Sequence 1670, Ap
430	32	50.0	251	7	US-11-054-515-1146	Sequence 1346, Ap	503	31.5	49.2	248	7	US-11-054-515-1679	Sequence 1679, Ap
431	32	50.0	252	7	US-11-054-515-1821	Sequence 1821, Ap	504	31.5	49.2	248	7	US-11-054-515-1681	Sequence 1681, Ap
432	32	50.0	253	7	US-11-054-515-1533	Sequence 1353, Ap	505	31.5	49.2	248	7	US-11-054-515-1755	Sequence 1755, Ap
433	32	50.0	254	7	US-11-054-515-1447	Sequence 1447, Ap	506	31.5	49.2	248	7	US-11-054-515-1763	Sequence 1765, Ap
434	32	50.0	256	7	US-11-054-515-843	Sequence 843, App	507	31.5	49.2	248	7	US-11-054-515-1823	Sequence 1823, Ap
435	32	50.0	256	7	US-11-054-515-872	Sequence 872, App	508	31.5	49.2	248	7	US-11-054-515-1876	Sequence 1876, Ap
436	32	50.0	256	7	US-11-054-515-1791	Sequence 1791, Ap	509	31.5	49.2	248	7	US-11-106-820-16	Sequence 16, Appl1
437	32	50.0	257	7	US-11-054-515-958	Sequence 958, App	510	31.5	49.2	250	7	US-11-054-515-859	Sequence 859, App
438	32	50.0	372	6	US-10-467-657-590	Sequence 590, App	511	31.5	49.2	250	7	US-11-054-515-1341	Sequence 1341, Ap
439	32	50.0	468	7	US-11-086-289-22	Sequence 22, Appl1	512	31.5	49.2	250	7	US-11-054-515-1247	Sequence 3247, Ap
440	32	50.0	470	7	US-11-086-289-18	Sequence 18, Appl1	513	31.5	49.2	251	7	US-11-054-515-845	Sequence 845, App
441	32	50.0	472	7	US-11-086-289-2	Sequence 2, Appl1	514	31.5	49.2	251	7	US-11-054-515-852	Sequence 852, App
442	32	50.0	485	6	US-10-630-203-2	Sequence 2, Appl1	515	31.5	49.2	251	7	US-11-054-515-853	Sequence 853, App
443	32	50.0	485	6	US-10-630-203-4	Sequence 4, Appl1	516	31.5	49.2	251	7	US-11-054-515-875	Sequence 875, App
444	32	50.0	485	6	US-11-103-037-1	Sequence 1, Appl1	517	31.5	49.2	251	7	US-11-054-515-879	Sequence 879, App
445	32	50.0	485	7	US-11-103-037-2	Sequence 2, Appl1	518	31.5	49.2	251	7	US-11-054-515-884	Sequence 884, App
446	32	50.0	531	6	US-10-517-939-70	Sequence 70, Appl1	519	31.5	49.2	251	7	US-11-054-515-886	Sequence 886, App
447	32	50.0	713	32	US-10-453-372-48	Sequence 48, Appl1	520	31.5	49.2	251	7	US-11-054-515-887	Sequence 887, App
448	32	50.0	776	6	US-10-453-372-44	Sequence 44, Appl1	521	31.5	49.2	251	7	US-11-054-515-940	Sequence 940, App
449	32	50.0	776	6	US-10-453-372-46	Sequence 46, Appl1	522	31.5	49.2	251	7	US-11-054-515-944	Sequence 944, App
450	32	50.0	847	6	US-10-995-561-634	Sequence 634, App	523	31.5	49.2	251	7	US-11-054-515-961	Sequence 961, App
451	32	50.0	869	6	US-10-453-372-50	Sequence 50, Appl1	524	31.5	49.2	251	7	US-11-054-515-962	Sequence 962, App
452	32	50.0	1259	6	US-10-995-561-625	Sequence 625, App	525	31.5	49.2	251	7	US-11-054-515-968	Sequence 968, App
453	32	50.0	1286	6	US-10-995-561-628	Sequence 628, App	526	31.5	49.2	251	7	US-11-054-515-975	Sequence 975, App
454	32	50.0	1315	6	US-10-995-561-630	Sequence 630, App	527	31.5	49.2	251	7	US-11-054-515-978	Sequence 978, App
455	32	50.0	1315	6	US-10-995-561-631	Sequence 621, App	528	31.5	49.2	251	7	US-11-054-515-986	Sequence 986, App
456	32	50.0	1348	6	US-10-995-561-624	Sequence 624, App	529	31.5	49.2	251	7	US-11-054-515-1051	Sequence 1051, App
457	32	50.0	2296	6	US-10-995-561-633	Sequence 633, App	530	31.5	49.2	251	7	US-11-054-515-1052	Sequence 1052, App
458	32	50.0	2355	6	US-10-995-561-623	Sequence 623, App	531	31.5	49.2	251	7	US-11-054-515-1055	Sequence 1055, App
459	32	50.0	2355	6	US-10-995-561-627	Sequence 627, App	532	31.5	49.2	251	7	US-11-054-515-1057	Sequence 1057, App
460	32	50.0	2384	6	US-10-821-223-1545	Sequence 1545, Ap	533	31.5	49.2	251	7	US-11-054-515-1062	Sequence 1062, App
461	32	50.0	2386	6	US-10-995-561-626	Sequence 626, App	534	31.5	49.2	251	7	US-11-054-515-1064	Sequence 1064, Ap
462	32	50.0	2612	6	US-10-453-372-38	Sequence 38, Appl1	535	31.5	49.2	251	7	US-11-054-515-1072	Sequence 1072, Ap
463	32	50.0	2669	6	US-10-453-372-36	Sequence 36, Appl1	536	31.5	49.2	251	7	US-11-054-515-1073	Sequence 1073, Ap

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538	31.5	49.2	251	7	US-11-054-515-1076	Sequence 1076, Ap	611	31	48.4	255	7	US-11-054-515-1914	Sequence 1914, Ap
539	31.5	49.2	251	7	US-11-054-515-1078	Sequence 1078, Ap	612	31	48.4	355	7	US-11-108-528-48	Sequence 48, Ap
540	31.5	49.2	251	7	US-11-054-515-1082	Sequence 1082, Ap	613	31	48.4	403	6	US-10-873-528-32	Sequence 32, Ap
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542	31.5	49.2	251	7	US-11-054-515-1086	Sequence 1086, Ap	615	31	48.4	455	7	US-11-059-867-17	Sequence 17, Ap
543	31.5	49.2	251	7	US-11-054-515-1103	Sequence 1103, Ap	616	31	48.4	478	7	US-11-139-499-8	Sequence 8, Ap
544	31.5	49.2	251	7	US-11-054-515-1106	Sequence 1106, Ap	617	31	48.4	528	7	US-11-052-554A-117	Sequence 117, Ap
545	31.5	49.2	251	7	US-11-054-515-1107	Sequence 1107, Ap	618	31	48.4	539	6	US-10-131-826A-140	Sequence 140, Ap
546	31.5	49.2	251	7	US-11-054-515-1132	Sequence 1132, Ap	619	31	48.4	565	6	US-10-793-626-2608	Sequence 2608, Ap
547	31.5	49.2	251	7	US-11-054-515-1172	Sequence 1172, Ap	620	31	48.4	645	6	US-10-793-626-1770	Sequence 1770, Ap
548	31.5	49.2	251	7	US-11-054-515-1176	Sequence 1176, Ap	621	31	48.4	892	7	US-11-082-389-396	Sequence 396, Ap
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551	31.5	49.2	251	7	US-11-054-515-1338	Sequence 1338, Ap	624	31	48.4	3194	7	US-11-052-554A-90	Sequence 90, Ap
552	31.5	49.2	251	7	US-11-054-515-1343	Sequence 1343, Ap	625	31	48.4	3300	7	US-11-052-554A-133	Sequence 133, Ap
553	31.5	49.2	251	7	US-11-054-515-1345	Sequence 1345, Ap	626	30.5	47.7	98	7	US-11-054-669-3	Sequence 3, Ap
554	31.5	49.2	251	7	US-11-054-515-1408	Sequence 1408, Ap	627	30.5	47.7	98	7	US-11-054-669-6	Sequence 6, Ap
555	31.5	49.2	251	7	US-11-054-515-1437	Sequence 1437, Ap	628	30.5	47.7	98	7	US-11-084-554-19	Sequence 19, Ap
556	31.5	49.2	251	7	US-11-054-515-1478	Sequence 1478, Ap	629	30.5	47.7	99	7	US-11-084-554-23	Sequence 23, Ap
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558	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	631	30.5	47.7	118	6	US-10-507-662-11	Sequence 31, Ap
559	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	632	30.5	47.7	118	6	US-10-507-662-32	Sequence 32, Ap
560	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	633	30.5	47.7	118	6	US-10-507-662-32	Sequence 32, Ap
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563	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	636	30.5	47.7	248	6	US-10-512-184-32	Sequence 32, Ap
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567	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	640	30.5	47.7	251	7	US-11-054-515-1805	Sequence 1805, Ap
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572	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	645	30.5	47.7	446	7	US-11-102-621-137	Sequence 137, Ap
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583	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	656	30.5	47.7	135	7	US-11-012-353-81	Sequence 81, Ap
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592	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	665	30.5	47.7	265	6	US-10-793-626-1790	Sequence 1790, Ap
593	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	666	30.5	47.7	270	7	US-11-054-515-1932	Sequence 932, Ap
594	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	667	30.5	47.7	270	7	US-10-467-657-2768	Sequence 2768, Ap
595	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	668	30.5	47.7	287	6	US-10-510-386-16	Sequence 16, Ap
596	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	669	30.5	47.7	297	6	US-10-453-372-332	Sequence 332, Ap
597	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	670	30.5	47.7	334	6	US-10-467-657-318	Sequence 318, Ap
598	31.5	49.2	251	7	US-11-054-515-1479	Sequence 1479, Ap	671	30.5	47.7	349	7	US-11-129-143-70	Sequence 70, Ap
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683	30	46.9	575	US-11-131-212-24	Sequence 24, Appl	756	29.5	46.1	251	7	US-11-054-515-21	Sequence 21, Appl
684	30	46.9	594	7 US-11-012-762-4	Sequence 4, Appl1	757	29.5	46.1	251	7	US-11-054-515-22	Sequence 22, Appl
685	30	46.9	602	6 US-10-793-626-2362	Sequence 2362, Ap	758	29.5	46.1	251	7	US-11-054-515-23	Sequence 23, Appl
686	30	46.9	612	7 US-11-120-308-174	Sequence 174, Appl	759	29.5	46.1	251	7	US-11-054-515-24	Sequence 24, Appl
687	30	46.9	795	7 US-11-109-157A-14	Sequence 14, Appl	760	29.5	46.1	251	7	US-11-054-515-25	Sequence 25, Appl
688	30	46.9	841	6 US-10-453-372-334	Sequence 334, App	761	29.5	46.1	251	7	US-11-054-515-26	Sequence 26, Appl
689	30	46.9	846	6 US-10-517-939-90	Sequence 90, Appl	762	29.5	46.1	251	7	US-11-054-515-27	Sequence 27, Appl
690	30	46.9	1037	6 US-10-392-234A-36	Sequence 36, Appl	763	29.5	46.1	251	7	US-11-054-515-28	Sequence 28, Appl
691	30	46.9	1061	7 US-11-059-814-18	Sequence 18, Appl	764	29.5	46.1	251	7	US-11-054-515-29	Sequence 29, Appl
692	30	46.9	1072	7 US-11-109-157A-13	Sequence 13, Appl	765	29.5	46.1	251	7	US-11-054-515-30	Sequence 30, Appl
693	30	46.9	1198	6 US-10-453-372-880	Sequence 880, App	766	29.5	46.1	251	7	US-11-054-515-31	Sequence 31, Appl
694	30	46.9	1275	6 US-10-821-234-1598	Sequence 1598, Ap	767	29.5	46.1	251	7	US-11-054-515-32	Sequence 32, Appl
695	30	46.9	1398	6 US-10-055-877-46	Sequence 46, Appl	768	29.5	46.1	251	7	US-11-054-515-33	Sequence 33, Appl
696	30	46.9	1398	6 US-10-453-372-872	Sequence 872, App	769	29.5	46.1	251	7	US-11-054-515-34	Sequence 34, Appl
697	30	46.9	1403	6 US-10-055-877-52	Sequence 52, Appl	770	29.5	46.1	251	7	US-11-054-515-35	Sequence 35, Appl
698	30	46.9	1403	6 US-10-453-372-878	Sequence 878, App	771	29.5	46.1	251	7	US-11-054-515-36	Sequence 36, Appl
699	30	46.9	1404	6 US-10-055-877-44	Sequence 44, Appl	772	29.5	46.1	251	7	US-11-054-515-37	Sequence 37, Appl
700	30	46.9	1404	6 US-10-453-372-870	Sequence 870, App	773	29.5	46.1	251	7	US-11-054-515-38	Sequence 38, Appl
701	30	46.9	1418	6 US-10-453-372-864	Sequence 864, App	774	29.5	46.1	251	7	US-11-054-515-39	Sequence 39, Appl
702	30	46.9	1450	6 US-10-055-877-48	Sequence 48, Appl	775	29.5	46.1	251	7	US-11-054-515-40	Sequence 40, Appl
703	30	46.9	1450	6 US-10-453-372-874	Sequence 874, App	776	29.5	46.1	251	7	US-11-054-515-41	Sequence 41, Appl
704	30	46.9	1547	6 US-10-453-372-886	Sequence 886, App	777	29.5	46.1	251	7	US-11-054-515-42	Sequence 42, Appl
705	30	46.9	1577	6 US-10-055-877-54	Sequence 54, Appl	778	29.5	46.1	251	7	US-11-054-515-43	Sequence 43, Appl
706	30	46.9	1577	6 US-10-453-372-882	Sequence 882, App	779	29.5	46.1	251	7	US-11-054-515-44	Sequence 44, Appl
707	30	46.9	1577	6 US-10-453-372-884	Sequence 884, App	780	29.5	46.1	251	7	US-11-054-515-45	Sequence 45, Appl
708	30	46.9	1594	6 US-10-453-372-860	Sequence 860, App	781	29.5	46.1	251	7	US-11-054-515-46	Sequence 46, Appl
709	30	46.9	1620	6 US-10-453-372-868	Sequence 868, App	782	29.5	46.1	251	7	US-11-054-515-47	Sequence 47, Appl
710	30	46.9	1653	6 US-10-453-372-866	Sequence 866, App	783	29.5	46.1	251	7	US-11-054-515-55	Sequence 55, Appl
711	30	46.9	2644	6 US-10-770-726-45	Sequence 45, Appl	784	29.5	46.1	251	7	US-11-054-515-61	Sequence 61, Appl

829	29.5	46.1	251	US-11-054-515-124	Sequence 124, App	902	29.5	46.1	251	US-11-054-515-203	Sequence 202, App
830	29.5	46.1	251	US-11-054-515-125	Sequence 125, App	903	29.5	46.1	251	US-11-054-515-203	Sequence 202, App
831	29.5	46.1	251	US-11-054-515-126	Sequence 126, App	904	29.5	46.1	251	US-11-054-515-204	Sequence 204, App
832	29.5	46.1	251	US-11-054-515-127	Sequence 127, App	905	29.5	46.1	251	US-11-054-515-205	Sequence 205, App
833	29.5	46.1	251	US-11-054-515-128	Sequence 128, App	906	29.5	46.1	251	US-11-054-515-206	Sequence 206, App
834	29.5	46.1	251	US-11-054-515-129	Sequence 129, App	907	29.5	46.1	251	US-11-054-515-207	Sequence 207, App
835	29.5	46.1	251	US-11-054-515-130	Sequence 130, App	908	29.5	46.1	251	US-11-054-515-208	Sequence 208, App
836	29.5	46.1	251	US-11-054-515-131	Sequence 131, App	909	29.5	46.1	251	US-11-054-515-209	Sequence 209, App
837	29.5	46.1	251	US-11-054-515-132	Sequence 132, App	910	29.5	46.1	251	US-11-054-515-210	Sequence 210, App
838	29.5	46.1	251	US-11-054-515-133	Sequence 133, App	911	29.5	46.1	251	US-11-054-515-211	Sequence 211, App
839	29.5	46.1	251	US-11-054-515-134	Sequence 134, App	912	29.5	46.1	251	US-11-054-515-212	Sequence 212, App
840	29.5	46.1	251	US-11-054-515-135	Sequence 135, App	913	29.5	46.1	251	US-11-054-515-213	Sequence 213, App
841	29.5	46.1	251	US-11-054-515-137	Sequence 137, App	914	29.5	46.1	251	US-11-054-515-214	Sequence 214, App
842	29.5	46.1	251	US-11-054-515-138	Sequence 138, App	915	29.5	46.1	251	US-11-054-515-215	Sequence 215, App
843	29.5	46.1	251	US-11-054-515-139	Sequence 139, App	916	29.5	46.1	251	US-11-054-515-216	Sequence 216, App
844	29.5	46.1	251	US-11-054-515-141	Sequence 141, App	917	29.5	46.1	251	US-11-054-515-217	Sequence 217, App
845	29.5	46.1	251	US-11-054-515-142	Sequence 142, App	918	29.5	46.1	251	US-11-054-515-218	Sequence 218, App
846	29.5	46.1	251	US-11-054-515-143	Sequence 143, App	919	29.5	46.1	251	US-11-054-515-219	Sequence 219, App
847	29.5	46.1	251	US-11-054-515-144	Sequence 144, App	920	29.5	46.1	251	US-11-054-515-220	Sequence 220, App
848	29.5	46.1	251	US-11-054-515-145	Sequence 145, App	921	29.5	46.1	251	US-11-054-515-221	Sequence 221, App
849	29.5	46.1	251	US-11-054-515-146	Sequence 146, App	922	29.5	46.1	251	US-11-054-515-222	Sequence 222, App
850	29.5	46.1	251	US-11-054-515-147	Sequence 147, App	923	29.5	46.1	251	US-11-054-515-223	Sequence 223, App
851	29.5	46.1	251	US-11-054-515-148	Sequence 148, App	924	29.5	46.1	251	US-11-054-515-225	Sequence 225, App
852	29.5	46.1	251	US-11-054-515-149	Sequence 149, App	925	29.5	46.1	251	US-11-054-515-226	Sequence 226, App
853	29.5	46.1	251	US-11-054-515-150	Sequence 150, App	926	29.5	46.1	251	US-11-054-515-227	Sequence 227, App
854	29.5	46.1	251	US-11-054-515-152	Sequence 152, App	927	29.5	46.1	251	US-11-054-515-228	Sequence 228, App
855	29.5	46.1	251	US-11-054-515-153	Sequence 153, App	928	29.5	46.1	251	US-11-054-515-229	Sequence 229, App
856	29.5	46.1	251	US-11-054-515-154	Sequence 154, App	929	29.5	46.1	251	US-11-054-515-230	Sequence 230, App
857	29.5	46.1	251	US-11-054-515-155	Sequence 155, App	930	29.5	46.1	251	US-11-054-515-231	Sequence 231, App
858	29.5	46.1	251	US-11-054-515-156	Sequence 156, App	931	29.5	46.1	251	US-11-054-515-232	Sequence 232, App
859	29.5	46.1	251	US-11-054-515-157	Sequence 157, App	932	29.5	46.1	251	US-11-054-515-233	Sequence 233, App
860	29.5	46.1	251	US-11-054-515-158	Sequence 158, App	933	29.5	46.1	251	US-11-054-515-234	Sequence 234, App
861	29.5	46.1	251	US-11-054-515-160	Sequence 160, App	934	29.5	46.1	251	US-11-054-515-235	Sequence 235, App
862	29.5	46.1	251	US-11-054-515-161	Sequence 161, App	935	29.5	46.1	251	US-11-054-515-236	Sequence 236, App
863	29.5	46.1	251	US-11-054-515-162	Sequence 162, App	936	29.5	46.1	251	US-11-054-515-237	Sequence 237, App
864	29.5	46.1	251	US-11-054-515-163	Sequence 163, App	937	29.5	46.1	251	US-11-054-515-238	Sequence 238, App
865	29.5	46.1	251	US-11-054-515-165	Sequence 165, App	938	29.5	46.1	251	US-11-054-515-239	Sequence 239, App
866	29.5	46.1	251	US-11-054-515-166	Sequence 166, App	939	29.5	46.1	251	US-11-054-515-240	Sequence 240, App
867	29.5	46.1	251	US-11-054-515-167	Sequence 167, App	940	29.5	46.1	251	US-11-054-515-241	Sequence 241, App
868	29.5	46.1	251	US-11-054-515-168	Sequence 168, App	941	29.5	46.1	251	US-11-054-515-242	Sequence 242, App
869	29.5	46.1	251	US-11-054-515-169	Sequence 169, App	942	29.5	46.1	251	US-11-054-515-243	Sequence 243, App
870	29.5	46.1	251	US-11-054-515-170	Sequence 170, App	943	29.5	46.1	251	US-11-054-515-244	Sequence 244, App
871	29.5	46.1	251	US-11-054-515-171	Sequence 171, App	944	29.5	46.1	251	US-11-054-515-245	Sequence 245, App
872	29.5	46.1	251	US-11-054-515-172	Sequence 172, App	945	29.5	46.1	251	US-11-054-515-246	Sequence 246, App
873	29.5	46.1	251	US-11-054-515-173	Sequence 173, App	946	29.5	46.1	251	US-11-054-515-247	Sequence 247, App
874	29.5	46.1	251	US-11-054-515-174	Sequence 174, App	947	29.5	46.1	251	US-11-054-515-248	Sequence 248, App
875	29.5	46.1	251	US-11-054-515-175	Sequence 175, App	948	29.5	46.1	251	US-11-054-515-249	Sequence 249, App
876	29.5	46.1	251	US-11-054-515-176	Sequence 176, App	949	29.5	46.1	251	US-11-054-515-250	Sequence 250, App
877	29.5	46.1	251	US-11-054-515-177	Sequence 177, App	950	29.5	46.1	251	US-11-054-515-251	Sequence 251, App
878	29.5	46.1	251	US-11-054-515-178	Sequence 178, App	951	29.5	46.1	251	US-11-054-515-252	Sequence 252, App
879	29.5	46.1	251	US-11-054-515-179	Sequence 179, App	952	29.5	46.1	251	US-11-054-515-253	Sequence 253, App
880	29.5	46.1	251	US-11-054-515-180	Sequence 180, App	953	29.5	46.1	251	US-11-054-515-254	Sequence 254, App
881	29.5	46.1	251	US-11-054-515-181	Sequence 181, App	954	29.5	46.1	251	US-11-054-515-255	Sequence 255, App
882	29.5	46.1	251	US-11-054-515-182	Sequence 182, App	955	29.5	46.1	251	US-11-054-515-256	Sequence 256, App
883	29.5	46.1	251	US-11-054-515-183	Sequence 183, App	956	29.5	46.1	251	US-11-054-515-257	Sequence 257, App
884	29.5	46.1	251	US-11-054-515-184	Sequence 184, App	957	29.5	46.1	251	US-11-054-515-258	Sequence 258, App
885	29.5	46.1	251	US-11-054-515-185	Sequence 185, App	958	29.5	46.1	251	US-11-054-515-259	Sequence 259, App
886	29.5	46.1	251	US-11-054-515-186	Sequence 186, App	959	29.5	46.1	251	US-11-054-515-260	Sequence 260, App
887	29.5	46.1	251	US-11-054-515-187	Sequence 187, App	960	29.5	46.1	251	US-11-054-515-262	Sequence 262, App
888	29.5	46.1	251	US-11-054-515-188	Sequence 188, App	961	29.5	46.1	251	US-11-054-515-263	Sequence 263, App
889	29.5	46.1	251	US-11-054-515-189	Sequence 189, App	962	29.5	46.1	251	US-11-054-515-264	Sequence 264, App
890	29.5	46.1	251	US-11-054-515-190	Sequence 190, App	963	29.5	46.1	251	US-11-054-515-265	Sequence 265, App
891	29.5	46.1	251	US-11-054-515-191	Sequence 191, App	964	29.5	46.1	251	US-11-054-515-266	Sequence 266, App
892	29.5	46.1	251	US-11-054-515-192	Sequence 192, App	965	29.5	46.1	251	US-11-054-515-267	Sequence 267, App
893	29.5	46.1	251	US-11-054-515-193	Sequence 193, App	966	29.5	46.1	251	US-11-054-515-268	Sequence 268, App
894	29.5	46.1	251	US-11-054-515-194	Sequence 194, App	967	29.5	46.1	251	US-11-054-515-269	Sequence 269, App
895	29.5	46.1	251	US-11-054-515-195	Sequence 195, App	968	29.5	46.1	251	US-11-054-515-270	Sequence 270, App
896	29.5	46.1	251	US-11-054-515-196	Sequence 196, App	969	29.5	46.1	251	US-11-054-515-271	Sequence 271, App
897	29.5	46.1	251	US-11-054-515-197	Sequence 197, App	970	29.5	46.1	251	US-11-054-515-272	Sequence 272, App
898	29.5	46.1	251	US-11-054-515-198	Sequence 198, App	971	29.5	46.1	251	US-11-054-515-273	Sequence 273, App
899	29.5	46.1	251	US-11-054-515-199	Sequence 199, App	972	29.5	46.1	251	US-11-054-515-274	Sequence 274, App
900	29.5	46.1	251	US-11-054-515-200	Sequence 200, App	973	29.5	46.1	251	US-11-054-515-275	Sequence 275, App
901	29.5	46.1	251	US-11-054-515-201	Sequence 201, App	974	29.5	46.1	251	US-11-054-515-276	Sequence 276, App

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996 29.5 46.1 251 7 US-11-054-515-300 Sequence 300, App
997 29.5 46.1 251 7 US-11-054-515-301 Sequence 301, App
998 29.5 46.1 251 7 US-11-054-515-302 Sequence 302, App
999 29.5 46.1 251 7 US-11-054-515-303 Sequence 303, App
1000 29.5 46.1 251 7 US-11-054-515-304 Sequence 304, App

ALIGNMENTS

RESULT 1
US-10-665-658-10
; Sequence 10, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-665-658-10

Query Match 100.0%; Score 64; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1,4e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GYSFTGHMNN 10
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Db 1 GYSFTGHMNN 10

RESULT 2

US-10-665-658-25
; Sequence 25, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-665-658-25
Query Match 100.0%; Score 64; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1,4e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GYSFTGHMNN 10
|||||
Db 1 GYSFTGHMNN 10

RESULT 3
US-10-665-658-4
Sequence 4, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-665-658-4
Query Match 100.0%; Score 64; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSFTGHMWN 10
Db 26 GYSFTGHMWN 35
RESULT 4
US-10-665-658-5
Sequence 5, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-665-658-5
Query Match 100.0%; Score 64; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYSFTGHMWN 10
Db 26 GYSFTGHMWN 35
RESULT 5
US-10-665-658-24
Sequence 24, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899

FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-665-658-24

Query Match 100.0%; Score 64; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||
Db 26 GYSFTGHMWN 35

RESULT 6
US-11-107-028-50
Sequence 50, Application US/11107028
Publication No. US20050276803A1
GENERAL INFORMATION:
APPLICANT: CHAN, ANDREW C.
APPLICANT: MARG, QIAN
APPLICANT: MARTIN, FLAVIUS
TITLE OF INVENTION: Method for Augmenting B Cell Depletion
FILE REFERENCE: P2112R1
CURRENT APPLICATION NUMBER: US/11/107,028
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/563,263
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 50
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-107-028-50

Query Match 100.0%; Score 64; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||
Db 26 GYSFTGHMWN 35

RESULT 7
US-11-107-028-52
Sequence 52, Application US/11107028
Publication No. US20050276803A1
GENERAL INFORMATION:
APPLICANT: CHAN, ANDREW C.
APPLICANT: GONG, QIAN
APPLICANT: MARTIN, FLAVIUS
TITLE OF INVENTION: Method for Augmenting B Cell Depletion
FILE REFERENCE: P2112R1
CURRENT APPLICATION NUMBER: US/11/107,028
CURRENT FILING DATE: 2005-04-15

PRIOR APPLICATION NUMBER: US 60/563,263
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 52
LENGTH: 121
TYPE: PRT
ORGANISM: Mus musculus
US-11-107-028-52

Query Match 100.0%; Score 64; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||
Db 26 GYSFTGHMWN 35

RESULT 8
US-10-665-658-27
Sequence 27, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
PRESTA, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-665-658-27

Query Match 95.3%; Score 61; DB 6; Length 10;
Best Local Similarity 90.0%; Pred. No. 4.5e-05;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
|||

Db 1 GYAFTGHMWN 10

RESULT 9

US-10-665-658-28

Sequence 28, Application US/10665658

Publication No. US20050276801A1

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

Presta, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESSES:

ADDRESS: Genentech, Inc.

STREET: 1 DNA way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658

FILING DATE: 19-Sep-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971

FILING DATE: 27-NOV-1996

APPLICATION NUMBER: 08/974899

FILING DATE: 20-NOV-1997

APPLICATION NUMBER: 09/420745

FILING DATE: 20-OCT-1999

APPLICATION NUMBER: 09/975798

FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:

NAME: Tan, Lee K.

REGISTRATION NUMBER: 39,447

REFERENCE/DOCKET NUMBER: P1014R1C1D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-4462

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: Amino Acid

TOPOLOGY: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-10-665-658-28

Query Match 92.2%; Score 59; DB 6; Length 10;

Best Local Similarity 90.0%; Pred. No. 9.9e-05;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMWN 10

Db 1 GYSFAGHMWN 10

RESULT 10

US-10-665-658-29

Sequence 29, Application US/10665658

Publication No. US20050276801A1

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

Presta, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESSES:

ADDRESS: Genentech, Inc.

STREET: 1 DNA way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658

FILING DATE: 19-Sep-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971

FILING DATE: 27-NOV-1996

APPLICATION NUMBER: 08/974899

FILING DATE: 20-NOV-1997

APPLICATION NUMBER: 09/420745

FILING DATE: 20-OCT-1999

APPLICATION NUMBER: 09/975798

FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:

NAME: Tan, Lee K.

REGISTRATION NUMBER: 39,447

REFERENCE/DOCKET NUMBER: P1014R1C1D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-4462

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: Amino Acid

TOPOLOGY: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-10-665-658-29

Query Match 90.6%; Score 58; DB 6; Length 10;

Best Local Similarity 90.0%; Pred. No. 0.00015;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMWN 10

Db 1 GYSFTAHMWN 10

RESULT 11

US-10-665-658-30

Sequence 30, Application US/10665658

Publication No. US20050276801A1

GENERAL INFORMATION:

APPLICANT: Jardieu, Paula M.

Presta, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESSES:

ADDRESS: Genentech, Inc.

STREET: 1 DNA way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658

FILING DATE: 19-Sep-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971

FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-665-658-30

Query Match 84.4%; Score 54; DB 6; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0007;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
Db 1 GYSFTGHMWN 10

RESULT 12
US-10-507-662-25
Sequence 25, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 25
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-10-507-662-25

Query Match 81.2%; Score 52; DB 6; Length 121;
Best Local Similarity 80.0%; Pred. No. 0.016;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
Db 26 GYSFTSYMWN 35

RESULT 13
US-10-507-662-26
Sequence 26, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662

CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 26
LENGTH: 121
TYPE: PRT
ORGANISM: Homo sapiens
US-10-507-662-26

Query Match 81.2%; Score 52; DB 6; Length 121;
Best Local Similarity 80.0%; Pred. No. 0.016;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMWN 10
Db 26 GYSFTSYMWN 35

RESULT 14
US-10-665-658-31
Sequence 31, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:

APPLICANT: Jardiou, Paula M.
PRESTA, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-SEP-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:

NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-665-658-31

Query Match 78.1%; Score 50; DB 6; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0033;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||:|:|:|

DB 1 GYSFTGHMNN 10

RESULT 15
US-10-880-238-63

; Sequence 63, Application US/10880238
; Publication No. US20050287538A1

; GENERAL INFORMATION:

; APPLICANT: Cheung, Wing-Tai

; APPLICANT: Cheung, Man

; TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE

; TITLE OF INVENTION: IMMUNOGLOBULIN GENES RETRIEVAL AND ANTIBODY ENGINEERING

; FILE REFERENCE: 17329-003001

; CURRENT APPLICATION NUMBER: US/10/880,238

; PRIOR FILING DATE: 2004-06-29

; NUMBER OF SEQ ID NOS: 214

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 63

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetically generated peptide

US-10-880-238-63

Query Match 75.0%; Score 48; DB 6; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.0073;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||:|:|:|

DB 1 GYSFTGYFMN 10

RESULT 16
US-10-507-662-22

; Sequence 22, Application US/10507662
; Publication No. US20050255102A1

; GENERAL INFORMATION:

; APPLICANT: BIOGEN, INC.

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES

; FILE REFERENCE: A136PCT

; CURRENT APPLICATION NUMBER: US/10/507,662

; PRIOR FILING DATE: 2004-09-13

; PRIOR APPLICATION NUMBER: 60/364,991

; PRIOR FILING DATE: 2002-03-13

; PRIOR APPLICATION NUMBER: 60/426,286

; PRIOR FILING DATE: 2002-11-13

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 22

; LENGTH: 119

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-507-662-22

Query Match 75.0%; Score 48; DB 6; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.075;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||:|:|:|

DB 26 GYSFTGYFMN 35

RESULT 17

US-11-051-481-46

; Sequence 46, Application US/11051481

; Publication No. US20060003387A1

; GENERAL INFORMATION:

; APPLICANT: PEBBLE, BEAU R.

; APPLICANT: BELCHER, ANGELA M.

; APPLICANT: WITTRUP, KARL DANE

; APPLICANT: KRAULAND, ERIC

; TITLE OF INVENTION: CELL DISPLAY LIBRARIES

; FILE REFERENCE: 027053-0150

; CURRENT APPLICATION NUMBER: US/11/051,481

; PRIOR FILING DATE: 2005-02-07

; PRIOR APPLICATION NUMBER: 60/541,757

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 46

; LENGTH: 49

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-11-051-481-46

Query Match 73.4%; Score 47; DB 7; Length 49;
Best Local Similarity 70.0%; Pred. No. 0.048;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||:|:|:|

DB 26 GYFTGHYMH 35

RESULT 18
US-11-051-481-45

; Sequence 45, Application US/11051481
; Publication No. US20060003387A1

; GENERAL INFORMATION:

; APPLICANT: PEBBLE, BEAU R.

; APPLICANT: BELCHER, ANGELA M.

; APPLICANT: WITTRUP, KARL DANE

; APPLICANT: KRAULAND, ERIC

; TITLE OF INVENTION: CELL DISPLAY LIBRARIES

; FILE REFERENCE: 027053-0150

; CURRENT APPLICATION NUMBER: US/11/051,481

; PRIOR FILING DATE: 2005-02-07

; PRIOR APPLICATION NUMBER: 60/541,757

; PRIOR FILING DATE: 2004-02-05

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 45

; LENGTH: 66

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-11-051-481-45

Query Match 73.4%; Score 47; DB 7; Length 66;
Best Local Similarity 70.0%; Pred. No. 0.064;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
|||:|:|:|

DB 26 GYFTGHYMH 35

RESULT 19

US-11-051-481-44

; Sequence 44, Application US/11051481

; Publication No. US20060003387A1

; GENERAL INFORMATION:

; APPLICANT: PEBBLE, BEAU R.

APPLICANT: BELCHER, ANGELA M.
APPLICANT: WITTRUP, KARL DANIE
TITLE OF INVENTION: CELL DISPLAY LIBRARIES
FILE REFERENCE: 027053-0150
CURRENT APPLICATION NUMBER: US/11/051,481
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: 60/541,757
PRIOR FILING DATE: 2004-02-05
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 44
LENGTH: 86
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-051-481-44

Query Match 73.4%; Score 47; DB 7; Length 86;
Best Local Similarity 70.0%; Pred. No. 0.082;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
||:||||:|
Db 26 GYFTGHMNN 35

RESULT 20
US-10-507-662-29
Sequence 29, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 119
TYPE: PRT
ORGANISM: Homo sapiens
US-10-507-662-29

Query Match 73.4%; Score 47; DB 6; Length 119;
Best Local Similarity 70.0%; Pred. No. 0.11;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
|||:|:|
Db 26 GYSFTGHMNN 35

RESULT 21
US-11-054-515-1161
Sequence 1161, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunologically Bind BlyS
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1161
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1161

Query Match 73.4%; Score 47; DB 7; Length 250;
Best Local Similarity 70.0%; Pred. No. 0.22;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYSFTGHMNN 10
||:||||:|
Db 26 GYFTGHMNN 35

RESULT 22
US-10-665-658-26
Sequence 26, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-665-658-26

Query Match      71.9%; Score 46; DB 6; Length 10;
Best Local Similarity 70.0%; Pred. No. 0.016;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GYSFTGHMWN 10
      ||:|||||
Db      1 GYAFAGAMWN 10

RESULT 23
US-11-097-812-27
; Sequence 27, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Kretz-Rommel, Katherine S.
; APPLICANT: Bowdish, Naveen
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 27
; LENGTH: 108
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59)..(59)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)..(62)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (66)..(66)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (99)..(99)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
```

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FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (103)..(103)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (106)..(106)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (108)..(108)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-097-812-27

Query Match      71.9%; Score 46; DB 7; Length 108;
Best Local Similarity 60.0%; Pred. No. 0.15;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYSFTGHMWN 10
      ||:|||||
Db      26 GYTFGYWIMH 35

RESULT 24
US-11-105-268-1
; Sequence 1, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
; APPLICANT: Allan, Christian
; TITLE OF INVENTION: ANTI-TL-9 ANTIBODY FORMULATIONS AND USES THEREOF
; FILE REFERENCE: 10271-126-999
; CURRENT APPLICATION NUMBER: US/11/105,268
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-1

Query Match      70.3%; Score 45; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 0.024;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYSFTGHMWN 9
      ||:|||||
Db      1 GYTFGYWIMH 9

RESULT 25
US-11-105-268-7
; Sequence 7, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
; APPLICANT: Allan, Christian
; TITLE OF INVENTION: ANTI-TL-9 ANTIBODY FORMULATIONS AND USES THEREOF
; FILE REFERENCE: 10271-126-999
; CURRENT APPLICATION NUMBER: US/11/105,268
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-7

Query Match      70.3%; Score 45; DB 7; Length 118;
```

Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTGHMM 9
||:||||:
Db 25 GYFTFGYWI 33

RESULT 26

US-11-105-268-17
; Sequence 17, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
; APPLICANT: Allan, Christian
; TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
; FILE REFERENCE: 10271-126-999
; CURRENT FILING DATE: 2005-04-12
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-17

Query Match 70.3%; Score 45; DB 7; Length 120;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTGHMM 9
||:||||:
Db 26 GYFTFGYWI 34

RESULT 27

US-11-105-268-9
; Sequence 9, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
; APPLICANT: Allan, Christian
; TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
; FILE REFERENCE: 10271-126-999
; CURRENT FILING DATE: 2005-04-12
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-105-268-9

Query Match 70.3%; Score 45; DB 7; Length 124;
Best Local Similarity 66.7%; Pred. No. 0.25;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GYSFTGHMM 9
||:||||:
Db 26 GYFTFGYWI 34

RESULT 28

US-11-069-834-2
; Sequence 2, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.

; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002_01
; CURRENT FILING DATE: 2005-03-01
; PRIOR FILING DATE: 2004-07-16
; PRIOR FILING DATE: 2004-07-16
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-069-834-2

Query Match 70.3%; Score 45; DB 7; Length 133;
Best Local Similarity 60.0%; Pred. No. 0.27;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYSFTGHMM 10
||:||||:
Db 26 GYAPSTYMN 35

RESULT 29

US-11-054-515-1957
; Sequence 1957, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523P3
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2002-11-14
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 2001-11-16
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1957
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1957

Query Match 70.3%; Score 45; DB 7; Length 249;
Best Local Similarity 66.7%; Pred. No. 0.49;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GYSFTGHMM 9
||:||||:
Db 26 GYNFKGHMI 34

```
RESULT 30
US-10-932-334-53
; Sequence 53, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-932-334-53

Query Match
Best Local Similarity 68.8%; Score 44; DB 6; Length 10;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
Db 1 GYFTFSYMMH 10

RESULT 31
US-10-932-334-57
; Sequence 57, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-932-334-57

Query Match
Best Local Similarity 68.8%; Score 44; DB 6; Length 98;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
Db 26 GYFTFSYMMH 35

RESULT 32
US-11-097-812-17
; Sequence 17, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
```

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; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-17

Query Match
Best Local Similarity 68.8%; Score 44; DB 7; Length 111;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
Db 26 GYFTFSYMMH 35

RESULT 33
US-11-097-812-20
; Sequence 20, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 111
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-20

Query Match
Best Local Similarity 68.8%; Score 44; DB 7; Length 111;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
Db 26 GYFTFSYMMH 35

RESULT 34
US-11-097-812-21
; Sequence 21, Application US/11097812
; Publication No. US20050281828A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Bowdish, Katherine S.
/ APPLICANT: Kretz-Rommel, Anke
/ APPLICANT: Dakapagari, Naveen
/ TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
/ FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
/ CURRENT APPLICATION NUMBER: US/11/097,812
/ PRIOR APPLICATION NUMBER: US 11/016,647
/ PRIOR FILING DATE: 2004-12-17
/ PRIOR APPLICATION NUMBER: PCT/US04/06570
/ PRIOR FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: US 60/548,385
/ PRIOR FILING DATE: 2004-02-28
/ PRIOR APPLICATION NUMBER: US 60/529,500
/ PRIOR FILING DATE: 2003-12-15
/ PRIOR APPLICATION NUMBER: US 60/451,816
/ PRIOR FILING DATE: 2003-03-04
/ NUMBER OF SEQ ID NOS: 207
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 21
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: mouse
US-11-097-812-21
```

```
Query Match      68.8%; Score 44; DB 7; Length 111;
Best Local Similarity 60.0%; Pred. No. 0.34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GYSFTGHMNN 10
      ||:||||:
Db      26 GYTFTSYMMH 35
```

```
RESULT 35
US-11-097-812-25
/ Sequence 25, Application US/11097812
/ Publication No. US20050281828A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdish, Katherine S.
/ APPLICANT: Kretz-Rommel, Anke
/ APPLICANT: Dakapagari, Naveen
/ TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
/ FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
/ CURRENT APPLICATION NUMBER: US/11/097,812
/ PRIOR APPLICATION NUMBER: US 11/016,647
/ PRIOR FILING DATE: 2004-12-17
/ PRIOR APPLICATION NUMBER: PCT/US04/06570
/ PRIOR FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: US 60/548,385
/ PRIOR FILING DATE: 2004-02-28
/ PRIOR APPLICATION NUMBER: US 60/529,500
/ PRIOR FILING DATE: 2003-12-15
/ PRIOR APPLICATION NUMBER: US 60/451,816
/ PRIOR FILING DATE: 2003-03-04
/ NUMBER OF SEQ ID NOS: 207
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 25
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: mouse
US-11-097-812-25
```

```
Query Match      68.8%; Score 44; DB 7; Length 111;
Best Local Similarity 60.0%; Pred. No. 0.34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GYSFTGHMNN 10
      ||:||||:
Db      26 GYTFTSYMMH 35
```

```
Db      26 GYTFTSYMMH 35

RESULT 36
US-11-097-812-30
/ Sequence 30, Application US/11097812
/ Publication No. US20050281828A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdish, Katherine S.
/ APPLICANT: Kretz-Rommel, Anke
/ APPLICANT: Dakapagari, Naveen
/ TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
/ FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
/ CURRENT APPLICATION NUMBER: US/11/097,812
/ PRIOR APPLICATION NUMBER: US 11/016,647
/ PRIOR FILING DATE: 2004-12-17
/ PRIOR APPLICATION NUMBER: PCT/US04/06570
/ PRIOR FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: US 60/548,385
/ PRIOR FILING DATE: 2004-02-28
/ PRIOR APPLICATION NUMBER: US 60/529,500
/ PRIOR FILING DATE: 2003-12-15
/ PRIOR APPLICATION NUMBER: US 60/451,816
/ PRIOR FILING DATE: 2003-03-04
/ NUMBER OF SEQ ID NOS: 207
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 30
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: mouse
US-11-097-812-30
```

```
Query Match      68.8%; Score 44; DB 7; Length 111;
Best Local Similarity 60.0%; Pred. No. 0.34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GYSFTGHMNN 10
      ||:||||:
Db      26 GYTFTSYMMH 35
```

```
RESULT 37
US-11-097-812-32
/ Sequence 32, Application US/11097812
/ Publication No. US20050281828A1
/ GENERAL INFORMATION:
/ APPLICANT: Bowdish, Katherine S.
/ APPLICANT: Kretz-Rommel, Anke
/ APPLICANT: Dakapagari, Naveen
/ TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
/ FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
/ CURRENT APPLICATION NUMBER: US/11/097,812
/ PRIOR APPLICATION NUMBER: US 11/016,647
/ PRIOR FILING DATE: 2004-12-17
/ PRIOR APPLICATION NUMBER: PCT/US04/06570
/ PRIOR FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: US 60/548,385
/ PRIOR FILING DATE: 2004-02-28
/ PRIOR APPLICATION NUMBER: US 60/529,500
/ PRIOR FILING DATE: 2003-12-15
/ PRIOR APPLICATION NUMBER: US 60/451,816
/ PRIOR FILING DATE: 2003-03-04
/ NUMBER OF SEQ ID NOS: 207
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 32
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: mouse
US-11-097-812-32
```

Query Match 68.8%; Score 44; DB 7; Length 111;
Best Local Similarity 60.0%; Pred. No. 0.34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:
26 GYFTSYMMH 35

Db

US-11-097-812-34

Sequence 34, Application US/11097812
Publication No. US20050281828A1
GENERAL INFORMATION:
APPLICANT: Howdlish, Katherine S.
APPLICANT: Kretz-Rommel, Naveen
TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 11/016,647
PRIOR FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PCT/US04/06570
PRIOR FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: US 60/548,385
PRIOR FILING DATE: 2004-02-28
PRIOR APPLICATION NUMBER: US 60/529,500
PRIOR FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 60/451,816
PRIOR FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34
LENGTH: 111
TYPE: PRT
ORGANISM: mouse
US-11-097-812-34

Query Match 68.8%; Score 44; DB 7; Length 111;
Best Local Similarity 60.0%; Pred. No. 0.34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:
26 GYFTSYMMH 35

Db

US-11-097-812-36

Sequence 36, Application US/11097812
Publication No. US20050281828A1
GENERAL INFORMATION:
APPLICANT: Howdlish, Katherine S.
APPLICANT: Kretz-Rommel, Naveen
TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
CURRENT APPLICATION NUMBER: US/11/097,812
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 11/016,647
PRIOR FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PCT/US04/06570
PRIOR FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: US 60/548,385
PRIOR FILING DATE: 2004-02-28
PRIOR APPLICATION NUMBER: US 60/529,500
PRIOR FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 60/451,816
PRIOR FILING DATE: 2003-03-04

NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn version 3.2
SEQ ID NO 36
LENGTH: 111
TYPE: PRT
ORGANISM: mouse
US-11-097-812-36

Query Match 68.8%; Score 44; DB 7; Length 111;
Best Local Similarity 60.0%; Pred. No. 0.34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:
26 GYFTSYMMH 35

Db

US-11-097-812-205

Sequence 205, Application US/11097812
Publication No. US20050281828A1
GENERAL INFORMATION:
APPLICANT: Howdlish, Katherine S.
APPLICANT: Kretz-Rommel, Naveen
TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
CURRENT APPLICATION NUMBER: US/11/097,812
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 11/016,647
PRIOR FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PCT/US04/06570
PRIOR FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: US 60/548,385
PRIOR FILING DATE: 2004-02-28
PRIOR APPLICATION NUMBER: US 60/529,500
PRIOR FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 60/451,816
PRIOR FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn version 3.2
SEQ ID NO 205
LENGTH: 111
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: majority antibody sequence
US-11-097-812-205

Query Match 68.8%; Score 44; DB 7; Length 111;
Best Local Similarity 60.0%; Pred. No. 0.34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYSFTGHMNN 10
||:|:|:
26 GYFTSYMMH 35

Db

US-11-054-669-119

Sequence 119, Application US/11054669
Publication No. US20050261480A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12

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; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 119
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-054-669-119

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Query Match      68.8%; Score 44; DB 7; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.35;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 GYSFTGHMMN 10
        |||||
Db      26 GYSFTDHMMN 35

```

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RESULT 42
US-11-010-954-5
; Sequence 5, Application US/11010954
; Publication No. US20050249735A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Le, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; APPLICANT: Shealy, David
; TITLE OF INVENTION: Methods of Treating Ankylosing Spondylitis Using Anti-TNF Antibod
; FILE REFERENCE: 0975.1005-043
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US/11/010,954
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 09/920,137
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 60/236,826
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/223,360
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-11-010-954-5

```

```

; APPLICANT: Le, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; APPLICANT: Shealy, David
; TITLE OF INVENTION: Methods of Treating Ankylosing Spondylitis Using Anti-TNF Antibod
; FILE REFERENCE: 0975.1005-043
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: US/11/010,954
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US 09/920,137
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 60/236,826
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/223,360
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-11-010-954-5

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Query Match      68.8%; Score 44; DB 7; Length 119;
Best Local Similarity 60.0%; Pred. No. 0.36;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 GYSFTGHMMN 10
        |||||
Db      26 GYFSNMMN 35

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RESULT 43
US-11-053-750-5
; Sequence 5, Application US/11053750
; Publication No. US20050255104A1
; GENERAL INFORMATION:

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; APPLICANT: Le, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; APPLICANT: Shealy, David
; TITLE OF INVENTION: Methods of Treating Rheumatoid Arthritis
; FILE REFERENCE: 0975.1005-040
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/11/053,749
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18

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; APPLICANT: Siegel, Scott
; APPLICANT: Scallion, Bernard
; TITLE OF INVENTION: Methods of Treating Psoriasis Using
; TITLE OF INVENTION: Anti-TNF Receptor Fusion Proteins
; FILE REFERENCE: 0975.1005-045
; CURRENT FILING DATE: US/11/053,750
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 09/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-11-053-750-5

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Query Match      68.8%; Score 44; DB 7; Length 119;
Best Local Similarity 60.0%; Pred. No. 0.36;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 GYSFTGHMMN 10
        |||||
Db      26 GYFSNMMN 35

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RESULT 44
US-11-053-749-5
; Sequence 5, Application US/11053749
; Publication No. US20050260201A1
; GENERAL INFORMATION:

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; APPLICANT: Le, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David
; APPLICANT: Siegel, Scott
; APPLICANT: Scallion, Bernard
; TITLE OF INVENTION: Methods of Treating Rheumatoid Arthritis
; TITLE OF INVENTION: Using Anti-TNF Receptor Fusion Proteins
; FILE REFERENCE: 0975.1005-040
; CURRENT FILING DATE: US/11/053,749
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18

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; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
; US-11-053-749-5

Query Match      68.8%; Score 44; DB 7; Length 119;
Best Local Similarity 60.0%; Pred. No. 0.36;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYSFTGHMNN 10
       ||:||||:
Db      26 GTFSTYMMH 35

RESULT 45
US-10-932-334-71
; Sequence 71, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 71
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
; US-10-932-334-71

Query Match      68.8%; Score 44; DB 6; Length 120;
Best Local Similarity 60.0%; Pred. No. 0.36;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMNN 10
       ||:||||:
Db      26 GTFSTYMMH 35

RESULT 46
US-10-932-334-72
; Sequence 72, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
```

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; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 72
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
; US-10-932-334-72

Query Match      68.8%; Score 44; DB 6; Length 120;
Best Local Similarity 60.0%; Pred. No. 0.36;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMNN 10
       ||:||||:
Db      26 GTFSTYMMH 35

RESULT 47
US-10-932-334-73
; Sequence 73, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 73
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
; US-10-932-334-73

Query Match      68.8%; Score 44; DB 6; Length 122;
Best Local Similarity 60.0%; Pred. No. 0.37;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYSFTGHMNN 10
       ||:||||:
Db      26 GTFSTYMMH 35

RESULT 48
US-10-932-334-87
; Sequence 87, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 87
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-932-334-87
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Query Match 68.8%; Score 44; DB 6; Length 123;
Best Local Similarity 60.0%; Pred. No. 0.37;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHWMN 10
||:||||:
Db 26 GYFTSYWMH 35

Db 26 GYFTSYWMH 35

Search completed: January 17, 2006, 12:13:31
Job time : 4.33333 secs

RESULT 49
US-10-932-334-88
; Sequence 88, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized EM164 antibody
US-10-932-334-88

Query Match 68.8%; Score 44; DB 6; Length 123;
Best Local Similarity 60.0%; Pred. No. 0.37;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHWMN 10
||:||||:
Db 26 GYFTSYWMH 35

RESULT 50
US-10-932-334-92
; Sequence 92, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variable region of humanized EM164 antibody - heavy chain
US-10-932-334-92

Query Match 68.8%; Score 44; DB 6; Length 123;
Best Local Similarity 60.0%; Pred. No. 0.37;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYSFTGHWMN 10
||:||||:
Db 26 GYFTSYWMH 35

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:46:53 : Search time 106.379 Seconds
(without alignments)
70.215 Million cell updates/sec

Title: US-10-665-658-11

Perfect score: 93

Sequence: 1 MIHPSDSETRYNQKFKD 17

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	17	2	AAW62011 Heavy cha
2	93	100.0	17	3	AAV82338 Humanised
3	93	100.0	17	8	ADG38999 Humanised
4	93	100.0	17	8	ADRO3389 Humanised
5	93	100.0	121	2	AAW62013 Heavy cha
6	93	100.0	121	2	AAW63532 Humanised
7	93	100.0	121	3	AAV82336 Humanised
8	93	100.0	121	8	ADG38993 Humanised
9	93	100.0	121	8	ADRO3368 Humanised
10	93	100.0	121	8	ADW38458 CD11a hea
11	93	100.0	121	8	ADW80646 Humanised
12	93	100.0	451	9	ADP11670 anti-CD11
13	90	96.8	17	8	ADRO3400 Humanised
14	90	96.8	17	8	ADRO3399 Humanised
15	90	96.8	17	8	ADRO3397 Humanised
16	89	95.7	17	8	ADRO3397 Humanised
17	87	93.5	17	8	ADRO3403 Humanised
18	87	93.5	17	8	ADRO3403 Humanised
19	87	93.5	17	8	ADRO3402 Humanised
20	87	93.5	17	8	ADRO3393 Humanised
21	87	93.5	17	8	ADRO3405 Humanised
22	87	93.5	17	8	ADRO3404 Humanised
23	87	93.5	17	8	ADRO3406 Humanised
24	85	91.4	17	8	ADRO3398 Humanised

25	85	91.4	17	8	ADU87697 Mouse Luc
26	85	91.4	118	2	AAW01579 Lead bind
27	85	91.4	118	2	AAW01576 Lead bind
28	85	91.4	119	8	ADG25812 Anti-CD30
29	85	91.4	120	8	ADU87690 Mouse Luc
30	85	91.4	120	2	AAW63531 Murine MH
31	85	91.4	121	2	AAV82346 Murine MH
32	85	91.4	121	8	ADG38992 Mouse ant
33	85	91.4	121	8	ADRO3367 Murine MH
34	85	91.4	121	8	ADRO3367 Murine MH
35	84	90.3	122	8	ADW38454 CD11a hea
36	83	89.2	117	8	ADRO3395 Humanised
37	82	88.2	66	6	ABU56854 BONT/A Hc
38	82	88.2	118	8	AD221535 Anti-Muc-
39	82	88.2	120	8	ADRO3650 Mouse hea
40	82	88.2	177	9	AD221543 Anti-Muc-
41	80	86.0	17	8	ADRO3392 Humanised
42	80	86.0	17	8	ADRO3394 Humanised
43	80	86.0	19	5	AAE22201 Murine MC
44	80	86.0	66	6	ABU56852 BONT/A Hc
45	80	86.0	117	5	AAE22192 Murine MC
46	80	86.0	125	8	ADRO3648 Mouse hea
47	80	86.0	138	5	AAE22191 Murine MC
48	80	86.0	495	5	AAE22193 Murine CC
49	82.8	82.8	17	8	ADRO3390 Humanised
50	82.8	82.8	17	8	AD245355 Murine fa
51	82.8	82.8	66	6	ABU56853 BONT/A Hc
52	77	82.8	121	8	ADRO3649 Mouse hea
53	77	82.8	121	8	AD245353 Murine an
54	77	79.6	17	2	AAE85500 SCFV(FWP5
55	74	79.6	66	6	ABU56835 BONT/A Hc
56	74	79.6	96	6	ADOC32145 Mouse ant
57	74	79.6	98	8	ADOC32145 Mouse ant
58	74	79.6	119	2	AAW01578 Lead bind
59	74	79.6	120	2	AAW47493 Murine an
60	74	79.6	125	8	ADRO3646 Mouse hea
61	74	79.6	240	2	AAE85495 SCFV(FWP5
62	74	79.6	241	2	AAE26981 FWP51 fus
63	74	79.6	637	2	AAE26983 (FRP51)-E
64	73	78.5	17	8	ADRO3391 Humanised
65	73	78.5	118	8	ADU39748 Human SLC
66	73	78.5	118	8	AD221533 Anti-Muc-
67	73	78.5	120	8	ADQ76069 Heteroec
68	73	78.5	120	9	AD251184 Amino acil
69	73	78.5	120	9	AD242058 Human ant
70	73	78.5	260	9	AD221542 Anti-Muc-
71	72	77.4	17	9	AEA43975 Anti-TPO
72	72	77.4	115	9	AEA89799 Antibody
73	72	77.4	115	9	AEA44081 Anti-TPO
74	70	75.3	116	9	ADW86143 Novel cyt
75	70	75.3	121	8	AD225819 Anti-alpha
76	70	75.3	121	8	AD225818 Anti-alpha
77	70	75.3	123	3	ADX39143 Mouse Mab
78	70	75.3	143	2	AAE12233 Heavy cha
79	70	75.3	144	2	AAE12355 Heavy cha
80	70	75.3	244	9	ADX39104 Humanized
81	70	75.3	315	4	AAE70843 SNV-env 1
82	70	75.3	466	9	ADX39100 Mouse mon
83	70	75.3	466	9	ADX39137 Mouse mon
84	70	75.3	473	3	ADX39139 Humanized
85	69	74.2	17	2	AAW62018 Complement
86	69	74.2	17	2	AAW62018 Complement
87	69	74.2	17	8	ADG39011 Rhesusise
88	69	74.2	17	8	ADG39011 Rhesusise
89	69	74.2	118	4	ABU56851 BONT/A Hc
90	69	74.2	121	2	AAE03753 Murine PS
91	69	74.2	121	2	AAE03753 Murine PS
92	69	74.2	121	2	AAW63542 Murine MH
93	69	74.2	121	8	AAV82348 Rhesusise
94	69	74.2	121	8	ADRO3380 Rhesusise
95	69	74.2	125	8	ADRO3380 Rhesusise
96	68	73.1	17	5	ADRO38647 Mouse hea
97	68	73.1	17	5	AAU72832 Anti-NKG2
			17	9	AEA43957 Anti-TPO

98	68	73.1	112	8	ADG25813	Adg25813	Anti-CD30	171	61	65.6	145	3	AAW90925	AAW90925	Humanised
99	68	73.1	114	6	ADG64770	Adg64770	Cl mouse	172	61	65.6	145	5	ABB74940	ABB74940	Humanised
100	68	73.1	115	6	ABR40167	Ab40167	Humanised	173	61	65.6	145	5	ABB74894	ABB74894	Humanised
101	68	73.1	115	9	AE444071	Ae444071	Anti-TP02	174	61	65.6	230	2	AAW07529	AAW07529	Anti-HGF
102	68	73.1	117	5	AAU72830	Aau72830	Anti-NKG2	175	61	65.6	464	2	AAW83041	AAW83041	Anti-Fas
103	68	73.1	117	5	AAE25526	Aae25526	S. aureus	176	61	65.6	464	2	AAH17747	AAH17747	Mouse ant
104	68	73.1	117	5	AAU72858	Aau72858	8G7C10x4-	177	61	65.6	464	3	AAW90897	AAW90897	Mouse ant
105	68	73.1	507	8	AAU72837	Ad43337	Anti-CD30	178	61	65.6	464	5	ABB74912	ABB74912	Humanised
106	67	72.0	709	8	ADG69518	Adg69518	Mouse ICA	179	61	65.6	464	5	ABB74866	ABB74866	Humanised
107	67	72.0	304	9	ADG69520	Adg69520	Mouse ICA	180	61	65.6	470	2	AAW83036	AAW83036	Anti-Fas
108	67	72.0	467	8	ADQ14477	Adq14477	Mouse ant	181	61	65.6	470	2	AAW83037	AAW83037	Anti-Fas
109	66	71.0	20	3	AAV70800	Aav70800	Murine an	182	61	65.6	470	3	AAH17779	AAH17779	Humanised
110	66	71.0	112	8	ADG25838	Adg25838	Anti-CD30	183	61	65.6	470	3	AAH14776	AAH14776	Humanised
111	66	71.0	129	3	AAV70789	Aav70789	Murine an	184	61	65.6	470	3	AAW90926	AAW90926	Humanised
112	64	68.8	120	2	AAH47491	Aeh47491	Humanised	185	61	65.6	470	3	AAW90934	AAW90934	Humanised
113	64	68.8	133	9	AE88772	Ae88772	Murine SA	186	61	65.6	470	3	AAW90935	AAW90935	Humanised
114	64	68.8	195	7	ABR84724	Ab84724	Vector pg	187	61	65.6	470	3	AAW90936	AAW90936	Humanised
115	64	68.8	195	7	ABR84722	Ab84722	Vector pg	188	61	65.6	470	3	AAW90937	AAW90937	Humanised
116	63	67.7	117	8	ADT75043	Adt75043	Murine he	189	61	65.6	470	5	ABB74941	ABB74941	Humanised
117	63	67.7	119	2	AAH79859	Aah79859	Anti-EGFR	190	61	65.6	470	5	ABB74944	ABB74944	Humanised
118	63	67.7	120	2	AAH19915	Aah19915	Heavy cha	191	61	65.6	470	5	ABB74945	ABB74945	Humanised
119	63	67.7	120	2	ADT75022	Adt75022	Heavy cha	192	61	65.6	470	5	ABB74898	ABB74898	Humanised
120	63	67.7	120	6	ABR40164	Ab40164	Humanised	193	61	65.6	470	5	ABB74904	ABB74904	Humanised
121	63	67.7	123	6	ABR40163	Ab40163	Humanised	194	61	65.6	470	5	ABB74902	ABB74902	Humanised
122	63	67.7	123	6	ABR40166	Ab40166	Humanised	195	61	65.6	470	5	ABB74903	ABB74903	Humanised
123	63	67.7	123	6	ABR40165	Ab40165	Humanised	196	61	65.6	470	5	ABB74895	ABB74895	Humanised
124	63	67.7	123	6	ADG64769	Adg64769	Cl mouse	197	61	65.6	470	5	ADR03429	ADR03429	Anti-glyre
125	63	67.7	123	8	ADG64767	Adg64767	Cl mouse	198	60	64.5	17	9	ADY80104	ADY80104	Anti-glyre
126	63	67.7	123	8	ADG64768	Adg64768	Cl mouse	199	60	64.5	17	9	ADY80111	ADY80111	Anti-glyre
127	63	67.7	124	4	AAE03750	Aae03750	Murine PS	200	60	64.5	114	9	ADY80111	ADY80111	Anti-glyre
128	63	67.7	125	7	ADP60842	Adp60842	Mouse hor	201	60	64.5	117	2	AAH90419	AAH90419	Anti-VAP-
129	63	67.7	125	8	ADM80371	Adm80371	Murine ho	202	61	63.4	17	2	AAH90419	AAH90419	Anti-body
130	63	67.7	447	7	AEH13531	Aeh13531	Mature ch	203	59	63.4	17	3	AAH55146	AAH55146	Anti-CD34
131	63	67.7	466	4	AAE03755	Aae03755	Chimeric	204	59	63.4	17	3	AAH68692	AAH68692	Human hae
132	62	66.7	17	2	AAH89153	Aah89153	Anti-p53	205	59	63.4	17	5	AAH11184	AAH11184	Mouse ant
133	62	66.7	104	2	AAH89170	Aah89170	Anti-p53	206	59	63.4	17	8	ADH87709	ADH87709	Mouse Luc
134	62	66.7	116	2	AAH29452	Aay29452	Human Igg	207	59	63.4	17	9	ADW97134	ADW97134	Murine MA
135	62	66.7	116	3	AAH77755	Aay77755	Human Igg	208	59	63.4	111	9	ADZ45471	ADZ45471	Murine fa
136	62	66.7	116	3	AAH30312	Aab30312	Human Igg	209	59	63.4	111	2	AAW04590	AAW04590	Anti-DNA
137	62	66.7	116	6	ABH13789	Abh13789	Human Igg	210	59	63.4	111	2	AAW04586	AAW04586	Anti-DNA
138	62	66.7	116	6	ABU59502	Abu59502	Human Igg	211	59	63.4	111	2	AAW04589	AAW04589	Anti-DNA
139	62	66.7	116	6	AAE39085	Aae39085	Human Igg	212	59	63.4	111	2	AAH21283	AAH21283	Murine VH
140	62	66.7	118	7	ADJ80431	Adj80431	Hybrid hu	213	59	63.4	114	2	AAH21264	AAH21264	Murine VH
141	62	66.7	118	7	ADJ80435	Adj80435	Hybrid hu	214	59	63.4	114	2	AAH21277	AAH21277	Murine VH
142	62	66.7	119	7	ADJ80432	Adj80432	Hybrid hu	215	59	63.4	114	2	AAH21281	AAH21281	Murine VH
143	62	66.7	119	7	ADJ80434	Adj80434	Hybrid hu	216	59	63.4	114	2	AAH21281	AAH21281	Murine VH
144	62	66.7	119	8	ADG25806	Adg25806	Anti-CD30	217	59	63.4	114	3	AAH71549	AAH71549	Humanised
145	61	65.6	16	3	AAW90892	Aaw90892	Murine an	218	59	63.4	114	3	AAH71550	AAH71550	Humanised
146	61	65.6	17	2	AAW83025	Aaw83025	Anti-Fas	219	59	63.4	117	2	AAH25732	AAH25732	Variable
147	61	65.6	17	2	AAH14742	Aab14742	Mouse ant	220	59	63.4	117	2	AAW00831	AAW00831	Anti-huma
148	61	65.6	17	5	ABH74907	Abh74907	Humanised	221	59	63.4	117	2	AAH71549	AAH71549	Humanised
149	61	65.6	17	5	ABH74861	Abh74861	Humanised	222	59	63.4	117	4	AAH69698	AAH69698	Human Bu
150	61	65.6	17	8	ADH85703	Adh85703	Human Bph	223	59	63.4	117	8	ADZ45469	ADZ45469	Murine fa
151	61	65.6	17	8	ADP79382	Adp79382	Thyriotrop	224	59	63.4	118	9	ADZ45469	ADZ45469	Anti-DNA
152	61	65.6	17	9	ADY32283	Ady32283	Human Bph	225	59	63.4	119	2	AAW26798	AAW26798	Anti-gp54
153	61	65.6	17	9	AEH17139	Aeh17139	BphA2-spe	226	59	63.4	119	2	AAH71548	AAH71548	Humanised
154	61	65.6	17	9	AEH42939	Aeh42939	BphA2 ant	227	59	63.4	121	2	AAH71548	AAH71548	Human-mou
155	61	65.6	17	9	AEH23164	Aeh23164	Human Bph	228	59	63.4	121	8	ADH87694	ADH87694	Mouse Luc
156	61	65.6	118	8	ADH85701	Adh85701	Human Bph	229	59	63.4	122	9	AEH21873	AEH21873	Human DC-
157	61	65.6	118	8	ADT61902	Adt61902	Anti-EpHa	230	59	63.4	131	3	AAH88771	AAH88771	Human SA-
158	61	65.6	118	8	ADU39962	Adu39962	Anti-body	231	59	63.4	136	3	AAH71546	AAH71546	Murine AR2
159	61	65.6	118	9	ADY32219	Ady32219	BphA2-spe	232	59	63.4	136	8	ADP91400	ADP91400	Human-mou
160	61	65.6	118	9	AEH17137	Aeh17137	BphA2 ant	233	59	63.4	137	2	AAH53818	AAH53818	Protein s
161	61	65.6	118	9	AEH42937	Aeh42937	BphA2 ant	234	59	63.4	137	2	AAH53815	AAH53815	Murine AC
162	61	65.6	119	2	AAH79861	Aah79861	Anti-EGFR	235	59	63.4	140	5	AAH11177	AAH11177	Mouse ant
163	61	65.6	119	2	AAH79863	Aah79863	Anti-EGFR	236	59	63.4	142	3	AAH53816	AAH53816	Heavy Cha
164	61	65.6	119	8	ADP79380	Adp79380	Thyriotrop	237	59	63.4	144	2	AAH69694	AAH69694	Murine AF
165	61	65.6	119	8	ADH69664	Adh69664	Humanized	238	59	63.4	152	4	ADH69694	ADH69694	Heavy cha
166	61	65.6	119	8	AEH23169	Aeh23169	Thyriotrop	239	59	63.4	152	8	AAH53813	AAH53813	Heavy cha
167	61	65.6	124	8	ADP79384	Adp79384	Thyriotrop	240	59	63.4	180	2	AAH11178	AAH11178	Mouse hum
168	61	65.6	145	2	AAH63038	Aah63038	Anti-Fas	241	59	63.4	180	5	AAH11178	AAH11178	Mouse hum
169	61	65.6	145	2	AAH14775	Aab14775	Fragment	242	59	63.4	245	2	AAH26800	AAH26800	Anti-gp54
170	61	65.6	145	3	AAH14775	Aab14775	Fragment	243	59	63.4	245	2	AAH26800	AAH26800	Anti-gp54

244	59	63.4	447	8	ADT51699	Adt51699	Fontolizn	317	58	62.4	135	2	AAW69310	AAW69310	Murine an
245	59	63.4	447	8	ADT51697	Adt51697	Fontolizn	318	58	62.4	135	2	AAW40125	AAW40125	Murine mo
246	59	63.4	447	8	ADT51700	Adt51700	Fontolizn	319	58	62.4	135	2	AAW29441	AAW29441	Murine 6G
247	59	63.4	447	8	ADT51701	Adt51701	Fontolizn	320	58	62.4	135	3	AAW77747	AAW77747	Humanised
248	59	63.4	447	8	ADT51698	Adt51698	Fontolizn	321	58	62.4	135	3	AAW30304	AAW30304	Murine 6G
249	59	63.4	462	2	AAW14933	AAW14933	2A2 (Chim	322	58	62.4	135	4	AAW69653	AAW69653	Humanised
250	59	63.4	462	2	AAW14934	AAW14934	2A2 (Chim	323	58	62.4	135	6	ABU13781	ABU13781	Mouse ant
251	59	63.4	463	2	AAW14932	AAW14932	Murine an	324	58	62.4	135	6	ABU59494	ABU59494	Mouse ant
252	59	63.4	463	2	AAW14935	AAW14935	Murine an	325	58	62.4	135	6	ABU39020	ABU39020	Murine 6G
253	58	62.4	463	2	AAW14935	AAW14935	2A2 Human	326	58	62.4	135	7	AAW39077	AAW39077	Murine 6G
254	58	62.4	17	4	AAW62862	AAW62862	Anti-SAP-	327	58	62.4	135	8	ADT47735	ADT47735	Humanised
255	58	62.4	17	9	AAW43978	AAW43978	Anti-TPO	328	58	62.4	146	3	AAW43874	AAW43874	Heavy cha
256	58	62.4	106	2	AAW91365	AAW91365	Anti-prior	329	58	62.4	219	7	ADT79230	ADT79230	OC125-3.1
257	58	62.4	113	9	ADW10186	ADW10186	Thy-1 Bas	330	58	62.4	226	9	AAW88770	AAW88770	Murine SA
258	58	62.4	113	2	AAW95483	AAW95483	Mouse der	331	58	62.4	239	3	AAW12563	AAW12563	Anti-TAC
259	58	62.4	114	2	AAW21270	AAW21270	Murine VH	332	58	62.4	248	7	AAW36826	AAW36826	Anti-TAC
260	58	62.4	114	2	AAW21285	AAW21285	Murine VH	333	58	62.4	248	7	ADG32327	ADG32327	Mouse scF
261	58	62.4	114	2	AAW21269	AAW21269	Murine VH	334	58	62.4	248	9	ADW95688	ADW95688	Anti-IL-6
262	58	62.4	114	2	AAW21279	AAW21279	Murine VH	335	58	62.4	248	9	ADW15693	ADW15693	Mouse ant
263	58	62.4	114	2	AAW21265	AAW21265	Murine VH	336	58	62.4	253	2	AAW86324	AAW86324	Anti-IL-8
264	58	62.4	114	2	AAW21282	AAW21282	Murine VH	337	58	62.4	253	2	AAW23791	AAW23791	Chimeric
265	58	62.4	114	2	AAW21280	AAW21280	Murine VH	338	58	62.4	253	2	AAW31581	AAW31581	Chimeric
266	58	62.4	114	2	AAW21280	AAW21280	Murine VH	339	58	62.4	253	2	AAW42324	AAW42324	Murine va
267	58	62.4	114	2	AAW21275	AAW21275	Murine VH	340	58	62.4	253	2	AAW33746	AAW33746	Chimeric
268	58	62.4	115	9	AAW44083	AAW44083	Anti-TPO	341	58	62.4	253	2	AAW69312	AAW69312	Anti-IL-8
269	58	62.4	115	2	AAW24103	AAW24103	Anti-Tac	342	58	62.4	253	2	AAW40127	AAW40127	Chimeric
270	58	62.4	116	2	AAW64224	AAW64224	Anti-(6-4	343	58	62.4	253	2	AAW29444	AAW29444	Humanised
271	58	62.4	116	2	AAW58514	AAW58514	Protein S	344	58	62.4	253	2	AAW29443	AAW29443	Chimeric
272	58	62.4	116	2	AAW58513	AAW58513	Protein S	345	58	62.4	253	2	AAW29454	AAW29454	Chimeric
273	58	62.4	116	2	AAW37812	AAW37812	Humanized	346	58	62.4	253	3	AAW29454	AAW29454	Humanised
274	58	62.4	116	4	AAW69645	AAW69645	Humanised	347	58	62.4	253	3	AAW77749	AAW77749	Humanised
275	58	62.4	116	4	AAW69643	AAW69643	Murine an	348	58	62.4	253	3	AAW77759	AAW77759	Humanised
276	58	62.4	116	4	AAW69646	AAW69646	Humanised	349	58	62.4	253	3	AAW30316	AAW30316	6G4-2-5V1
277	58	62.4	116	4	AAW69649	AAW69649	Murine an	350	58	62.4	253	3	AAW30314	AAW30314	Humanised
278	58	62.4	116	5	ABJ10401	ABJ10401	Mutant an	351	58	62.4	253	3	AAW30306	AAW30306	Murine 6G
279	58	62.4	116	5	ABJ10402	ABJ10402	Mutant an	352	58	62.4	253	6	ABU13791	ABU13791	Humanised
280	58	62.4	116	5	ABJ10400	ABJ10400	Disulphid	353	58	62.4	253	6	ABU13783	ABU13783	Mouse ant
281	58	62.4	116	6	AAW36054	AAW36054	atacVH pr	354	58	62.4	253	6	ABU13793	ABU13793	Humanised
282	58	62.4	116	6	ADT01226	ADT01226	Protein 8	355	58	62.4	253	6	ABU59506	ABU59506	Humanised
283	58	62.4	116	8	ADT01227	ADT01227	Murine an	356	58	62.4	253	6	ABU59496	ABU59496	Mouse ant
284	58	62.4	116	8	ADT01227	ADT01227	Murine an	357	58	62.4	253	6	ABU59504	ABU59504	Humanised
285	58	62.4	116	8	ADT01227	ADT01227	Murine an	358	58	62.4	253	6	AAW39079	AAW39079	Murine 6G
286	58	62.4	116	8	ADT01227	ADT01227	Murine an	359	58	62.4	253	7	AAW39089	AAW39089	Humanised
287	58	62.4	116	8	ADT01227	ADT01227	Murine an	360	58	62.4	253	7	AAW39089	AAW39089	Humanised
288	58	62.4	116	8	ADT01227	ADT01227	Murine an	361	58	62.4	253	7	AAW39089	AAW39089	Humanised
289	58	62.4	116	8	ADT01227	ADT01227	Murine an	362	58	62.4	253	7	AAW39089	AAW39089	Humanised
290	58	62.4	116	8	ADT01227	ADT01227	Murine an	363	58	62.4	253	7	AAW39089	AAW39089	Humanised
291	58	62.4	116	8	ADT01227	ADT01227	Murine an	364	58	62.4	253	7	AAW39089	AAW39089	Humanised
292	58	62.4	116	8	ADT01227	ADT01227	Murine an	365	58	62.4	253	7	AAW39089	AAW39089	Humanised
293	58	62.4	116	8	ADT01227	ADT01227	Murine an	366	58	62.4	253	7	AAW39089	AAW39089	Humanised
294	58	62.4	116	8	ADT01227	ADT01227	Murine an	367	58	62.4	253	7	AAW39089	AAW39089	Humanised
295	58	62.4	116	8	ADT01227	ADT01227	Murine an	368	58	62.4	253	7	AAW39089	AAW39089	Humanised
296	58	62.4	116	8	ADT01227	ADT01227	Murine an	369	58	62.4	253	7	AAW39089	AAW39089	Humanised
297	58	62.4	116	8	ADT01227	ADT01227	Murine an	370	58	62.4	253	7	AAW39089	AAW39089	Humanised
298	58	62.4	116	8	ADT01227	ADT01227	Murine an	371	58	62.4	253	7	AAW39089	AAW39089	Humanised
299	58	62.4	116	8	ADT01227	ADT01227	Murine an	372	58	62.4	253	7	AAW39089	AAW39089	Humanised
300	58	62.4	116	8	ADT01227	ADT01227	Murine an	373	58	62.4	253	7	AAW39089	AAW39089	Humanised
301	58	62.4	116	8	ADT01227	ADT01227	Murine an	374	58	62.4	253	7	AAW39089	AAW39089	Humanised
302	58	62.4	116	8	ADT01227	ADT01227	Murine an	375	58	62.4	253	7	AAW39089	AAW39089	Humanised
303	58	62.4	116	8	ADT01227	ADT01227	Murine an	376	58	62.4	253	7	AAW39089	AAW39089	Humanised
304	58	62.4	116	8	ADT01227	ADT01227	Murine an	377	58	62.4	253	7	AAW39089	AAW39089	Humanised
305	58	62.4	116	8	ADT01227	ADT01227	Murine an	378	58	62.4	253	7	AAW39089	AAW39089	Humanised
306	58	62.4	116	8	ADT01227	ADT01227	Murine an	379	58	62.4	253	7	AAW39089	AAW39089	Humanised
307	58	62.4	116	8	ADT01227	ADT01227	Murine an	380	58	62.4	253	7	AAW39089	AAW39089	Humanised
308	58	62.4	116	8	ADT01227	ADT01227	Murine an	381	58	62.4	253	7	AAW39089	AAW39089	Humanised
309	58	62.4	116	8	ADT01227	ADT01227	Murine an	382	58	62.4	253	7	AAW39089	AAW39089	Humanised
310	58	62.4	116	8	ADT01227	ADT01227	Murine an	383	58	62.4	253	7	AAW39089	AAW39089	Humanised
311	58	62.4	116	8	ADT01227	ADT01227	Murine an	384	58	62.4	253	7	AAW39089	AAW39089	Humanised
312	58	62.4	116	8	ADT01227	ADT01227	Murine an	385	58	62.4	253	7	AAW39089	AAW39089	Humanised
313	58	62.4	116	8	ADT01227	ADT01227	Murine an	386	58	62.4	253	7	AAW39089	AAW39089	Humanised
314	58	62.4	116	8	ADT01227	ADT01227	Murine an	387	58	62.4	253	7	AAW39089	AAW39089	Humanised
315	58	62.4	116	8	ADT01227	ADT01227	Murine an	388	58	62.4	253	7	AAW39089	AAW39089	Humanised
316	58	62.4	116	8	ADT01227	ADT01227	Murine an	389	58	62.4	253	7	AAW39089	AAW39089	Humanised

390	58	62.4	452	3	AAB30322	Humanised	463	57	61.3	139	2	AAW62204	Humanised
391	58	62.4	452	6	ABU13799	Humanised	464	57	61.3	139	2	AAW62211	Humanised
392	58	62.4	452	6	ABU59512	Humanised	465	57	61.3	139	2	AAW62199	Humanised
393	58	62.4	452	7	AAE39094	Protein #	466	57	61.3	139	2	AAW62214	Humanised
394	58	62.4	470	8	ADM72031	Chimeric	467	57	61.3	139	2	AAW62217	Humanised
395	58	62.4	599	2	AAW37132	Anti-Tac (468	57	61.3	139	2	AAW62196	Humanised
396	58	62.4	599	2	AAW95462	Anti-Tac (469	57	61.3	139	2	AAW62188	Mouse ant
397	58	62.4	599	2	AAW87477	Anti-Tac (470	57	61.3	139	2	AAW62201	Humanised
398	58	62.4	615	7	ADG32341	Fusion pr	471	57	61.3	139	2	AAW62210	Humanised
399	57	61.3	17	8	ADO60472	Mouse ant	472	57	61.3	139	2	AAW62205	Humanised
400	57	61.3	17	8	ADM47109	Anti-CD20	473	57	61.3	139	2	AAW62206	Humanised
401	57	61.3	17	9	ADY80105	Anti-ghre	474	57	61.3	139	2	AAW62209	Humanised
402	57	61.3	17	9	ADZ45483	Murine fa	475	57	61.3	139	2	AAW62198	Humanised
403	57	61.3	17	9	ADZ45467	Murine fa	476	57	61.3	139	2	AAW62218	Humanised
404	57	61.3	17	9	ADZ83468	Anti-CD3	477	57	61.3	139	2	AAW62197	Humanised
405	57	61.3	17	9	AEb24624	Humanised	478	57	61.3	139	2	AAW62202	Humanised
406	57	61.3	102	2	AAE91363	Anti-proe	479	57	61.3	139	2	AAW62212	Humanised
407	57	61.3	102	2	AAE91369	Anti-proe	480	57	61.3	139	2	AAW62200	Humanised
408	57	61.3	102	2	AAE91370	Anti-proe	481	57	61.3	139	2	AAW62203	Humanised
409	57	61.3	113	8	ADO60449	Humanised	482	57	61.3	139	2	AAW62213	Humanised
410	57	61.3	113	8	ADO60448	Humanised	483	57	61.3	139	2	AAW77295	Humanised
411	57	61.3	113	8	ADO60444	Humanised	484	57	61.3	139	2	AAW02557	Humanised
412	57	61.3	113	8	ADO60442	Mouse ant	485	57	61.3	139	2	AAW02568	Humanised
413	57	61.3	113	8	ADO60450	Humanised	486	57	61.3	139	2	AAW02573	Humanised
414	57	61.3	113	8	ADO60447	Humanised	487	57	61.3	139	2	AAW02561	Humanised
415	57	61.3	113	8	ADO60446	Humanised	488	57	61.3	139	2	AAW02558	Humanised
416	57	61.3	113	8	AEb24594	Murine MA	489	57	61.3	139	2	AAW02546	H chain V
417	57	61.3	113	9	AEb24596	Humanised	490	57	61.3	139	2	AAW02570	Humanised
418	57	61.3	113	9	AEb24602	Humanised	491	57	61.3	139	2	AAW02575	Humanised
419	57	61.3	113	9	AEb24600	Humanised	492	57	61.3	139	2	AAW02564	Humanised
420	57	61.3	113	9	AEb24598	Humanised	493	57	61.3	139	2	AAW02565	Humanised
421	57	61.3	113	9	AEb24599	Humanised	494	57	61.3	139	2	AAW02572	Humanised
422	57	61.3	113	9	AEb24601	Humanised	495	57	61.3	139	2	AAW02571	Humanised
423	57	61.3	114	9	ADY80112	Anti-ghre	496	57	61.3	139	2	AAW02555	Humanised
424	57	61.3	115	2	AAW39812	Variable	497	57	61.3	139	2	AAW02559	Humanised
425	57	61.3	115	2	ADZ45481	Murine fa	498	57	61.3	139	2	AAW02560	Humanised
426	57	61.3	116	2	AAE79241	Heavy cha	499	57	61.3	139	2	AAW02563	Humanised
427	57	61.3	119	2	AAE13092	Grafted h	500	57	61.3	139	2	AAW02567	Humanised
428	57	61.3	119	2	AAE13099	Grafted h	501	57	61.3	139	2	AAW02566	Humanised
429	57	61.3	119	2	AAE67449	OKT3 huma	502	57	61.3	139	2	AAW02574	Humanised
430	57	61.3	119	2	AAE75224	OKT3 huma	503	57	61.3	139	2	AAW02562	Humanised
431	57	61.3	119	2	AAE67447	OKT3 huma	504	57	61.3	139	2	AAW02556	Humanised
432	57	61.3	119	2	AAW73531	Humanised	505	57	61.3	139	2	AAW02569	Humanised
433	57	61.3	119	2	AAW73529	Humanised	506	57	61.3	139	2	AAW32771	Anti-HM1
434	57	61.3	119	4	AAW80851	Anti-CD3	507	57	61.3	139	2	AAW32770	Humanised
435	57	61.3	119	6	AAO16693	Anti-ovar	508	57	61.3	139	2	AAW05487	H chain V
436	57	61.3	119	8	ADQ91061	Murine OK	509	57	61.3	139	2	AAW05486	H chain V
437	57	61.3	119	8	ADR42625	Mouse ant	510	57	61.3	139	5	AAW52354	H chain V
438	57	61.3	119	9	ADV66154	CD3-spect	511	57	61.3	139	5	AAW52355	H chain V
439	57	61.3	119	9	ADV66149	CD3-spect	512	57	61.3	139	6	ABG71946	Human res
440	57	61.3	119	9	ADV26037	Mouse OKT	513	57	61.3	139	8	ADO60011	H chain V
441	57	61.3	119	9	ADV26040	Mouse OKT	514	57	61.3	139	8	ADO60010	H chain V
442	57	61.3	119	9	ADV26042	Mouse OKT	515	57	61.3	140	2	AAW77294	HM1.24 an
443	57	61.3	119	9	ADZ64980	Non-deimm	516	57	61.3	219	9	ADZ00217	Mouse OKT
444	57	61.3	119	9	ADZ64972	Deimmuniz	517	57	61.3	232	9	ADW13531	Anti-anti
445	57	61.3	119	9	ADZ83454	Deimmuniz	518	57	61.3	240	9	ADV14577	VL(CD3)-V
446	57	61.3	119	9	ADZ83488	Non-deimm	519	57	61.3	243	8	ADR43341	scFv anti
447	57	61.3	119	9	ADZ83484	Non-deimm	520	57	61.3	243	9	ADV14573	VH(CD3)-V
448	57	61.3	120	9	ADM13533	Anti-anti	521	57	61.3	243	9	ADZ64955	Anti-CD3
449	57	61.3	121	5	AAE22195	CD3-spect	522	57	61.3	243	9	ADZ64951	Anti-CD3
450	57	61.3	121	8	ADQ91076	Modified	523	57	61.3	243	9	ADZ64912	Anti-CD3
451	57	61.3	122	9	ADM47050	Heavy cya	524	57	61.3	243	9	ADZ64953	Anti-CD3
452	57	61.3	122	9	ADM86135	Novel cyt	525	57	61.3	243	9	ADZ83405	Anti-CD3
453	57	61.3	122	9	ADZ45465	Murine fa	526	57	61.3	243	9	ADZ83380	Non-deimm
454	57	61.3	123	9	ADV26052	Mouse OKT	527	57	61.3	243	9	ADZ83401	Anti-CD3
455	57	61.3	123	9	ADM71839	Murine OK	528	57	61.3	243	9	ADZ83403	Anti-CD3
456	57	61.3	138	8	AD126639	Mouse ant	529	57	61.3	256	4	AAE82897	Anti-p53
457	57	61.3	138	8	ADQ91059	Murine OK	530	57	61.3	258	4	AAE82898	Anti-p53
458	57	61.3	138	9	ADM71844	Human OKT	531	57	61.3	267	8	ADM32742	Amino aci
459	57	61.3	138	9	ADM71854	APEx-3PMO	532	57	61.3	269	8	ADR28054	NPB polyP
460	57	61.3	139	2	AAW65774	Anti-huma	533	57	61.3	273	2	AAE52865	Anti-infl
461	57	61.3	139	2	AAW65773	Anti-huma	534	57	61.3	288	2	AAW82317	Mouse bis
462	57	61.3	139	2	AAW62216	Humanised	535	57	61.3	288	2	AAW82316	Mouse OKT

AAW62204	Humanised
AAW62211	Humanised
AAW62199	Humanised
AAW62214	Humanised
AAW62217	Humanised
AAW62196	Humanised
AAW62188	Mouse ant
AAW62201	Humanised
AAW62210	Humanised
AAW62205	Humanised
AAW62206	Humanised
AAW62209	Humanised
AAW62198	Humanised
AAW62218	Humanised
AAW62197	Humanised
AAW62202	Humanised
AAW62212	Humanised
AAW62200	Humanised
AAW62203	Humanised
AAW62213	Humanised
AAW77295	Humanised
AAW02557	Humanised
AAW02568	Humanised
AAW02573	Humanised
AAW02561	Humanised
AAW02558	Humanised
AAW02546	H chain V
AAW02570	Humanised
AAW02575	Humanised
AAW02564	Humanised
AAW02565	Humanised
AAW02572	Humanised
AAW02571	Humanised
AAW02555	Humanised
AAW02559	Humanised
AAW02560	Humanised
AAW02563	Humanised
AAW02567	Humanised
AAW02566	Humanised
AAW02574	Humanised
AAW02562	Humanised
AAW02556	Humanised
AAW02569	Humanised
AAW32771	Anti-HM1
AAW32770	Humanised
AAW05487	H chain V
AAW05486	H chain V
AAW52354	H chain V
AAW52355	H chain V
ABG71946	Human res
ADO60011	H chain V
ADO60010	H chain V
AAW77294	HM1.24 an
ADZ00217	Mouse OKT
ADW13531	Anti-anti
ADV14577	VL(CD3)-V
ADR43341	scFv anti
ADV14573	VH(CD3)-V
ADZ64955	Anti-CD3
ADZ64951	Anti-CD3
ADZ64912	Anti-CD3
ADZ64953	Anti-CD3
ADZ83405	Anti-CD3
ADZ83380	Non-deimm
ADZ83401	Anti-CD3
ADZ83403	Anti-CD3
AAE82897	Anti-p53
AAE82898	Anti-p53
ADM32742	Amino aci
ADR28054	NPB polyP
AAE52865	Anti-infl
AAW82317	Mouse bis
AAW82316	Mouse OKT

536	57	61.3	378	9	AEA36900	Anti-CD3x	609	57	61.3	499	9	AD283735	Ad283735	CD3 speci
537	57	61.3	409	5	AB07680	MOGxCD3 f	610	57	61.3	499	9	AD283751	Ad283751	CD3 speci
538	57	61.3	409	6	ADA14263	Human MOG	611	57	61.3	499	9	AD283781	Ad283781	CD3 speci
539	57	61.3	449	9	AD280769	Amino aci	612	57	61.3	500	9	ADV66137	ADV66137	Anti-CD3-
540	57	61.3	467	9	AD26107	Mouse OXt	613	57	61.3	500	9	ADV66095	ADV66095	Anti-CD3-
541	57	61.3	467	9	ADW71833	Murine OX	614	57	61.3	500	9	ADV66097	ADV66097	Anti-CD3-
542	57	61.3	468	2	AAR13061	Monoclonoma	615	57	61.3	500	9	AD283703	Ad283703	CD3 speci
543	57	61.3	468	2	ADQ91057	Murine OX	616	57	61.3	500	9	AD283687	Ad283687	CD3 speci
544	57	61.3	491	9	AD283606	CD3 speci	617	57	61.3	500	9	AD283695	Ad283695	CD3 speci
545	57	61.3	491	9	AD283602	CD3 speci	618	57	61.3	500	9	AD283683	Ad283683	CD3 speci
546	57	61.3	491	9	AD283604	CD3 speci	619	57	61.3	500	9	AD283691	Ad283691	CD3 speci
547	57	61.3	492	8	ADQ91080	Antibody	620	57	61.3	502	9	ADV14530	ADV14530	Anti-CD3-
548	57	61.3	492	8	ADQ91090	Antibody	621	57	61.3	503	9	ADV66131	ADV66131	Anti-CD3-
549	57	61.3	492	8	ADQ91082	Antibody	622	57	61.3	503	9	ADV66133	ADV66133	Anti-CD3-
550	57	61.3	492	8	ADQ91084	Antibody	623	57	61.3	503	9	ADV66087	ADV66087	Anti-CD3-
551	57	61.3	492	8	ADQ91104	Antibody	624	57	61.3	503	9	ADV66093	ADV66093	Anti-CD3-
552	57	61.3	492	8	ADQ91106	Antibody	625	57	61.3	503	9	ADV66135	ADV66135	Anti-CD3-
553	57	61.3	492	8	ADQ91088	Antibody	626	57	61.3	503	9	ADV66091	ADV66091	Anti-CD3-
554	57	61.3	492	8	ADQ91086	Antibody	627	57	61.3	503	9	ADV66081	ADV66081	Anti-CD3-
555	57	61.3	492	8	ADQ91092	Antibody	628	57	61.3	503	9	ADV14538	ADV14538	Bi-specifi
556	57	61.3	492	8	ADQ91094	Antibody	629	57	61.3	503	9	ADV14532	ADV14532	Bi-specifi
557	57	61.3	492	8	ADQ91100	Antibody	630	57	61.3	503	9	ADV14540	ADV14540	Bi-specifi
558	57	61.3	492	8	ADQ91096	Antibody	631	57	61.3	503	9	AEA52452	AEA52452	Human CD3
559	57	61.3	492	8	ADQ91098	Antibody	632	57	61.3	503	9	AEA52450	AEA52450	Human CD3
560	57	61.3	492	8	ADQ91102	Antibody	633	57	61.3	504	9	ADV14534	ADV14534	Bi-specifi
561	57	61.3	492	8	ADQ91078	Bi-specifi	634	57	61.3	504	9	ADV14536	ADV14536	Bi-specifi
562	57	61.3	492	8	ADZ83590	CD3 speci	635	57	61.3	504	9	ADV14536	ADV14536	Bi-specifi
563	57	61.3	492	9	ADZ83580	CD3 speci	636	57	61.3	504	9	AEA52451	AEA52451	Human CD3
564	57	61.3	492	9	ADZ83592	Anti-CD3-	637	57	61.3	504	9	AEA52447	AEA52447	Human CD3
565	57	61.3	494	9	ADV66089	Anti-CD3-	638	57	61.3	504	9	AEA52449	AEA52449	Human CD3
566	57	61.3	496	9	ADZ83641	CD3 speci	639	57	61.3	505	9	AEA52448	AEA52448	Human CD3
567	57	61.3	496	9	ADZ83653	CD3 speci	640	57	61.3	505	9	ADV66079	ADV66079	Anti-CD3-
568	57	61.3	496	9	ADZ83637	CD3 speci	641	57	61.3	506	9	ADV66085	ADV66085	Anti-CD3-
569	57	61.3	496	9	ADZ83649	CD3 speci	642	57	61.3	506	9	ADV66129	ADV66129	Anti-CD3-
570	57	61.3	496	9	ADZ83657	CD3 speci	643	57	61.3	506	9	ADV66127	ADV66127	Anti-CD3-
571	57	61.3	496	9	ADZ836123	Anti-CD3-	644	57	61.3	506	9	ADV66129	ADV66129	Anti-CD3-
572	57	61.3	497	9	ADV66125	Anti-CD3-	645	57	61.3	515	9	ADV66113	ADV66113	Anti-CD3-
573	57	61.3	497	9	ADZ83659	CD3 speci	646	57	61.3	521	9	ADV66116	ADV66116	Anti-CD3-
574	57	61.3	497	9	ADZ83659	CD3 speci	647	57	61.3	521	9	ADV66121	ADV66121	Anti-CD3-
575	57	61.3	497	9	ADZ83647	CD3 speci	648	57	61.3	524	8	AD816612	AD816612	Human ant
576	57	61.3	497	9	ADZ83655	CD3 speci	649	57	61.3	526	9	ADV66119	ADV66119	Anti-CD3-
577	57	61.3	497	9	ADZ83651	CD3 speci	650	57	61.3	526	9	ADV66107	ADV66107	Anti-CD3-
578	57	61.3	497	9	ADZ83651	CD3 speci	651	57	61.3	526	9	ADV66113	ADV66113	Anti-CD3-
579	57	61.3	497	9	ADZ83653	CD3 speci	652	57	61.3	531	3	AAV43749	AAV43749	Fv-antibo
580	57	61.3	498	9	ADZ83574	Vector pB	653	57	61.3	533	8	ADR42630	ADR42630	Mouse ant
581	57	61.3	498	9	ADZ83741	CD3 speci	654	57	61.3	539	9	AAV50822	AAV50822	Fv-antibo
582	57	61.3	498	9	ADZ83731	CD3 speci	655	57	61.3	554	3	AAV50822	AAV50822	Fv-antibo
583	57	61.3	498	9	ADZ83578	Vector pB	656	57	61.3	562	6	ABR57058	ABR57058	Plaemid p
584	57	61.3	498	9	ADZ83749	CD3 speci	657	57	61.3	562	6	ABR57058	ABR57058	Plaemid p
585	57	61.3	498	9	ADZ83729	CD3 speci	658	57	61.3	574	7	ADZ83729	ADZ83729	CD3 speci
586	57	61.3	498	9	ADZ83773	CD3 speci	659	57	61.3	2606	7	ADZ83729	ADZ83729	CD3 speci
587	57	61.3	498	9	ADZ83785	CD3 speci	660	57	61.3	2606	7	ADZ83729	ADZ83729	CD3 speci
588	57	61.3	498	9	ADZ83576	Vector pB	661	57	61.3	17	9	ADV86697	ADV86697	Anti-FLJ3
589	57	61.3	498	9	ADZ83582	Non-delimm	662	57	61.3	17	9	AEA43966	AEA43966	Anti-TPO
590	57	61.3	498	9	ADZ83779	CD3 speci	663	57	61.3	17	9	AEA43945	AEA43945	Anti-TPO
591	57	61.3	498	9	ADZ83779	CD3 speci	664	57	61.3	17	9	AEA43945	AEA43945	Anti-TPO
592	57	61.3	498	9	ADZ83745	CD3 speci	665	57	61.3	98	8	ADO58549	ADO58549	GAMP gene
593	57	61.3	499	8	ADZ83745	CD3 speci	666	57	61.3	111	2	AAW04588	AAW04588	Anti-DNA
594	57	61.3	499	8	ADZ83743	CD3 speci	667	57	61.3	113	2	AAW89348	AAW89348	Mouse 23P
595	57	61.3	499	9	ADZ83697	CD3 speci	668	57	61.3	116	8	ADV86727	ADV86727	Anti-FLJ3
596	57	61.3	499	9	ADZ83787	CD3 speci	669	57	61.3	118	8	ADZ83787	ADZ83787	Anti-FLJ3
597	57	61.3	499	9	ADZ83747	CD3 speci	670	57	61.3	118	8	ADZ83787	ADZ83787	Anti-FLJ3
598	57	61.3	499	9	ADZ83747	CD3 speci	671	57	61.3	118	8	ADZ83787	ADZ83787	Anti-FLJ3
599	57	61.3	499	9	ADZ83685	CD3 speci	672	57	61.3	118	9	AEA44063	AEA44063	Anti-TPO
600	57	61.3	499	9	ADZ83701	CD3 speci	673	57	61.3	118	9	AEA44077	AEA44077	Anti-TPO
601	57	61.3	499	9	ADZ83681	CD3 speci	674	57	61.3	120	2	AAW47934	AAW47934	Humanised
602	57	61.3	499	9	ADZ83771	CD3 speci	675	57	61.3	120	2	AAW89350	AAW89350	Humanised
603	57	61.3	499	9	ADZ83693	CD3 speci	676	57	61.3	120	8	ADW17834	ADW17834	Murine an
604	57	61.3	499	9	ADZ83739	CD3 speci	677	57	61.3	120	8	ADW17834	ADW17834	Murine an
605	57	61.3	499	9	ADZ83775	CD3 speci	678	57	61.3	124	2	AAW47931	AAW47931	Mutated h
606	57	61.3	499	9	ADZ83783	CD3 speci	679	57	61.3	124	2	AAW82973	AAW82973	FBS human
607	57	61.3	499	9	ADZ83689	CD3 speci	680	57	61.3	124	2	AAW82974	AAW82974	FBS human
608	57	61.3	499	9	ADZ83777	CD3 speci	681	57	61.3	124	2	AAW82974	AAW82974	FBS human

682	56	60.2	124	2	AAR82972	Aar82972	FB5 human	755	54	58.1	102	2	AAR91371	Aar91371	Anti-proe
683	56	60.2	124	2	AAR82969	Aar82969	FB5 antib	756	54	58.1	113	8	AD032161	Ado32161	Mouse ant
684	56	60.2	124	2	AAR82971	Aar82971	FB5 human	757	54	58.1	114	8	ADM33984	Adm33984	Anti-Nogo
685	56	60.2	140	2	AAR12234	Aar12234	Mouse Mab	758	54	58.1	114	8	ADO32164	Ado32164	Mouse ant
686	56	60.2	141	2	AAR12356	Aar12356	Heavy Cha	759	54	58.1	114	8	ADY34451	Ady34451	Nogo rece
687	56	60.2	246	8	ADG64766	Adg64766	C1 mouse	760	54	58.1	117	8	ADL02304	Adl02304	Mouse Im
688	55	59.1	17	3	AAV92159	Aav92159	Murine 15	761	54	58.1	118	4	AAB85349	Aab85349	Antibody
689	55	59.1	17	7	AABR63921	Aab63921	Murine C5	762	54	58.1	118	8	ADL02308	Adl02308	Chimeric
690	55	59.1	17	8	ADG19053	Adg19053	Murine A5	763	54	58.1	118	6	ABJ18572	Abj18572	Gangliosid
691	55	59.1	17	9	ADZ45387	Adz45387	Murine fa	764	54	58.1	119	6	ABJ18570	Abj18570	Gangliosid
692	55	59.1	17	9	AEB23188	Aeb23188	Anti-trkC	765	54	58.1	119	6	AEB18772	Aeb18772	Hybridoma
693	55	59.1	114	2	AAK21284	Aak21284	Murine VH	766	54	58.1	119	7	AER82782	Aer82782	Hybridoma
694	55	59.1	118	2	AAW27122	Aaw27122	Murine an	767	54	58.1	119	9	ADZ45389	Adz45389	Murine fa
695	55	59.1	118	8	ADN49403	Adn49403	Murine ant	768	54	58.1	119	9	ADZ45381	Adz45381	Murine fa
696	55	59.1	119	3	AAV92156	Aav92156	Murine 15	769	54	58.1	119	9	ABP59952	Abp59952	Monoclonal
697	55	59.1	119	3	ADZ45385	Adz45385	Murine fa	770	54	58.1	120	6	ABP59987	Abp59987	Antibody
698	55	59.1	121	7	AER63917	Aer63917	Murine C5	771	54	58.1	120	6	ADP69657	Adp69657	Humanised
699	55	59.1	123	7	ADQ31356	Adq31356	Anti-trkC	772	54	58.1	120	7	ADP69652	Adp69652	Humanised
700	55	59.1	123	8	ADG19050	Adg19050	Human A5	773	54	58.1	120	7	ADJ94601	Adj94601	Anti-CD30
701	55	59.1	123	9	AEB23185	Aeb23185	Anti-trkC	774	54	58.1	120	8	ADG25810	Adg25810	Mouse ant
702	55	59.1	130	9	ADY96825	Ady96825	Human imm	775	54	58.1	120	8	ADR15133	Adr15133	Mouse ant
703	55	59.1	130	9	ADY96944	Ady96944	Human imm	776	54	58.1	120	8	AEB03871	Aeb03871	B-CLL pha
704	55	59.1	130	9	ADY96932	Ady96932	Human imm	777	54	58.1	120	9	AEB03876	Aeb03876	B-CLL pha
705	55	59.1	214	2	AAV44176	Aav44176	MAB FabJ3	778	54	58.1	120	2	AAW46484	Aaw46484	SIC5 VH a
706	55	59.1	243	2	AAW09436	Aaw09436	Anti-CD19	779	54	58.1	121	9	AAB69667	Aab69667	Murine Fd
707	55	59.1	243	2	AAW86002	Aaw86002	Murine an	780	54	58.1	121	4	AAB69668	Aab69668	Humanised
708	55	59.1	243	2	AAV42294	Aav42294	Anti-5T4	781	54	58.1	121	4	AAB69667	Aab69667	Humanised
709	55	59.1	243	2	AAV27407	Aav27407	5T4 bCFV	782	54	58.1	121	7	ADJ94605	Adj94605	Chimeric
710	55	59.1	243	4	AAB83835	Aab83835	Amino aci	783	54	58.1	121	7	ADJ94608	Adj94608	Humanised
711	55	59.1	244	8	ADG17481	Adg17481	Anti-CD22	784	54	58.1	121	7	ADJ94607	Adj94607	Chimeric
712	55	59.1	244	8	ADG17477	Adg17477	Anti-CD22	785	54	58.1	121	7	ADJ94607	Adj94607	Chimeric
713	55	59.1	244	8	ADG17482	Adg17482	Anti-CD22	786	54	58.1	121	8	ADO47714	Ado47714	Mouse Fd1
714	55	59.1	244	8	ADG17480	Adg17480	Anti-CD22	787	54	58.1	121	8	ADO47766	Ado47766	Mouse Fd1
715	55	59.1	244	8	ADG17478	Adg17478	Anti-CD22	788	54	58.1	121	8	ADU80275	Adu80275	CD20 bind
716	55	59.1	244	8	ADG17484	Adg17484	Anti-CD22	789	54	58.1	121	9	ADW03412	Adw03412	Murine an
717	55	59.1	250	8	ADG09249	Adg09249	Human C-M	790	54	58.1	121	9	ADX16288	Adx16288	2B8 antib
718	55	59.1	268	8	ADR03085	Adr03085	Polioviru	791	54	58.1	121	9	ADX16286	Adx16286	2B8 antib
719	55	59.1	268	8	ADR70319	Adr70319	Polioviru	792	54	58.1	121	9	ADX16329	Adx16329	Modified
720	55	59.1	268	8	ADR70386	Adr70386	Polioviru	793	54	58.1	121	9	ADX16287	Adx16287	Modified
721	55	59.1	450	9	AEB23211	Aeb23211	Anti-trkC	794	54	58.1	122	6	AAO27203	Aao27203	Chimeric
722	55	59.1	474	8	ADS98007	Ads98007	Protein F	795	54	58.1	122	8	ADP79573	Adp79573	Murine 2H
723	55	59.1	488	2	AAW86004	Aaw86004	Human B7-	796	54	58.1	122	8	ADP79574	Adp79574	Humanised
724	55	59.1	488	6	AAB83836	Aab83836	Amino aci	797	54	58.1	122	8	ADV33302	Adv33302	Anti-CD20
725	55	59.1	488	6	ABU07262	Abu07262	Human exp	798	54	58.1	122	9	ADV21492	Adv21492	Human ant
726	55	59.1	488	6	ABU07253	Abu07253	Human exp	799	54	58.1	122	9	ADW47044	Adw47044	Heavy Cha
727	55	59.1	488	6	AAB83838	Aab83838	Amino aci	800	54	58.1	122	9	ADW03408	Adw03408	Humanised
728	55	59.1	592	4	AAW86003	Aaw86003	Anti-5T4	801	54	58.1	122	9	ADW21310	Adw21310	Mouse ant
729	55	59.1	595	2	ABP58454	Abp58454	Engineere	802	54	58.1	122	9	ADM21309	Adm21309	Mouse ant
730	54	58.1	672	6	AAW80140	Aaw80140	Chimeric	803	54	58.1	122	9	ADX00803	Adx00803	Humanized
731	54	58.1	17	3	AAI12175	Aai12175	Human CDR	804	54	58.1	122	9	ADY21867	Ady21867	Human ant
732	54	58.1	17	4	AAO14423	Aao14423	CD25 bind	805	54	58.1	122	9	ADX16331	Adx16331	Modified
733	54	58.1	17	5	AAU81235	Aau81235	Murine tr	806	54	58.1	122	9	ADX16294	Adx16294	Lue16 ant
734	54	58.1	17	6	ABJ18551	Abj18551	Gangli1081	807	54	58.1	122	9	ADX16295	Adx16295	Vhy Light
735	54	58.1	17	6	ABB82655	Abb82655	CDR2 fireg	808	54	58.1	122	9	ADY62623	Ady62623	Humanized
736	54	58.1	17	7	ADC66265	Adc66265	Mouse pro	809	54	58.1	122	9	ADZ83548	Adz83548	CD20 VH
737	54	58.1	17	7	ADJ94575	Adj94575	Humanised	810	54	58.1	122	9	AEB27726	Aeb27726	Variable
738	54	58.1	17	8	ADJ02228	Adj02228	Murine Im	811	54	58.1	122	9	AEB17636	Aeb17636	Variable
739	54	58.1	17	8	ADR15150	Adr15150	Mouse ant	812	54	58.1	123	6	AAO27195	Aao27195	Chimeric
740	54	58.1	17	8	ADP79604	Adp79604	Murine 2H	813	54	58.1	123	6	AAO27201	Aao27201	Murine an
741	54	58.1	17	8	ADU80241	Adu80241	CD20 bind	814	54	58.1	123	9	ADW47048	Adw47048	Heavy Cha
742	54	58.1	17	8	ADU80237	Adu80237	CD20 bind	815	54	58.1	123	9	ADW47042	Adw47042	Heavy Cha
743	54	58.1	17	9	ADM47107	Adm47107	Anti-CD20	816	54	58.1	123	9	AEB23214	Aeb23214	Mouse ant
744	54	58.1	17	9	ADM47106	Adm47106	Anti-CD20	817	54	58.1	126	5	AAU81272	Aau81272	Murine tr
745	54	58.1	17	9	ADM21313	Adm21313	Mouse ant	818	54	58.1	136	2	AAI14153	Aai14153	Ig heavy
746	54	58.1	17	9	ADZ45544	Adz45544	Murine fa	819	54	58.1	136	3	AAB23815	Aab23815	Plasmid P
747	54	58.1	17	9	ADZ45383	Adz45383	Murine fa	820	54	58.1	136	4	AAW67491	Aaw67491	Amino aci
748	54	58.1	17	9	ADZ45391	Adz45391	Murine fa	821	54	58.1	136	5	AAW47629	Aaw47629	Murine MA
749	54	58.1	17	9	AEB33206	Aeb33206	Mouse ant	822	54	58.1	136	5	ABG97806	Abg97806	Mouse Mab
750	54	58.1	17	9	ABP33225	Abp33225	Human imm	823	54	58.1	136	5	ABG35309	Abg35309	Thrombopo
751	54	58.1	17	9	ADP69304	Adp69304	Human lun	824	54	58.1	136	9	AEO06268	Aeo06268	Anti-CD47
752	54	58.1	17	9	AAV56644	Aav56644	Partial P	825	54	58.1	136	9	AE062671	Aeo06271	Anti-CD47
753	54	58.1	102	2	AAV56645	Aav56645	Partial P	826	54	58.1	136	9	AE062671	Aeo06271	Anti-CD47
754	54	58.1	102	2	AAV56645	Aav56645	Partial P	827	54	58.1	136	9	AE062671	Aeo06271	Anti-CD47

828	54	58.1	136	9	AEA06269	Aea06269 Anti-CD47	901	54	58.1	368	9	ADM77074	Adh77074 Heavy cha
829	54	58.1	136	9	AEA06270	Aea06270 Anti-CD47	902	54	58.1	412	4	AA30694	AA30694 A fusion
830	54	58.1	136	9	AEA06265	Aea06265 Anti-CD47	903	54	58.1	412	6	AA39009	AA39009 B9E9 scFv
831	54	58.1	140	1	AA94780	AA94780 2 H7 VH g	904	54	58.1	422	5	ABG31032	ABG31032 Synthetic
832	54	58.1	140	2	AA95215	AA95215 Murine va	905	54	58.1	422	7	ADD25591	ADD25591 Binding d
833	54	58.1	140	2	AAW10242	AAW10242 Heavy cha	906	54	58.1	422	7	ADDM25473	ADDM25473 Binding d
834	54	58.1	140	2	AAW10588	AAW10588 2H7 antib	907	54	58.1	422	7	ADDM42748	ADDM42748 2H7scFv-I
835	54	58.1	140	2	AAW16343	AAW16343 2H7 heavy	908	54	58.1	422	7	AE95416	AE95416 Mouse 2H7
836	54	58.1	140	2	AAW89540	AAW89540 Mouse ant	909	54	58.1	422	4	AE994450	AE994450 Mouse ant
837	54	58.1	140	2	AA989092	AA989092 2H7 heavy	910	54	58.1	423	4	AA30695	AA30695 A fusion
838	54	58.1	140	6	ABR55873	ABR55873 Anti-CD20	911	54	58.1	423	6	ABJ39010	ABJ39010 B9E9 scFv
839	54	58.1	140	6	ABU08394	ABU08394 Murine an	912	54	58.1	426	9	ADY22144	ADY22144 Antibody
840	54	58.1	140	7	ADC66270	ADC66270 Mouse ant	913	54	58.1	426	9	AE95423	AE95423 Mouse 2H7
841	54	58.1	140	7	ADC65027	ADC65027 Immunoglo	914	54	58.1	426	9	AE994457	AE994457 Mouse ant
842	54	58.1	140	7	AD856569	AD856569 Murine im	915	54	58.1	451	8	ADL92472	ADL92472 Antibody
843	54	58.1	140	7	AD873084	AD873084 Murine FU	916	54	58.1	451	8	ADL92473	ADL92473 Improved
844	54	58.1	140	7	AD670661	AD670661 Proteain r	917	54	58.1	451	8	ADN97545	ADN97545 Artificialia
845	54	58.1	140	7	ADJ94616	ADJ94616 Human ant	918	54	58.1	451	8	ADU68155	ADU68155 Novel var
846	54	58.1	140	7	ADJ94618	ADJ94618 Human ant	919	54	58.1	451	8	ADU68154	ADU68154 Novel var
847	54	58.1	140	8	ADN494618	ADN494618 Mature va	920	54	58.1	452	8	ADS33304	ADS33304 Anti-CD20
848	54	58.1	140	8	ADU74410	ADU74410 Mouse ant	921	54	58.1	452	9	ADM03410	ADM03410 Humanized
849	54	58.1	140	9	ADY92492	ADY92492 2B8 heavy	922	54	58.1	452	9	ADM03411	ADM03411 Humanized
850	54	58.1	140	9	ADY98555	ADY98555 Novel chl	923	54	58.1	452	9	AE927728	AE927728 Humanized
851	54	58.1	140	9	ADZ59909	ADZ59909 Glycoprot	924	54	58.1	452	9	AE917638	AE917638 Heavy cha
852	54	58.1	142	3	AAV56708	AAV56708 Amino aci	925	54	58.1	465	2	AA966758	AA966758 Anti-tcoba
853	54	58.1	142	3	AAV56709	AAV56709 Amino aci	926	54	58.1	470	3	AA980826	AA980826 A dimeric
854	54	58.1	142	3	AAV56709	AAV56709 Amino aci	927	54	58.1	470	5	AA927923	AA927923 Human C2B
855	54	58.1	142	3	AAV56709	AAV56709 Amino aci	928	54	58.1	470	6	AB882832	AB882832 Antibody
856	54	58.1	140	9	AA945442	AA945442 Sequence	929	54	58.1	470	9	ADY92496	ADY92496 Humanized
857	54	58.1	140	9	AA945442	AA945442 Sequence	930	54	58.1	470	9	ADY98559	ADY98559 Novel chl
858	54	58.1	140	9	AA945442	AA945442 Sequence	931	54	58.1	471	8	ADP79584	ADP79584 2H7.v16 L
859	54	58.1	140	9	AA945442	AA945442 Sequence	932	54	58.1	471	8	ADP79585	ADP79585 2H7.v31 L
860	54	58.1	140	9	AA945442	AA945442 Sequence	933	54	58.1	471	9	ADM03399	ADM03399 Human ant
861	54	58.1	140	9	AA945442	AA945442 Sequence	934	54	58.1	471	9	ADM03406	ADM03406 Human ant
862	54	58.1	140	9	AA945442	AA945442 Sequence	935	54	58.1	471	9	ADM21319	ADM21319 Mouse ant
863	54	58.1	140	9	AA945442	AA945442 Sequence	936	54	58.1	471	9	ADM21320	ADM21320 Mouse ant
864	54	58.1	140	9	AA945442	AA945442 Sequence	937	54	58.1	471	9	ADM21320	ADM21320 Humanized
865	54	58.1	140	9	AA945442	AA945442 Sequence	938	54	58.1	471	9	ADY62625	ADY62625 Humanized
866	54	58.1	140	9	AA945442	AA945442 Sequence	939	54	58.1	471	9	ABG31031	ABG31031 Synthetic
867	54	58.1	140	9	AA945442	AA945442 Sequence	940	54	58.1	471	9	ADD25472	ADD25472 Binding d
868	54	58.1	140	9	AA945442	AA945442 Sequence	941	54	58.1	471	9	ADD25589	ADD25589 Binding d
869	54	58.1	140	9	AA945442	AA945442 Sequence	942	54	58.1	471	9	ADM42747	ADM42747 2H7-CD154
870	54	58.1	140	9	AA945442	AA945442 Sequence	943	54	58.1	471	9	AE994415	AE994415 Mouse 2H7
871	54	58.1	140	9	AA945442	AA945442 Sequence	944	54	58.1	471	9	AE994449	AE994449 Mouse ant
872	54	58.1	140	9	AA945442	AA945442 Sequence	945	54	58.1	471	9	ADN97549	ADN97549 Artificialia
873	54	58.1	140	9	AA945442	AA945442 Sequence	946	54	58.1	471	9	ADY22142	ADY22142 Antibody
874	54	58.1	140	9	AA945442	AA945442 Sequence	947	54	58.1	471	9	AE994425	AE994425 Mouse 2H7
875	54	58.1	140	9	AA945442	AA945442 Sequence	948	54	58.1	471	9	AE994456	AE994456 Mouse ant
876	54	58.1	140	9	AA945442	AA945442 Sequence	949	54	58.1	471	9	ADY21539	ADY21539 Mature fo
877	54	58.1	140	9	AA945442	AA945442 Sequence	950	54	58.1	471	9	ADZ83598	ADZ83598 CD3 speci
878	54	58.1	140	9	AA945442	AA945442 Sequence	951	54	58.1	471	9	ADZ83596	ADZ83596 CD3 speci
879	54	58.1	140	9	AA945442	AA945442 Sequence	952	54	58.1	471	9	ADZ83600	ADZ83600 CD3 speci
880	54	58.1	140	9	AA945442	AA945442 Sequence	953	54	58.1	471	9	ADY21537	ADY21537 Mature fo
881	54	58.1	140	9	AA945442	AA945442 Sequence	954	54	58.1	471	9	ADY21537	ADY21537 Mature fo
882	54	58.1	140	9	AA945442	AA945442 Sequence	955	54	58.1	471	9	ADY21647	ADY21647 Antibody
883	54	58.1	140	9	AA945442	AA945442 Sequence	956	54	58.1	471	9	AE968722	AE968722 scFv23-ge
884	54	58.1	140	9	AA945442	AA945442 Sequence	957	54	58.1	471	9	ABG31026	ABG31026 Synthetic
885	54	58.1	140	9	AA945442	AA945442 Sequence	958	54	58.1	471	9	ABG31027	ABG31027 Synthetic
886	54	58.1	140	9	AA945442	AA945442 Sequence	959	54	58.1	471	9	ABG31025	ABG31025 Synthetic
887	54	58.1	140	9	AA945442	AA945442 Sequence	960	54	58.1	471	9	ADZ25587	ADZ25587 Binding d
888	54	58.1	140	9	AA945442	AA945442 Sequence	961	54	58.1	471	9	ADZ25454	ADZ25454 Binding d
889	54	58.1	140	9	AA945442	AA945442 Sequence	962	54	58.1	471	9	ADZ25456	ADZ25456 Binding d
890	54	58.1	140	9	AA945442	AA945442 Sequence	963	54	58.1	471	9	ADZ25455	ADZ25455 Binding d
891	54	58.1	140	9	AA945442	AA945442 Sequence	964	54	58.1	471	9	ADM42731	ADM42731 2H7scFv-I
892	54	58.1	140	9	AA945442	AA945442 Sequence	965	54	58.1	471	9	ADM42729	ADM42729 2H7scFv-I
893	54	58.1	140	9	AA945442	AA945442 Sequence	966	54	58.1	471	9	ADM42730	ADM42730 2H7scFv-I
894	54	58.1	140	9	AA945442	AA945442 Sequence	967	54	58.1	471	9	AE955397	AE955397 Mouse hum
895	54	58.1	140	9	AA945442	AA945442 Sequence	968	54	58.1	471	9	AE955398	AE955398 Mouse hum
896	54	58.1	140	9	AA945442	AA945442 Sequence	969	54	58.1	471	9	AE955399	AE955399 Mouse hum
897	54	58.1	140	9	AA945442	AA945442 Sequence	970	54	58.1	471	9	AE994431	AE994431 Mouse ant
898	54	58.1	140	9	AA945442	AA945442 Sequence	971	54	58.1	471	9	AE994433	AE994433 Mouse ant
899	54	58.1	140	9	AA945442	AA945442 Sequence	972	54	58.1	471	9	AE994432	AE994432 Mouse ant
900	54	58.1	140	9	AA945442	AA945442 Sequence	973	54	58.1	471	9	ADD25826	ADD25826 Binding d

CC anti-CD11a antibody MEM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MEM24 had IC50 0.13 nM. The present
 CC sequence represents the heavy chain variable region CDR2 of the humanised
 CC anti-CD11a Ab

SO Sequence 17 AA:

Query Match 100.0%; Score 93; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.5e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPSPDSETRYNQKPKD 17
 |||
 DB 1 MHPSPDSETRYNQKPKD 17

RESULT 3
 ADG38999
 ID ADG38999 standard; peptide; 17 AA.
 AC ADG38999;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Humanised Mouse anti-CD11a antibody heavy chain variable region CDR2.
 XX
 KW Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
 KW VH; cluster of differentiation 11a; mixed lymphocyte response assay;
 KW Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 KW ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 KW psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; prodrug activating enzyme; humanised;
 KW complementarity determining region; CDR.

OS Synthetic.
 OS Mus sp.
 XX
 PN US2003207336-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 28-FEB-2001; 2001US-00795798.
 XX
 PR 27-NOV-1996; 96US-0031971P.
 PR 20-NOV-1997; 97US-00974899.
 PR 20-OCT-1999; 99US-00420745.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-051511/05.
 PT Humanized anti-CD11a antibody useful for treating lymphocyte function-
 PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 XX
 PS Claim 6; SEQ ID NO 11; 43pp; English.

CC The invention relates to a Humanised anti-cluster of differentiation
 CC (CD11a) antibody having specificity to human CD11a I-domain or CD11a with
 CC a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nm) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MEM24 on CD11a. The

CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is a CDR (complementarity determining region) of the
 CC heavy chain variable region (VH) of the humanised mouse anti-CD11a I
 CC domain monoclonal antibody MEM24.

SO Sequence 17 AA:

Query Match 100.0%; Score 93; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.5e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPSPDSETRYNQKPKD 17
 |||
 DB 1 MHPSPDSETRYNQKPKD 17

RESULT 4
 ADR03389
 ID ADR03389 standard; peptide; 17 AA.
 AC ADR03389;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MEM24 CDR-H2 peptide #1.
 XX
 KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain;
 KW VH; murine; human; fusion protein; complementarity determining region;
 KW CDR.

OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX
 PF 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 26; 54pp; English.

CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful

CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MHM24) CDR-H2 peptide. This sequence is used in the exemplification of
 CC the invention.
 CC
 XX Sequence 17 AA;
 SO

Query Match 100.0%; Score 93; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.5e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MHPSDSTRYNQKFKD 17
 |||||
 Db 1 MHPSDSTRYNQKFKD 17

RESULT 5
 AAW62013
 ID AAW62013 standard; peptide; 121 AA.
 AC AAW62013;
 XX
 DT 01-OCT-1998 (first entry)
 DE Heavy chain variable region of humanised anti-CD11a antibody.
 XX
 KW Complementarity determining region; heavy chain variable region;
 KW humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;
 KW human CD11a I domain; MHM24 epitope; alpha subunit;
 KW lymphocyte function-associated antigen 1; LFA-1; immunoassay;
 KW in vivo imaging; diagnosis; CD11a-associated disease.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS
 PN WO9823761-A1.
 XX
 PD 04-JUN-1998.
 XX
 PF 20-OCT-1997; 97WO-US019041.
 XX
 PR 27-NOV-1996; 96US-00757205.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 1998-322737/28.
 PT New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
 PT also to treat conditions such as immunological or inflammatory disease.
 XX
 PS Claim 7; Page 50; 66pp; English.

CC The present sequence represents the heavy chain variable region of a
 CC humanised anti-CD11a antibody that binds specifically to the human CD11a
 CC I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte
 CC function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-
 CC CD11a antibodies are used to determine presence of CD11a in usual
 CC immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-
 CC associated diseases (typically immune responses and inflammation such as
 CC psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,

CC leukaemia, etc
 XX
 XX Sequence 121 AA;
 SO

Query Match 100.0%; Score 93; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MHPSDSTRYNQKFKD 17
 |||||
 Db 50 MHPSDSTRYNQKFKD 66

RESULT 6
 AAW63532
 ID AAW63532 standard; protein; 121 AA.
 AC AAW63532;
 XX
 DT 06-OCT-1998 (first entry)
 DE Humanised MHM24 heavy chain.
 XX
 KW Antibody mutant production; species-dependent antibody; malignancy;
 KW infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KW intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 KW autoimmune disease; transplant rejection; tumour cell invasion;
 KW human immune deficiency virus infection; heavy chain.
 XX
 OS Synthetic.
 OS
 PN WO9823746-A1.
 XX
 PD 04-JUN-1998.
 XX
 PF 29-OCT-1997; 97WO-US020169.
 XX
 PR 27-NOV-1996; 96US-00756150.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 1998-322726/28.
 PT Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in theus monkey(s) of therapeutic antibodies
 PT directed against CD11a.
 XX
 PS Disclosure; Page 55; 71pp; English.

CC This sequence represents the heavy chain of the humanised antibody MHM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 XX
 SO Sequence 121 AA;
 Query Match 100.0%; Score 93; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHPSDSETRYNQKFKD 17
 |||||
 Db 50 MIHPSDSETRYNQKFKD 66

RESULT 7
 AAY82336
 ID AAY82336 standard; protein; 121 AA.

AC AAY82336;

DT 22-JUN-2000 (first entry)

DE Humanised anti-CD11a antibody heavy chain variable region SEQ ID NO:5.

XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 XX antitumour; antiviral; inflammation; immunological response; LFA-1;
 KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KW viral infection; transplant rejection; graft rejection.

XX Homo sapiens.

OS Mus sp.

PN US6037454-A.

PD 14-MAR-2000.

PF 20-NOV-1997; 97US-00974899.

PR 27-NOV-1996; 96US-0031971P.

PA (GETH) GENENTECH INC.

PI Jardieu PM, Preesta LG;

DR WPI; 2000-282241/24.

PT New humanised anti-CD11a antibody, useful for treating or preventing e.g.
 PT inflammation and transplant rejection, contains human heavy variable
 PT region complementarity determining regions.

PS Claim 1; Fig 1; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that
 CC binds specifically to the human CD11a I-domain. The Ab has anti-
 CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
 CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 CC involved in leucocyte adhesion associated with inflammatory and
 CC immunological responses. The Ab are used: (i) optionally when coupled to
 CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
 CC rhinitis, leukaemia, viral infections and many others, also for
 CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine
 CC anti-CD11a antibody MM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MM24 had IC50 0.13 nM. The present
 CC sequence represents the heavy chain variable region of the humanised anti
 CC -CD11a Ab
 XX

SQ Sequence 121 AA;

Query Match 100.0%; Score 93; DB 3; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHPSDSETRYNQKFKD 17
 |||||
 Db 50 MIHPSDSETRYNQKFKD 66

RESULT 8
 ADG38993
 ID ADG38993 standard; protein; 121 AA.

AC ADG38993;

DT 26-FEB-2004 (first entry)

DE Humanised Mouse anti-CD11a antibody heavy chain variable region.

XX Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
 KW VH; cluster of differentiation 11a; mixed lymphocyte response assay;
 KW Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 KW ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 KW psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; prodrug activating enzyme; humanised.

XX Synthetic.

OS Mus sp.

PN US2003207336-A1.

PD 06-NOV-2003.

PF 28-FEB-2001; 2001US-00795798.

PR 27-NOV-1996; 96US-0031971P.

PR 20-NOV-1997; 97US-00974899.

PR 20-OCT-1999; 99US-00420745.

PA (GETH) GENENTECH INC.

PI Jardieu PM, Preesta LG;

DR WPI; 2004-051511/05.

PT Humanised anti-CD11a antibody useful for treating lymphocyte function-
 PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

PS Claim 7; SEQ ID NO 5; 43pp; English.

XX The invention relates to a Humanised anti-cluster of differentiation
 CC (CD11a) antibody having specificity to human CD11a I-domain or CD11a with
 CC a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MM24 on CD11a. The
 CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis; Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is the heavy chain variable region (VH) of the humanised
 CC mouse anti-CD11a I domain monoclonal antibody MM24.

SQ Sequence 121 AA;

Query Match 100.0%; Score 93; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHPDSETRYNOKFKD 17
 |||||||
 Db 50 MIHPDSETRYNOKFKD 66

RESULT 9
 ADK03368
 ID ADK03368 standard; protein, 121 AA.
 XX
 AC ADK03368;
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MHM24 F(ab)-8 antibody variable heavy chain protein.
 XX
 KM CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KM rhinovirus infection; inflammatory skin disease; psoriasis;
 KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculous; sarcoidosis; polymyositis;
 KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KM skin hypersensitivity disorder; poison ivy; poison oak;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 VH; murine; human; fusion protein.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX
 PP 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GETH) GENENTECH INC.
 PI Jardiou PM, Presta LG;
 DR WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 5; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MHM24) F(ab)-8 variable heavy chain protein. This sequence is used in
 CC the exemplification of the invention.

XX
 SQ Sequence 121 AA;

Query Match 100.0%; Score 93; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHPDSETRYNOKFKD 17
 |||||||
 Db 50 MIHPDSETRYNOKFKD 66

RESULT 10
 ADK38458
 ID ADK38458 standard; protein, 121 AA.
 XX
 AC ADK38458;
 DT 24-MAR-2005 (first entry)
 XX
 DE CD11a heavy chain variable region #2.
 XX
 KM monoclonal antibody; CD11a; light-chain variable region;
 KM heavy-chain variable region.
 XX
 OS Homo sapiens.
 XX
 PN CN1439651-A.
 XX
 PD 03-SEP-2003.
 XX
 PP 20-FEB-2002; 2002CN-00110866.
 XX
 PR 20-FEB-2002; 2002CN-00110866.
 XX
 PA (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
 PI Wang H, Wang J;
 DR WPI; 2004-169719/17.
 XX
 PT Recombinant human CD11a monoclonal antibody and its preparation and
 PT medicinal composition.
 XX
 PS Claim 1; Page 14-15; 16pp; Chinese.
 XX
 CC The present invention relates to a recombinant monoclonal antibody for
 CC human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
 CC No.5 in light-chain variable region and the amino acid sequence shown by
 CC SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
 CC bioactivity and the expression in host cell are greatly increased. The
 CC DNA molecule for coding the antibody, its preparation process and the
 CC medicinal composition containing it are also disclosed. The present
 CC sequence represents a heavy chain variable region of human CD11a.
 XX
 SQ Sequence 121 AA;

Query Match 100.0%; Score 93; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHPDSETRYNOKFKD 17
 |||||||
 Db 50 MIHPDSETRYNOKFKD 66

RESULT 11
 ADK80646
 ID ADK80646 standard; protein, 121 AA.
 XX
 AC ADK80646;
 DT 05-MAY-2005 (first entry)

XX Humanized CD11a variable heavy chain amino acid sequence, seq id 6.
 DE Protein purification; leaching; protein A affinity chromatography; CD11a;
 XX antibody.
 KW
 XX
 OS Synthetic.
 XX
 PN US2005038231-A1.
 XX
 PD 17-FEB-2005.
 XX
 PF 24-JUN-2004; 2004US-00877532.
 XX
 PR 28-JUL-2003; 2003US-0490500P.
 XX
 PS (GETH) GENENTECH INC.
 XX
 PI Fahrner RL, Laverdiere A, McDonald PJ, O'Leary RM;
 XX
 DR WPI; 2005-172327/18.
 XX
 PT Purifying a protein, e.g. antibody or immunoadhesin, comprises reducing
 PT the temperature of a composition subjected to protein A affinity
 PT chromatography to 3-20 degrees C, where protein A leaching is reduced.
 XX
 PS Disclosure; SEQ ID NO 6; 27pp; English.
 XX
 CC The invention relates to a method of purifying a protein which comprises
 CC a CH2/CH3 region by protein A affinity chromatography. The method
 CC involves reducing the temperature of a composition comprising the protein
 CC and one or more impurities subjected to protein A affinity chromatography
 CC to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably
 CC the protein is antibody. The antibody is selected from Trastuzumab,
 CC humanized 2C4, humanized CD11a antibody, and humanized VEGF antibody.
 CC Preferably, the antibody binds HER2 antigen, where the antibody is
 CC Trastuzumab or humanized 2C4. The protein is an immunoadhesin.
 CC Specifically a TNF receptor immunoadhesin. The methods are useful for
 CC purifying a protein, which comprises a CH2/CH3 region by protein A
 CC affinity chromatography and for reducing leaching of protein A during
 CC protein A affinity chromatography. The current sequence represents the
 CC variable heavy chain amino acid sequence of CD11a.
 XX
 SQ Sequence 121 AA:
 QY
 DB 1 MHPSDSETRYNOXKFD 17
 |||||
 50 MHPSDSETRYNOXKFD 66

Query Match 100.0%; Score 93; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 8.1e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 ADP11670
 ID ADP11670 standard; protein; 451 AA.
 XX
 AC ADP11670;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE anti-CD11a rhumAb heavy chain amino acid sequence #SEQ ID 4.
 XX
 KW Purifying; target protein; non-affinity purification;
 KW high-performance tangential flow filtration; HPLFF; pharmaceutical;
 KW diagnostic; therapeutic; antibody.
 XX
 OS Synthetic.
 XX
 PN WO2003102132-A2.
 XX
 PD 11-DEC-2003.

XX
 PF 25-APR-2003; 2003WO-US013054.
 XX
 PR 26-APR-2002; 2002US-0375953P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fahrner RL, Pollman D, Lebretton B, Van Reis R;
 XX
 DR WPI; 2004-043096/04.
 XX
 PT Purifying target protein from mixture containing host cell protein
 PT involves subjecting mixture to non-affinity purification, high-
 PT performance tangential flow filtration and isolating purified protein.
 XX
 PS Disclosure; SEQ ID NO 4; 77pp; English.
 XX
 CC The invention relates to a method for purifying a target protein from a
 CC mixture containing a host cell protein. This method comprises subjecting
 CC the mixture to a non-affinity purification followed by high-performance
 CC tangential flow filtration (HPLFF) and isolating the protein in a purity
 CC containing less than 100 parts/million (ppm) of the host cell protein,
 CC where the method of the invention includes no affinity purification
 CC process. The method of the invention is useful for purifying a target
 CC protein from a mixture containing a host cell protein, and is useful for
 CC incorporating the isolated protein into a pharmaceutical formulation.
 CC Proteins purified using the method of the invention are useful in a
 CC pharmaceutical respect, and are also useful in various diagnostic and
 CC therapeutic purposes. The method of the invention is efficient in
 CC purifying a target protein from a mixture containing a host cell protein,
 CC and may also be effectively performed at low cost. The current sequence
 CC represents the anti-CD11a rhumAb heavy chain amino acid sequence. This
 CC particular protein was used to demonstrate the method of the invention.
 XX
 SQ Sequence 451 AA:
 QY
 DB 1 MHPSDSETRYNOXKFD 17
 |||||
 50 MHPSDSETRYNOXKFD 66

Query Match 100.0%; Score 93; DB 8; Length 451;
 Best Local Similarity 100.0%; Pred. No. 3.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 ADR03400
 ID ADR03400 standard; peptide; 17 AA.
 XX
 AC ADR03400;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MEM24 CDR-H2 mutant peptide, SerH55Aan.
 XX
 KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; Rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain;
 KW VH; murine; human; fusion protein; complementarity determining region;
 KW CDR; mutant; mutein.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.

XX		US2004146507-A1.
PN		
PD		29-JUL-2004.
PF		
PR	03-DEC-2003;	2003US-00727737.
XX		
XX	27-NOV-1996;	96US-0031945P.
PR	20-NOV-1997;	97US-00975329.
XX		
PA	(GENETH) GENENTECH INC.	
PI	Jardieu PM,	Presta LG;
XX		
DR	WPI; 2004-552640/53.	
PT	New antibody mutant of a species-dependent antibody, useful for treating	
PT	and preventing infectious diseases, psoriasis, inflammatory bowel	
PT	disease, allergic conditions, autoimmune diseases, or cancer.	
XX		
PS	Example; SEQ ID NO 37; 54pp; English.	
XX		
CC	The present invention relates to an antibody mutant of a species-	
CC	dependent antibody with beneficial properties. The invention is useful	
CC	for treating and preventing infectious diseases such as human	
CC	immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin	
CC	disease such as psoriasis, inflammatory bowel diseases such as Crohn's	
CC	disease and ulcerative colitis, adult respiratory distress syndrome,	
CC	allergic diseases such as eczema and asthma, autoimmune diseases such as	
CC	rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes	
CC	mellitus, Reynaud's syndrome, immunological diseases such as	
CC	tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary	
CC	disease (COPD), CNS inflammatory disorder, skin hypersensitivity	
CC	disorders such as poison ivy and poison oak, B-cell malignancies such as	
CC	chronic lymphocytic leukemia and hairy cell leukaemia, graft versus host	
CC	disease and cancer. The invention is also useful in gene therapy. The	
CC	present sequence is humanised murine anti-human CD14 monoclonal antibody	
CC	(MHM24) CDR-H2 mutant peptide. This sequence is used in the	
CC	exemplification of the invention.	
XX		
SQ	Sequence 17 AA:	
	Query Match	96.8%; Score 90; DB 8; Length 17;
	Best Local Similarity	94.1%; Pred. No. 2.8e-08;
	Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0	
OY	1 MIHPSPDETTRYNOKPKD 17	
	:	
Db	1 MIHPSPDETTRYNOKFKD 17	
	:	
	RESULT 14	
	ADR03399 .	
ID	ADR03399 standard; peptide; 17 AA.	
XX		
AC	ADR03399;	
XX		
DT	21-OCT-2004 (first entry)	
XX		
DE	Humanised MHM24 CDR-H2 mutant peptide, SerH55Ala.	
XX		
KW	CD14 antibody; human immunodeficiency virus infection; HIV infection;	
KW	rhinovirus infection; inflammatory skin disease; psoriasis;	
KW	inflammatory bowel disease; Crohn's disease; ulcerative colitis;	
KW	adult respiratory distress syndrome; allergic disease; eczema; asthma;	
KW	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;	
KW	SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;	
KW	tuberculosis; sarcoidosis; polymyositis;	
KW	chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;	
KW	skin hypersensitivity disorder; poison ivy; poison oak;	
KW	B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;	
KW	graft versus host disease; cancer; gene therapy;	
KW	murine anti-human CD14 monoclonal antibody; MHM24; variable heavy chain;	

KW	VH:	murine; human; fusion protein; complementarity determining region;
KM	CDR:	mutant; mutein.
XX		
OS	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
XX		
PN	US2004146507-A1.	
XX		
PD	29-JUL-2004.	
XX		
PF	03-DEC-2003; 2003US-00727737.	
XX		
PR	27-NOV-1996; 96US-0031945P.	
PR	20-NOV-1997; 97US-00975329.	
XX		
PA	(GETH) GENENTECH INC.	
PI	Jardieu PM, Presta LG;	
DR	WPI; 2004-552640/53.	
XX		
PT	New antibody mutant of a species-dependent antibody, useful for treating and preventing infectious diseases, psoriasis, inflammatory bowel disease, allergic conditions, autoimmune diseases, or cancer.	
PS	Example; SEQ ID NO 36; 54pp; English.	
XX		
CC	The present invention relates to an antibody mutant of a species-dependent antibody with beneficial properties. The invention is useful for treating and preventing infectious diseases such as human immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin disease such as psoriasis, inflammatory bowel diseases such as Crohn's disease and ulcerative colitis, adult respiratory distress syndrome, allergic diseases such as eczema and asthma, autoimmune diseases such as rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes mellitus, Reynaud's syndrome, immunological diseases such as tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary disease (COPD), CNS inflammatory disorder, skin hypersensitivity disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is humanised murine anti-human CD1a monoclonal antibody (MHM24) CDR-H2 mutant peptide. This sequence is used in the exemplification of the invention.	
SO	Sequence 17 AA;	
Query Match	96.8%; Score 90; DB 8; Length 17;	
Best Local Similarity	94.1%; Pred. No. 2.8e-08;	
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
OY	1 MIHPDSSTRYNOKFD 17 :	
Db	1 MIHPSDAETRYNOKFD 17	
RESULT 15		
ADR03397		
ID	ADR03397 standard; peptide; 17 AA.	
AC	ADR03397;	
XX		
DT	21-OCT-2004 (first entry)	
XX		
DE	Humanised MHM24 CDR-H2 mutant peptide, Ser53Ala.	
XX		
KW	CD1a antibody; human immunodeficiency virus infection; HIV infection;	
KM	rhinovirus infection; inflammatory skin disease; psoriasis;	
KW	inflammatory bowel disease; Crohn's disease; ulcerative colitis;	
KM	adult respiratory distress syndrome; allergic disease; eczema; asthma;	
KW	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;	
KW	SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;	

KM	tuberculosis; sarcoidosis; polymyositis;				
KM	chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;				
KM	skin hypersensitivity disorder; poison ivy; poison oak;				
KM	B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;				
KM	graft versus host disease; cancer; gene therapy;				
KM	murine anti-human CD1a monoclonal antibody; MHM24; variable heavy chain;				
KM	VH; murine; human; fusion protein; complementarity determining region;				
KM	CDR; mutant; mutein.				
OS	Mus sp.				
OS	Homo sapiens.				
OS	Chimeric.				
XX	US2004146507-A1.				
XX	29-JUL-2004.				
XX	03-DEC-2003; 2003US-00727737.				
XX	27-NOV-1996; 96US-0031945P.				
XX	20-NOV-1997; 97US-00975329.				
XX	(GETH) GENENTECH INC.				
XX	Jardieu PM, Presta LG;				
XX	WPI; 2004-552640/53.				
XX	New antibody mutant of a species-dependent antibody, useful for treating				
XX	and preventing infectious diseases, psoriasis, inflammatory bowel				
XX	disease, allergic conditions, autoimmune diseases, or cancer.				
XX	Example; SEQ ID NO 34; 54pp; English.				
XX	The present invention relates to an antibody mutant of a species-				
XX	dependent antibody with beneficial properties. The invention is useful				
XX	for treating and preventing infectious diseases such as human				
XX	immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin				
XX	disease such as psoriasis, inflammatory bowel diseases such as Crohn's				
XX	disease and ulcerative colitis, adult respiratory distress syndrome,				
XX	allergic diseases such as eczema and asthma, autoimmune diseases such as				
XX	rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes				
XX	mellitus, Reynaud's syndrome, immunological diseases such as				
XX	tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary				
XX	disease (COPD), CNS inflammatory disorder, skin hypersensitivity				
XX	disorders such as poison ivy and poison oak, B-cell malignancies such as				
XX	chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host				
XX	disease and cancer. The invention is also useful in gene therapy. The				
XX	present sequence is humanised murine anti-human CD1a monoclonal antibody				
XX	(MHM24) CDR-H2 mutant peptide. This sequence is used in the				
XX	exemplification of the invention.				
XX	Sequence 17 AA:				
XX					
QY	1 MTHPSDSETRYNOKFPD 17				
QY	:				
Db	1 MTHPADSETRYNOKFPD 17				
XX					
XX	Query Match	96.8%;	Score 90;	DB 8;	Length 17;
XX	Best Local Similarity	94.1%;	Pred. No. 2.8e-08;		
XX	Matches 16; Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0	
XX	RESULT 16				
XX	ADR03401				
XX	ADR03401 standard; peptide; 17 AA.				
XX	ADR03401;				
XX	21-OCT-2004 (first entry)				
XX	Humanised MHM24 CDR-H2 mutant peptide, SerH55Gln.				
XX					

```

KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
KW rhinovirus infection; inflammatory skin disease; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
KW tuberculosis; sarcoidosis; polymyositis;
KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KW skin hypersensitivity disorder; poison ivy; poison oak; hairy cell leukemia;
KW B-cell malignancy; chronic lymphocytic leukemia; hairy cell leukemia;
KW graft versus host disease; cancer; gene therapy;
KW murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
KW VH; murine; human; fusion protein; complementarity determining region;
KW CDR; mutant; mutein.
XX
XX Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
XX US2004146507-A1.
PN 29-JUL-2004.
PD
PE 03-DEC-2003; 2003US-00727737.
XX
XX 27-NOV-1996; 96US-0031945P.
PR 20-NOV-1997; 97US-00975329.
XX
XX (GERTH ) GENENTECH INC.
PA
XX
XX Jardieu PM, Presta LG;
PI
XX WPI; 2004-552640/53.
XX
XX New antibody mutant of a species-dependent antibody, useful for treating
PT and preventing infectious diseases, psoriasis, inflammatory bowel
PT disease, allergic conditions, autoimmune diseases, or cancer.
XX
XX Example; SEQ ID NO 38; 54pp; English.
PS
XX
XX The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC diseases such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such as
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as
CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC disorders such as poison ivy and poison oak, B-cell malignancies such as
CC chronic lymphocytic leukemia and hairy cell leukemia, graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is humanised murine anti-human CD11a monoclonal antibody
CC (MHM24) CDR-H2 mutant peptide. This sequence is used in the
CC exemplification of the invention.
XX
XX
SQ Sequence 17 AA;
XX
XX Query Match 95.7%; Score 89; DB 8; Length 17;
XX Best Local Similarity 94.1%; Pred. No. 4.2e-08;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MIHPSDSTRYNQKFKD 17
XX ||||| ||||| |||||
XX 1 MIHPSDQETRYNQKFKD 17
XX
XX RESULT 17
XX ID ADR03403 standard; peptide; 17 AA.
XX

```

AC ADR03403;
 XX 21-OCT-2004 (first entry)
 XX
 DE Humanised MM24 CDR-H2 mutant peptide, ARGH58A1a.
 XX
 KM CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KM rhinovirus infection; inflammatory skin disease; psoriasis;
 KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculosis; sarcoidosis; polymyositis;
 KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KM skin hypersensitivity disorder; poison ivy; poison oak;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD11a monoclonal antibody; MM24; variable heavy chain;
 KM VH; murine; human; fusion protein; complementarity determining region;
 KM CDR; mutant; mutein.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX
 PF 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GERTH) GENENTECH INC.
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 40; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MM24) CDR-H2 mutant peptide. This sequence is used in the
 CC exemplification of the invention.
 CC
 XX Sequence 17 AA;
 SQ
 Query Match 93.5%; Score 87; DB 8; Length 17;
 Best Local Similarity 94.1%; Pred. No. 9.2e-08;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 MIHPDSSTRYNOKRFD 17
 |||||
 Db 1 MIHPDSSTRYNOKRFD 17

RESULT 18
 ADR03402
 ID ADR03402 standard; peptide, 17 AA.
 XX
 AC ADR03402;
 XX
 DE 21-OCT-2004 (first entry)
 XX
 KM Humanised MM24 CDR-H2 mutant peptide, GLUH56A1a.
 XX
 KM CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KM rhinovirus infection; inflammatory skin disease; psoriasis;
 KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculosis; sarcoidosis; polymyositis;
 KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KM skin hypersensitivity disorder; poison ivy; poison oak;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD11a monoclonal antibody; MM24; variable heavy chain;
 KM VH; murine; human; fusion protein; complementarity determining region;
 KM CDR; mutant; mutein.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX
 PF 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GERTH) GENENTECH INC.
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 39; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MM24) CDR-H2 mutant peptide. This sequence is used in the
 CC exemplification of the invention.
 CC
 XX Sequence 17 AA;
 SQ
 Query Match 93.5%; Score 87; DB 8; Length 17;

Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKFKD 17
Db 1 MIHPDSETRYNOKFKD 17

RESULT 19

ADRO3393
ID ADRO3393 standard; peptide; 17 AA.

AC ADR03393;

DT 21-OCT-2004 (first entry)

DE Humanised MM24 CDR-H2 mutant peptide, H2A2.

KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
KW rhinovirus infection; inflammatory skin disease; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
KW tuberculosis; sarcoidosis; polymyositis;
KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KW skin hypersensitivity disorder; poison ivy; poison oak;
KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
KW graft versus host disease; cancer; gene therapy;
KW murine anti-human CD11a monoclonal antibody; MM24; variable heavy chain;
KW VH; murine; human; fusion protein; complementarity determining region;
KW CDR; mutant; mutein.

OS Mus sp.
OS Homo sapiens.
OS Chimeric.

XX US2004146507-A1.

PD 29-JUL-2004.

PF 03-DEC-2003; 2003US-00727737.

XX 27-NOV-1996; 96US-0031945P.

PR 20-NOV-1997; 97US-00975329.

XX (GETH) GENENTECH INC.

PA Jardieu PM, Presta LG;

PI WPI; 2004-552640/53.

DR New antibody mutant of a species-dependent antibody, useful for treating
XX and preventing infectious diseases, psoriasis, inflammatory bowel
XX disease, allergic conditions, autoimmune diseases, or cancer.

PS Example; SEQ ID NO 30; 54pp; English.

CC The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such as
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as
CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC disorders such as poison ivy and poison oak, B-cell malignancies such as
CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is humanised murine anti-human CD11a monoclonal antibody

CC (MM24) CDR-H2 mutant peptide. This sequence is used in the
CC exemplification of the invention.

XX Sequence 17 AA;

Qy Query Match 93.5%; Score 87; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 9.2e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKFKD 17
Db 1 MIHPDSETRYNOKFKD 17

RESULT 20

ADRO3405
ID ADRO3405 standard; peptide; 17 AA.

AC ADR03405;

DT 21-OCT-2004 (first entry)

DE Humanised MM24 CDR-H2 mutant peptide, LysH62A1a.

KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
KW rhinovirus infection; inflammatory skin disease; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
KW tuberculosis; sarcoidosis; polymyositis;
KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KW skin hypersensitivity disorder; poison ivy; poison oak;
KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
KW graft versus host disease; cancer; gene therapy;
KW murine anti-human CD11a monoclonal antibody; MM24; variable heavy chain;
KW VH; murine; human; fusion protein; complementarity determining region;
KW CDR; mutant; mutein.

OS Mus sp.
OS Homo sapiens.
OS Chimeric.

XX US2004146507-A1.

PD 29-JUL-2004.

PF 03-DEC-2003; 2003US-00727737.

XX 27-NOV-1996; 96US-0031945P.

PR 20-NOV-1997; 97US-00975329.

XX (GETH) GENENTECH INC.

PA Jardieu PM, Presta LG;

PI WPI; 2004-552640/53.

DR New antibody mutant of a species-dependent antibody, useful for treating
XX and preventing infectious diseases, psoriasis, inflammatory bowel
XX disease, allergic conditions, autoimmune diseases, or cancer.

PS Example; SEQ ID NO 42; 54pp; English.

CC The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such as
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as

CC	tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC	disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC	disorders such as poison ivy and poison oak; B-cell malignancies such as
CC	chronic lymphocytic leukemia and hairy cell leukaemia, graft versus host
CC	disease and cancer. The invention is also useful in gene therapy. The
CC	present sequence is humanised murine anti-human CD1a monoclonal antibody
CC	(MHM24) CDR-H2 mutant peptide. This sequence is used in the
CC	exemplification of the invention.
XX	
SQ	Sequence 17 AA:
Query Match	93.5%; Score 87; DB 8; Length 17;
Beech Local Similarity	94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative	0; Mismatches 1; Indels 0; Gaps 0
OY	1 MHPSDSERTYNQKFKD 17
Db	1 MHPSDSERTYNQAFKD 17
RESULT 21	
ID	ADRO3404
XX	ADRO3404 standard; peptide; 17 AA.
AC	ADRO3404;
DT	21-OCT-2004 (first entry)
DE	Humanised MHM24 CDR-H2 mutant peptide, GlNH61Aa.
XX	
KW	CD1a antibody; human immunodeficiency virus infection; HIV infection;
KW	rhinovirus infection; inflammatory skin disease; psoriasis;
KW	inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW	adult respiratory distress syndrome; allergic disease; eczema; asthma;
KW	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW	SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
KW	tuberculosis; sarcoidosis; polyomyelitis;
KW	chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KW	skin hypersensitivity disorder; poison ivy; poison oak;
KW	B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
KW	graft versus host disease; cancer; gene therapy;
KW	murine anti-human CD1a monoclonal antibody; MHM24; variable heavy chain,
KW	VH; murine; human; fusion protein; complementarity determining region;
KW	CDR; mutant; mutain.
XX	
OS	Mus sp.
OS	Homo sapiens.
OS	Chimeric.
PN	US2004146507-A1.
PD	29-JUL-2004.
Pf	03-DEC-2003; 2003US-00727737.
XX	
XX	27-NOV-1996; 96US-003194SP.
PR	20-NOV-1997; 97US-00975329.
XX	
PA	(GERT) GENENTECH INC.
PI	Jardieu PM, Presta IG;
DR	WPI; 2004-552640/53.
PT	New antibody mutant of a species-dependent antibody, useful for treating
PT	and preventing infectious diseases, psoriasis, inflammatory bowel
PT	disease, allergic conditions, autoimmune diseases, or cancer.
XX	
PS	Example; SEQ ID NO 41: 54pp; English.
XX	
CC	The present invention relates to an antibody mutant of a species-
CC	dependent antibody with beneficial properties. The invention is useful
CC	for treating and preventing infectious diseases such as human

CC		immunodeficiency virus (HIV) and rhinovirus infections; inflammatory skin
CC		disease such as psoriasis; inflammatory bowel diseases such as Crohn's
CC		disease and ulcerative colitis; adult respiratory distress syndrome;
CC		allergic diseases such as eczema and asthma; autoimmune diseases such as
CC		rheumatoid arthritis; systemic lupus erythematosus (SLE); diabetes
CC		mellitus; Reynaud's syndrome; immunological diseases such as
CC		tuberculosis; sarcoidosis; polymyositis and chronic obstructive pulmonary
CC		disease (COPD); CNS inflammatory disorder; skin hypersensitivity
CC		disorders such as poison ivy and poison oak; B-cell malignancies such as
CC		chronic lymphocytic leukaemia and hairy cell leukaemia; graft versus host
CC		disease and cancer. The invention is also useful in gene therapy. The
CC		present sequence is humanised murine anti-human CD1a monoclonal antibody
CC		(MHM24) CDR-H2 mutant peptide. This sequence is used in the
CC		exemplification of the invention.
XX		
SQ	Sequence 17 AA:	
OY		
Query Match	93.5%; Score 87; DB 8; Length 17;	
Best Local Similarity	94.1%; Pred. No. 9.2e-08;	
Matches 16; Conservative	0; Mismatches 1; Indels 0; Gaps 0	
Db	1 MHPSDETTRYNQKFXD 17 1 MHPSDETTRYNAKFXD 17	
RESULT 22		
ADRO3406		
ID	ADRO3406 standard; peptide; 17 AA.	
AC	ADRO3406;	
XX		
DT	21-OCT-2004 (first entry)	
XX		
DE	Humanised MHM24 CDR-H2 mutant peptide, LysH64Ala.	
XX		
KW	CD1a antibody; human immunodeficiency virus infection; HTV infection;	
KW	rhinovirus infection; inflammatory skin disease; psoriasis;	
KW	inflammatory bowel disease; Crohn's disease; ulcerative colitis;	
KW	adult respiratory distress syndrome; allergic disease; eczema; asthma;	
KW	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;	
KW	SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;	
KW	tuberculosis; sarcoidosis; polymyositis;	
KW	chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;	
KW	skin hypersensitivity disorder; poison ivy; poison oak;	
KW	B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;	
KW	graft versus host disease; cancer; gene therapy;	
KW	murine anti-human CD1a monoclonal antibody; MHM24; variable heavy chain;	
KW	VH; murine; human; fusion protein; complementarity determining region;	
KW	CDR; mutant; mutlein.	
XX		
OS	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
PX	US2004146507-A1.	
PX		
PD	29-JUL-2004.	
PX		
PF	03-DEC-2003; 2003US-00727737.	
PX		
PR	27-NOV-1996; 96US-0031945P.	
PR	20-NOV-1997; 97US-00975329.	
PX		
PA	(GETH) GENENTECH INC.	
PX		
P1	Jardieu PM, Presta LG;	
DR	WPI; 2004-552640/53.	
PT	New antibody mutant of a species-dependent antibody, useful for treating	
PT	and preventing infectious diseases; psoriasis, inflammatory bowel	
PT	disease, allergic conditions, autoimmune disease, or cancer.	

XX Example; SEQ ID NO 43; 54bp; English.

CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MHM24) CDR-H2 mutant peptide. This sequence is used in the
 CC exemplification of the invention.

XX Sequence 17 AA:

Query Match 93.5%; Score 87; DB 8; Length 17;
 Best Local Similarity 94.1%; Pred. No. 9.2e-08;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNQKFKD 17
 DB 1 MHPSDSETRYNQKFKD 17

RESULT 23

ADRO3407 standard; peptide; 17 AA.

AC ADRO3407;

DT 21-OCT-2004 (first entry)

DE Humanised MHM24 CDR-H2 mutant peptide, AepH65A1a.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 KW VH; murine; human; fusion protein; complementarity determining region;
 KW CDR; mutant; mutein.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

PN US2004146507-A1.

PD 29-JUL-2004.

PF 03-DEC-2003; 2003US-00727737.

PR 27-NOV-1996; 96US-0031945P.

PR 20-NOV-1997; 97US-00975329.

PA (GERTH) GENENTECH INC.
 PI Jardieu PM, Presta LG;

XX WPI; 2004-552640/53.

XX New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.

PS Example; SEQ ID NO 44; 54bp; English.

CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MHM24) CDR-H2 mutant peptide. This sequence is used in the
 CC exemplification of the invention.

XX Sequence 17 AA:

Query Match 93.5%; Score 87; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.2e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNQKFK 16
 DB 1 MHPSDSETRYNQKFK 16

RESULT 24

ADRO3398 standard; peptide; 17 AA.

AC ADRO3398;

DT 21-OCT-2004 (first entry)

DE Humanised MHM24 CDR-H2 mutant peptide, AepH54A1a.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 KW VH; murine; human; fusion protein; complementarity determining region;
 KW CDR; mutant; mutein.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

PN US2004146507-A1.

PD 29-JUL-2004.

PF 03-DEC-2003; 2003US-00727737.

PR 27-NOV-1996; 96US-0031945P.
PR 20-NOV-1997; 97US-00975329.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardiou PM, Presta LG;
XX
DR WPI, 2004-552640/53.
XX
PT New antibody mutant of a species-dependent antibody, useful for treating
PT and preventing infectious diseases, psoriasis, inflammatory bowel
PT disease, allergic conditions, autoimmune diseases, or cancer.
XX
PS Example; SEQ ID NO 35; 54pp; English.
XX
CC The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such as
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as
CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC disorders such as poison ivy and poison oak, B-cell malignancies such as
CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is humanised murine anti-human CD11a monoclonal antibody
CC (MHM24) CDR-H2 mutant peptide. This sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 17 AA;
OY
Query Match 91.4%; Score 85; DB 8; Length 17;
Best Local Similarity 94.1%; Pred. No. 2e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 MIHPSDSETRYNQKFKD 17
1 MIHPSASETRYNQKFKD 17
RESULT 25
ADU87697
ID ADU87697 standard; peptide; 17 AA.
XX
AC ADU87697;
XX
DT 10-FEB-2005 (first entry)
XX
DE Mouse Luc90 heavy chain variable region, CDR2.
XX
XX Antibody; CS1; SLAMF7; immunoglobulin;
XX pharmaceutical; antibody-dependent cellular cytotoxicity;
XX Fc gamma R receptor; cell proliferation; leukocyte; cancer;
XX multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
XX macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
XX autoimmune disease; inflammatory bowel disease;
XX systemic lupus erythematosus; cytostatic; immunosuppressive;
XX antineoplastic; gastrointestinal-gen.; dermatological; luc90;
XX heavy chain variable region; complementarity determining region; CDR.
OS Mus sp.
XX
XX WO2004100898-A2.
XX
XX 25-NOV-2004.
XX
XX 10-MAY-2004; 2004WO-US014866.
XX
XX 08-MAY-2003; 2003US-0469211P.
PR

PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Williams M, Tso YJ, Landolfi NF;
XX
XX WPI, 2004-821790/81.
XX
DR
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
XX
PS Claim 12; SEQ ID NO 10; 15pp; English.
XX
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a Fc gamma R receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc90 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc90 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenström's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents a CDR from a CS1 antibody.
XX
SQ Sequence 17 AA;
OY
Query Match 91.4%; Score 85; DB 8; Length 17;
Best Local Similarity 94.1%; Pred. No. 2e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1 MIHPSDSETRYNQKFKD 17
1 MIHPSASETRYNQKFKD 17
RESULT 26
AAW01579
ID AAW01579 standard; protein; 118 AA.
XX
XX
AC AAW01579;
XX
XX 22-AUG-1997 (first entry)
DT

```

XX DE Lead binding Mab 10G5 heavy chain variable region.
XX XX
XX XX Monoclonal antibody; Pd fragment; lead cation; perfume; cosmetic;
XX KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
XX KW heavy metal.
XX OS
XX OS Mus musculus.
XX PN WO9639518-A1.
XX PD 12-DEC-1996.
XX XX
XX PF 05-JUN-1996; 96WO-US009258.
XX XX
XX PR 05-JUN-1995; 95US-00462798.
XX PR 10-OCT-1995; 95US-00541373.
XX XX
XX PA (BION-) BIONEERASKA INC.
XX XX
XX PI Wylie DE, Lopez O, Murray PJ;
XX XX WPI; 1997-043140/04.
XX DR N-PSDB; AAT58253.
XX XX
XX PT DNA encoding heavy metal binding polypeptide sequences - used for
XX PT detecting, removing, adding or neutralising heavy metals, such as lead
XX PT cations.
XX PS
XX PS Claim 12; Page 61; 125pp; English.
XX CC
XX CC The present sequence represents the heavy chain variable region for
XX CC monoclonal antibody (Mab) 10G5, which immunoreacts with a lead cation.
XX CC The sequence was derived from RNA isolated from mouse hybridoma cells.
XX CC The protein can be used for binding heavy metals, such as lead cations.
XX CC It can be used for detecting, removing, adding or neutralising the heavy
XX CC metals in biological and inanimate systems. It can be used in e.g.
XX CC aqueous liquid systems, in biological or environmental systems or in such
XX CC compositions as perfumes, cosmetics, pharmaceuticals, health care
XX CC products, skin treatment products, pesticides, herbicides, solvents used
XX CC in the production of semi-conductor and integrated circuit components and
XX CC production materials for electronic components. The products can provide
XX CC for applications involving minute amounts of specific heavy metals
XX XX
XX SQ Sequence 118 AA;
XX
XX Query Match 91.4%; Score 85; DB 2; Length 118;
XX Best Local Similarity 94.1%; Pred. No. 1.9e-06;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MHPDSETRYNOKFXD 17
XX |||||
XX DB 50 MHPDSETRYNOKFXD 66
XX
XX RESULT 27
XX ID AAM01576 standard; protein; 118 AA.
XX XX
XX AC AAM01576;
XX XX
XX DT 22-AUG-1997 (first entry)
XX DE Lead binding Mab 6B11 heavy chain variable region.
XX XX
XX KW Monoclonal antibody; Pd fragment; lead cation; perfume; cosmetic;
XX KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
XX KW heavy metal.
XX XX
XX OS Mus musculus.
XX OS
XX PN WO9639518-A1.
XX XX

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XX PD 12-DEC-1996.
XX XX
XX PF 05-JUN-1996; 96WO-US009258.
XX XX
XX PR 05-JUN-1995; 95US-00462798.
XX PR 10-OCT-1995; 95US-00541373.
XX XX
XX PA (BION-) BIONEERASKA INC.
XX XX
XX PI Wylie DE, Lopez O, Murray PJ;
XX XX WPI; 1997-043140/04.
XX DR N-PSDB; AAT58250.
XX XX
XX PT DNA encoding heavy metal binding polypeptide sequences - used for
XX PT detecting, removing, adding or neutralising heavy metals, such as lead
XX PT cations.
XX PS
XX PS Claim 12; Page 56; 125pp; English.
XX CC
XX CC The present sequence represents the heavy chain variable region for
XX CC monoclonal antibody (Mab) 6B11, which immunoreacts with a lead cation.
XX CC The sequence was derived from RNA isolated from mouse hybridoma cells.
XX CC The protein can be used for binding heavy metals, such as lead cations.
XX CC It can be used for detecting, removing, adding or neutralising the heavy
XX CC metals in biological and inanimate systems. It can be used in e.g.
XX CC aqueous liquid systems, in biological or environmental systems or in such
XX CC compositions as perfumes, cosmetics, pharmaceuticals, health care
XX CC products, skin treatment products, pesticides, herbicides, solvents used
XX CC in the production of semi-conductor and integrated circuit components and
XX CC production materials for electronic components. The products can provide
XX CC for applications involving minute amounts of specific heavy metals
XX XX
XX SQ Sequence 118 AA;
XX
XX Query Match 91.4%; Score 85; DB 2; Length 118;
XX Best Local Similarity 94.1%; Pred. No. 1.9e-06;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MHPDSETRYNOKFXD 17
XX |||||
XX DB 50 MHPDSETRYNOKFXD 66
XX
XX RESULT 28
XX ID ADG25812 standard; protein; 119 AA.
XX XX
XX AC ADG25812;
XX XX
XX DT 11-MAR-2004 (first entry)
XX DE Anti-CD30 monoclonal antibody VH variable region T427 SEQ ID NO.12.
XX XX
XX KW antibody; CD30; anti-CD30 antibody; cytostatic; gene therapy; cancer.
XX KW Synthetic.
XX OS
XX OS WO2003104432-A2.
XX PN
XX PD 18-DEC-2003.
XX PF 09-JUN-2003; 2003WO-US018373.
XX XX
XX PR 07-JUN-2002; 2002US-0387293P.
XX PR 16-SEP-2002; 2002US-0411032P.
XX XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Pastan IH, Nagata S, Onda M, Numata Y, Santora K, Beers R;
XX PI Kreitman R, Sinha A;
XX DR WPI; 2004-062352/06.
XX

```

XX New antibody that binds specifically to a stalk of CD30 of a cell, or to
PT an epitope destroyed upon cleavage of soluble CD30 (sCD30) from intact
PT CD30, useful for inhibiting the growth of a CD30+ cancer cell.
XX
PS Claim 66; SEQ ID NO 12; 102pp; English.
XX
CC The present invention describes an isolated antibody that binds
CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed
CC upon cleavage of soluble CD30 (sCD30) from intact CD30. Also described:
CC (1) a composition comprising the antibody conjugated or fused to a
CC therapeutic part; (2) a nucleic acid encoding an antibody that binds
CC specifically to a stalk of CD30 of a cell, or to an epitope destroyed
CC upon cleavage of sCD30 from intact CD30; (3) an expression vector
CC comprising the nucleic acid operably linked to a promoter; (4) inhibiting
CC growth of a CD30+ cancer cell; (5) detecting the presence of a CD30+ cell
CC in a biological sample; (6) a host cell expressing the isolated nucleic
CC acid encoding the antibody having variable heavy and variable light
CC chains; and (7) a kit for detecting the presence of a CD30+ cancer cell
CC in a biological sample comprising a container and an anti-CD30 antibody.
CC An anti-CD30 antibody has cytostatic activity, and can be used in gene
CC therapy. The anti-CD30 antibody that binds specifically to a stalk of
CC CD30 of a cell, or to an epitope destroyed upon cleavage of sCD30 from
CC intact CD30 is useful for the manufacture of a medicament for inhibiting
CC the growth of a CD30+ cancer cell. The present sequence is used in the
CC exemplification of the present invention.
XX
SQ Sequence 119 AA;

Query Match 91.4%; Score 85; DB 8; Length 119;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIHPDSETRVNOKFKD 17
| | | | | | | | | | | | | | | | | | | |
Db 50 MIHPDSETRVNOKFKD 66

RESULT 29
ADU87690
ID ADU87690 standard; protein; 120 AA.
XX
AC ADU87690;
XX
DT 10-FEB-2005 (first entry)
XX
DE Mouse Luc90 heavy chain variable region.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW Fc gamma receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; Luc90;
KW heavy chain variable region.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX

PI Williams M, Tso YJ, Landolfi NF;
XX WPI, 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer; myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 12; SEQ ID NO 3; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a Fc gamma receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc3 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc3 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenström's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents a CS1 antibody.
XX
SQ Sequence 120 AA;

Query Match 91.4%; Score 85; DB 8; Length 120;
Best Local Similarity 94.1%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIHPDSETRVNOKFKD 17
| | | | | | | | | | | | | | | | | | | |
Db 50 MIHPDSETRVNOKFKD 66

RESULT 30
AAW63531
ID AAW63531 standard; protein; 121 AA.
XX
AC AAW63531;
XX
DT 06-OCT-1998 (first entry)
XX
DE Murine M24 heavy chain.
XX
KW Antibody mutant production; species-dependent antibody; malignancy;
KW infection; haematopoiesis; lymphocyte function-associated antigen-1;
KW intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
KW

KM autoimmune disease; transplant rejection; tumour cell invasion;
 XX human immune deficiency virus infection; heavy chain.
 XX Mus sp.
 XX WO9823746-A1.
 XX 04-JUN-1998.
 XX 29-OCT-1997; 97WO-US020169.
 XX 27-NOV-1996; 96US-00756150.
 XX (GENTH) GENENTECH INC.
 XX Jardiou PM, Presta LG;
 XX WPI; 1998-322726/28.
 XX Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD11a.
 XX PS
 XX Disclosure; Page 54; 71pp; English.
 XX This sequence represents the heavy chain of the murine antibody MHM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 XX SQ
 XX Sequence 121 AA;
 XX
 XX Query Match 91.4%; Score 85; DB 2; Length 121;
 XX Best Local Similarity 94.1%; Pred. No. 2e-06;
 XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MHPSDSETRYNQKFXD 17
 DB 50 MHPSDSETRYNQKFXD 66
 XX
 XX RESULT 31
 XX ID AAY82346 standard; protein; 121 AA.
 XX AC AAY82346;
 XX DT 22-JUN-2000 (first entry)
 XX DE Murine MHM24 heavy chain amino acid sequence SEQ ID NO.4.
 XX KM Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 XX KM antitumour; antiviral; inflammation; immunological response; LFA-1;
 XX KM lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 XX KM inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 XX KM viral infection; transplant rejection; graft rejection.
 XX Mus sp.
 XX OS US6037454-A.
 XX PN

XX 14-MAR-2000.
 PD 20-NOV-1997; 97US-00974899.
 XX 27-NOV-1996; 96US-0031971P.
 XX (GENTH) GENENTECH INC.
 XX Jardiou PM, Presta LG;
 XX WPI; 2000-282241/24.
 XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 PT inflammation and transplant rejection, contains human heavy variable
 PT region complementarily determining regions.
 XX Example; Fig 1; 38pp; English.
 XX PS
 XX The present invention describes a humanised anti-CD11a antibody (Ab) that
 CC binds specifically to the human CD11a I-domain. The Ab has anti-
 CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
 CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 CC involved in leucocyte adhesion associated with inflammatory and
 CC immunological responses. The Ab are used: (i) optionally when coupled to
 CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
 CC rhinitis, leukaemia, viral infections and many others, also for
 CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine
 CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanised version of MHM24 had IC50 0.13 nM. The present
 CC sequence represents the amino acid sequence of murine MHM24 heavy chain,
 CC which is used in the exemplification of the present invention
 XX SQ
 XX Sequence 121 AA;
 XX
 XX Query Match 91.4%; Score 85; DB 3; Length 121;
 XX Best Local Similarity 94.1%; Pred. No. 2e-06;
 XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MHPSDSETRYNQKFXD 17
 DB 50 MHPSDSETRYNQKFXD 66
 XX
 XX RESULT 32
 XX ID ADG38992 standard; protein; 121 AA.
 XX AC ADG38992;
 XX DT 26-FEB-2004 (first entry)
 XX DE Mouse anti-CD11a antibody heavy chain variable region.
 XX KM Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
 XX KM VH; cluster of differentiation 11a; mixed lymphocyte response assay;
 XX KM Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 XX KM ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 XX KM psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 XX KM rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 XX KM diabetes mellitus; prodrug activating enzyme.
 XX Mus sp.
 XX OS US2003207336-A1.
 XX PN

XX 06-NOV-2003.
 PD 28-FEB-2001; 2001US-00795798.
 XX 27-NOV-1996; 96US-0031971P.
 PR 20-NOV-1997; 97US-00974899.
 PR 20-OCT-1999; 99US-00420745.
 XX (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG;
 PI WPI; 2004-051511/05.
 DR Humanized anti-CD11a antibody useful for treating lymphocyte function-
 XX associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 PS Example; SEQ ID NO 4; 43pp; English.
 XX The invention relates to a Humanised anti-cluster of differentiation
 CC (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 CC a Kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (mM) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The
 CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is the heavy chain variable region (VH) of the wild-type
 CC mouse anti-CD11a I domain monoclonal antibody MHM24.
 XX Sequence 121 AA;
 SQ

Query Match 91.4%; Score 85; DB 8; Length 121;
 Best Local Similarity 94.1%; Pred. No. 2e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MIHPSDSETRYNOKFKD 17
 |||||
 Db 50 MIHPSDSETRYNOKFKD 66

RESULT 33
 ADR03367
 ID ADR03367 standard; protein; 121 AA.
 AC ADR03367;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Murine MHM24 antibody variable heavy chain protein.
 XX
 XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;

KW murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 KW VH; murine.
 XX
 XX Mus sp.
 XX US2004146507-A1.
 XX 29-JUL-2004.
 XX 03-DEC-2003; 2003US-00727737.
 XX 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG;
 PI WPI; 2004-552640/53.
 DR
 XX
 XX New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 PS Example; SEQ ID NO 4; 54pp; English.
 XX The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is murine anti-human CD11a monoclonal antibody (MHM24)
 CC variable heavy chain protein. This sequence is used in the
 CC exemplification of the invention.
 XX Sequence 121 AA;
 SQ

Query Match 91.4%; Score 85; DB 8; Length 121;
 Best Local Similarity 94.1%; Pred. No. 2e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MIHPSDSETRYNOKFKD 17
 |||||
 Db 50 MIHPSDSETRYNOKFKD 66

RESULT 34
 ADR03396
 ID ADR03396 standard; peptide; 17 AA.
 AC ADR03396;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MHM24 CDR-H2 mutant peptide, H1SH52Ser.
 XX
 XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;

OS	Mus sp.
OS	Homo sapiens.
OS	Chimeric.
PN	US2004146507-A1.
XX	
PD	29-JUL-2004.
XX	
PF	03-DEC-2003; 2003US-00727737.
XX	
PR	27-NOV-1996; 96US-0031945P.
PR	20-NOV-1997; 97US-00975329.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Jardieu PM, Presta LG;
XX	
DR	WPI; 2004-552640/53.
XX	
PT	New antibody mutant of a species-dependent antibody, useful for treating
PT	and preventing infectious diseases, psoriasis, inflammatory bowel
PT	disease, allergic conditions, autoimmune diseases, or cancer.
XX	
PS	Example; SEQ ID NO 33; 54pp; English.
XX	
CC	The present invention relates to an antibody mutant of a species-
CC	dependent antibody with beneficial properties. The invention is useful
CC	for treating and preventing infectious diseases such as human
CC	immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC	disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC	disease and ulcerative colitis, adult respiratory distress syndrome, as
CC	allergic diseases such as eczema and asthma, autoimmune diseases such as
CC	rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC	mellitus, Reynaud's syndrome, immunological diseases such as
CC	tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC	disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC	disorders such as poison ivy and poison oak, B-cell malignancies such as
CC	chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
CC	disease and cancer. The invention is also useful in gene therapy. The
CC	present sequence is humanised murine anti-human CD11a monoclonal antibody
CC	(MHM24) CDR-H2 mutant peptide. This sequence is used in the
CC	embodiment of the invention.
XX	
XX	
SQ	Sequence 17 AA;
XX	
Query Match	90.3%; Score 84; DB 8; Length 17;
Best Local Similarity	94.1%; Pred. No. 3e-07;
Matches 16; Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	1 MIHPSDSETRYNQKFKD 17
DB	1 MISPSPDSETRYNQKFKD 17
XX	
RESULT 35	
ADM38454	
ID	ADM38454 standard; protein; 122 AA.
XX	
AC	ADM38454;
XX	
DT	24-MAR-2005 (first entry)
XX	
DE	CD11a heavy chain variable region #1.
XX	
KM	monoclonal antibody; CD11a; light-chain variable region;
KM	heavy-chain variable region.

XX	OS	Homo sapiens.
XX	XX	CN1433651-A.
PN	PD	03-SEP-2003.
XX	PF	20-FEB-2002; 2002CN-00110866.
XX	PR	20-FEB-2002; 2002CN-00110866.
XX	PA	(ZHON-) ZHONGXIN GOOJIAN PHARM CO LTD SHANGHAI.
XX	PI	Wang H, Wang J;
XX	DR	WP1; 2004-169719/17.
XX	DR	N-PSDB; ADW38456.
XX	PT	Recombinant human CD11a monoclonal antibody and its preparation and medicinal composition.
XX	PS	Claim 1; Page 12-13; 16pp; Chinese.
XX	CC	The present invention relates to a recombinant monoclonal antibody for human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID No.5 in 11gth-chain variable region and the amino acid sequence shown by SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its biologically active form and the expression in host cell are greatly increased. The DNA molecule for coding the antibody, its preparation process and the medicinal composition containing it are also disclosed. The present sequence represents a heavy chain variable region of human CD11a.
XX	SO	Sequence 122 AA:
OY	Query Match	90.3%; Score 84; DB 8; Length 122; Best Local Similarity 100.0%; Pred. No. 2.9e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	3 HPSPSETRYNQKFXD 17 52 HPSPSETRYNQKFXD 66	
RESULT 36		
ADRO3395	ID	ADRO3395 standard; peptide; 17 AA.
AC	ADRO3395;	
DT	21-OCT-2004	(first entry)
DE	Humanised MEM24 CDR-H2 mutant peptide, HisH52A1a.	
XX	CD11a antibody; human immunodeficiency virus infection; HIV infection; rhinovirus infection; inflammatory skin disease; psoriasis; inflammatory bowel disease; Crohn's disease; ulcerative colitis; adult respiratory distress syndrome; allergic disease; eczema; asthma; autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus; SLR; diabetes mellitus; Reynaud's syndrome; immunological disease; tuberculosis; sarcoidosis; polymyositis; chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder; skin hypersensitivity disorder; poison ivy; poison oak; hairy cell leukaemia; B-cell malignancy; chronic lymphocytic leukaemia; gene therapy; graft versus host disease; cancer; murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain; VH; murine; human; fusion protein; complementarity determining region; CDR; mutant; mutein.	
OS	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
XX	US2004146507-A1.	

XX 29-JUN-2004.
PD 03-DEC-2003; 2003US-00727737.
XX 27-NOV-1996; 96US-0031945P.
PR 20-NOV-1997; 97US-00975329.
XX (GETH) GENENTECH INC.
PA Jardieu PM, Presta LG;
PI WPI; 2004-552640/53.
DR
XX
XX New antibody mutant of a species-dependent antibody, useful for treating
PT and preventing infectious diseases, psoriasis, inflammatory bowel
PT diseases, allergic conditions, autoimmune diseases, or cancer.
FT
PS Example; SEQ ID NO 32; 54pp; English.
XX
XX The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such as
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as
CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC disorders such as poison ivy and poison oak, B-cell malignancies such as
CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is humanised murine anti-human CD14 monoclonal antibody
CC (MEM24) CDR-H2 mutant peptide. This sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 17 AA;
Query Match 89.2%; Score 83; DB 8; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.5e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNQKFKD 17
Db 1 MIHPDSETRYNQKFKD 17
RESULT 37
ABUS6854
ID ABUS6854 standard; protein; 66 AA.
XX
XX ABUS6854;
AC
XX
XX 04-APR-2003 (first entry)
DT
XX
XX BONT/A Hc binding antibody scfv VH region from S25 #1.
DE
XX
XX Botulinum neurotoxin type A; BONT/A; mouse; heavy chain variable region;
KW scfv; antibody; botulinum; antibacterial; single chain antibody; VH;
KW immunoglobulin.
XX
XX Mus sp.
OS
XX
XX US2002155114-A1.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 31-AUG-1998; 98US-00144886.
PF
XX
XX 31-AUG-1998; 98US-00144886.
PR
XX

PA (MARK/) MARKS J D.
PA (AMER/) AMERSDORFER P.
XX
XX Marks JD, Amersdorfer P;
PI WPI; 2003-182618/18.
DR
XX
XX Novel antibody that specifically binds and neutralizes botulinum
PT neurotoxin type A useful for neutralizing botulinum neurotoxin and
PT treating botulism.
XX
PS Claim 6; Page 22; 31pp; English.
XX
XX The invention relates to an isolated antibody that specifically binds to
CC an epitope specifically bound by an antibody expressed by a clone such as
CC clone S25, C35, C39, 1C6 and clone 1F3, where the antibody binds to and
CC neutralises botulinum neurotoxin type A (BONT/A). Also included are a
CC polypeptide comprising BONT/A neutralising epitope comprising an epitope
CC which is specifically bound by the antibody, where the polypeptide is not
CC a full-length botulinum neurotoxin H c fragment and making an anti-BONT/A
CC antibody that neutralises BONT/A (by contacting several antibodies with
CC an epitope specifically bound by an antibody expressed by any of the
CC novel clones and isolating an antibody that specifically binds to the
CC epitope). The antibody is useful for neutralising a BONT/A, by contacting
CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
CC chain variable region complementarily determining region) and with a
CC second anti-BONT/A antibody which comprises a VH CDR, where the second
CC antibody binds to a different epitope than the first anti-BONT/A
CC antibody. The antibody is useful in the treatment of pathologies
CC associated with botulinum neurotoxin poisoning, for rapid
CC detection/diagnosis of botulism and in the detection and/or
CC quantification of BONT/A in a biological sample obtained from an organism.
CC Which is indicative of a Clostridium botulinum infection of the organism.
CC The present sequence is a heavy chain variable region (VH) of a single
CC chain antibody (scfv) of the invention
XX
SQ Sequence 66 AA;
Query Match 88.2%; Score 82; DB 6; Length 66;
Best Local Similarity 82.4%; Pred. No. 3.2e-06;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNQKFKD 17
Db 50 MIHPDSDPTREYNQKFKD 66
RESULT 38
ADZ21535
ID ADZ21535 standard; protein; 118 AA.
XX
XX ADZ21535;
AC
XX
XX 30-JUN-2005 (first entry)
DT
XX
XX Anti-Muc-1 single chain antibody B9 VH polypeptide.
DE
XX
XX Single chain antibody; MUC-1; tumor-associated antigen;
KW heavy chain variable region; antibody therapy; cytosstatic.
KW
XX
XX Mus sp.
OS
XX
XX WO2005032454-A2.
PN
XX
XX 14-APR-2005.
PD
XX
XX 07-MAY-2004; 2004WO-US014159.
PF
XX
XX 09-MAY-2003; 2003US-00435614.
PR
XX
XX (RBGC) UNIV CALIFORNIA.
PA
XX

PI Denardo SJ, Winthrop MD, Denardo GL, Xiong C;
 XX
 DR WPI; 2005-285319/29.
 XX
 PT New antibodies that specifically bind to cancer antigen MUC-1, useful for
 PT tumor targeting, for inhibiting the growth or proliferation of cancer
 PT cells or as diagnostic agents to identify tumors and monitor levels of
 PT circulating antigen.
 XX
 PS Claim 6; SEQ ID NO 13; 79pp; English.
 XX
 CC The invention provides novel antibodies that specifically bind to the MUC
 CC -1 cancer antigen. Preferred single chain antibodies were obtained from a
 CC phage display library and were designated as 12E, 3D, A5, C4, B5, E1 and
 CC B9 AD221537-AD221543. The heavy chain variable regions (VH) and light
 CC chain variable regions (VL) of these antibodies are also provided
 CC AD221523-AD221536. The VH and VL domains govern the construction of a
 CC binding affinity of the antibodies and permit the construction of a
 CC variety of antibodies that specifically target the MUC-1 antigen and
 CC cells bearing/displaying the antigen. The antibodies are useful targeting
 CC moieties for specifically directing imaging agents and various
 CC therapeutic moieties to a cancer. A claimed method of inhibiting the
 CC growth or proliferation of a cell bearing a MUC-1 antigen comprises
 CC contacting the cell with a chimeric molecule comprising an anti-MUC-1
 CC antibody attached to a cytotoxicin, a radionuclide, a liposome comprising
 CC an anti-cancer drug, a prodrug or an anti-cancer drug. The present
 CC sequence is that of the VH region of single chain antibody B9 AD221543.
 XX
 SQ Sequence 118 AA;
 XX
 Query Match 88.2%; Score 82; DB 9; Length 118;
 Best Local Similarity 88.2%; Pred. No. 6.2e-06;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MHPSPDSETRYNQKFPD 17
 |||||:|||||:
 Db 50 MHPSPDSETRYNQKFPD 66
 XX
 RESULT 39
 ADR38650
 ID ADR38650 standard; peptide; 120 AA.
 XX
 AC ADR38650;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Mouse heavy chain variable region scFv seqid 52.
 XX
 KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KW heavy chain variable region; single chain antibody; scFv.
 XX
 OS Mus sp.
 XX
 PN US2004175385-A1.
 XX
 PD 09-SEP-2004.
 XX
 PF 01-AUG-2003; 2003US-00632706.
 XX
 PR 31-AUG-1998; 98US-00144886.
 XX
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Marks JD, Amersdorfer P;
 XX
 DR WPI; 2004-652009/63.
 XX
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated

PT with botulinum neurotoxin poisoning.
 XX
 PS Example 1; SEQ ID NO 52; 110pp; English.
 XX
 CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin
 CC scFv.
 XX
 SQ Sequence 120 AA;
 XX
 Query Match 88.2%; Score 82; DB 8; Length 120;
 Best Local Similarity 82.4%; Pred. No. 6.4e-06;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHPSPDSETRYNQKFPD 17
 |||||:|||||:
 Db 50 MHPSPDSETRYNQKFPD 66
 XX
 RESULT 40
 AD221543
 ID AD221543 standard; protein; 177 AA.
 XX
 AC AD221543;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Anti-Muc-1 single chain antibody B9.
 XX
 KW Single chain antibody; MUC-1; tumor-associated antigen; antibody therapy;
 KW cytostatic.
 XX
 OS Mus sp.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Domain 3..120
 FT /label = VH
 FT Domain 136..177
 FT /label = VL
 XX
 PN WO2005032454-A2.
 XX
 PD 14-APR-2005.
 XX
 PF 07-MAY-2004; 2004WO-US014159.
 XX
 PR 09-MAY-2003; 2003US-00435614.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX

XX Denardo SJ, Winthrop MD, Denardo GL, Xiong C;
 XX WPI, 2005-285319/29.
 XX
 PT New antibodies that specifically bind to cancer antigen MUC-1, useful for
 PT tumor targeting, for inhibiting the growth or proliferation of cancer
 PT cells or as diagnostic agents to identify tumors and monitor levels of
 PT circulating antigen.
 XX
 PS Claim 7; SEQ ID NO 21; 79pp; English.
 XX
 CC The invention provides novel antibodies that specifically bind to the MUC
 CC -1 cancer antigen. Preferred single chain antibodies were obtained from a
 CC phage display library and were designated as 12E, 3D, A5, C4, B5, B1 and
 CC B9 ADZ21537-ADZ21543. The heavy chain variable regions (VH) and light
 CC chain variable regions (VL) of these antibodies are also provided
 CC ADZ21533-ADZ21536. The VH and VL domains govern the specificity and
 CC binding affinity of the antibodies and permit the construction of a
 CC variety of antibodies that specifically target the MUC-1 antigen and
 CC cells bearing/displaying the antigen. The antibodies are useful targeting
 CC moieties for specifically directing imaging agents and various
 CC therapeutic moieties to a cancer. A claimed method of inhibiting the
 CC growth or proliferation of a cell bearing a MUC-1 antigen comprises
 CC contacting the cell with a chimeric molecule comprising an anti-MUC-1
 CC antibody attached to a cytotoxin, a radionuclide, a liposome comprising
 CC an anti-cancer drug, a prodrug or an anti-cancer drug. The present
 CC sequence is that of single chain antibody B9.
 XX
 SQ Sequence 177 AA;
 XX
 Query Match 88.2%; Score 82; DB 9; Length 177;
 Best Local Similarity 88.2%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MIHPDSETRYNQKFKD 17
 Db 52 MIHPDSETRYNQKFKD 68
 XX
 RESULT 41
 ADR03392 standard; peptide; 17 AA.
 XX
 AC ADR03392;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MEM24 CDR-H2 mutant peptide, H2A1.
 XX
 KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak; hairy cell leukaemia;
 KW B-cell malignancy; chronic lymphocytic leukaemia; graft versus host
 KW disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain;
 KW VH; murine; human; fusion protein; complementarity determining region;
 KW CDR; mutant; mutein.
 XX
 XX Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX

PF 03-DEC-2003; 2003US-00727737.
 XX
 XX 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GERTH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI, 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 29; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MEM24) CDR-H2 mutant peptide. This sequence is used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 17 AA;
 XX
 Query Match 86.0%; Score 80; DB 8; Length 17;
 Best Local Similarity 86.2%; Pred. No. 1.5e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MIHPDSETRYNQKFKD 17
 Db 1 MIHPDSETRYNQKFKD 17
 XX
 RESULT 42
 ADR03394 standard; peptide; 17 AA.
 XX
 AC ADR03394;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MEM24 CDR-H2 mutant peptide, H2A2.
 XX
 KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak; hairy cell leukaemia;
 KW B-cell malignancy; chronic lymphocytic leukaemia; graft versus host
 KW disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain;
 KW VH; murine; human; fusion protein; complementarity determining region;
 KW CDR; mutant; mutein.
 XX
 XX Mus sp.
 OS Homo sapiens.
 OS

OS Chimeric.
XX
XX US2004146507-A1.
XX
XX 29-JUL-2004.
XX
XX 03-DEC-2003; 2003US-00727737.
XX
XX 27-NOV-1996; 96US-0031945P.
XX 20-NOV-1997; 97US-00975329.
XX
XX (GERTH) GENENTECH INC.
XX
XX Jardiou PM, Preeta LG;
XX WPI, 2004-552640/53.
XX
XX New antibody mutant of a species-dependent antibody, useful for treating
XX PT and preventing infectious diseases, psoriasis, inflammatory bowel
XX PT disease, allergic conditions, autoimmune diseases, or cancer.
XX
XX Example; SEQ ID NO 31; 54pp; English.
XX
XX The present invention relates to an antibody mutant of a species-
XX CC dependent antibody with beneficial properties. The invention is useful
XX CC for treating and preventing infectious diseases such as human
XX CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
XX CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
XX CC disease and ulcerative colitis, adult respiratory distress syndrome,
XX CC allergic diseases such as eczema and asthma, autoimmune diseases such as
XX CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
XX CC mellitus, Reynaud's syndrome, immunological diseases such as
XX CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
XX CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
XX CC disorders such as poison ivy and poison oak, B-cell malignancies such as
XX CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
XX CC disease and cancer. The invention is also useful in gene therapy. The
XX CC present sequence is humanized murine anti-human CD14 monoclonal antibody
XX CC (MHM24) CDR-H2 mutant peptide. This sequence is used in the
XX CC exemplification of the invention.
XX
XX Sequence 17 AA;
SQ

Query Match 86.0%; Score 80; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MIHPDSESTRYNQKFKD 17
|||:|||||
DB 1 MIAPSDAETRYNQKFKD 17

RESULT 43
AAE22201
ID AAE22201 standard; peptide; 19 AA.
XX
XX AAE22201;
XX
XX 25-JUL-2002 (first entry)
XX
XX Murine MC-1 antibody heavy chain variable domain (VH) CDR2 peptide.
XX
XX Chemokine construct; human immunodeficiency virus 1; allergic disease;
XX KM skin disease; immunological disorder; autoimmune disease; psoriasis;
XX KM multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
XX KM diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
XX KM inflammatory renal disease; HIV-1; transplant rejection; murine; CDR2;
XX KM heavy chain variable domain; VH; complementarity determining region 2;
XX KM MC-1; antibody.
XX
XX Mus sp.
XX OS
XX PN WO200220615-A2.

XX
XX 14-MAR-2002.
XX PD
XX 10-SEP-2001; 2001WO-EP010433.
XX PF
XX 08-SEP-2000; 2000EP-00119694.
XX PR 05-SEP-2001; 2001US-00948004.
XX
XX (MICR-) MICROMET AG.
XX
XX Mack M, Schloendorff D, Spring M;
XX WPI, 2002-362240/39.
XX
XX Use of an antibody and/or chemokine construct that binds to a chemokine
XX PT receptor, for eliminating cells latently infected with primate
XX PT immunodeficiency virus, or treating, preventing and alleviating immune
XX PT disorders.
XX
XX Disclosure; Page 117; 117pp; English.
XX
XX The invention relates to the use of an antibody and/or chemokine
XX CC construct that binds a chemokine receptor for preparing a pharmaceutical
XX CC composition for eliminating cells latently infected with a primate
XX CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They
XX CC are used in gene therapy and as vaccines. The antibody and/or chemokine
XX CC construct is also used for preparing a pharmaceutical composition for
XX CC treating, preventing and/or alleviating immunological disorders including
XX CC autoimmune diseases (e.g. multiple sclerosis, type I diabetes and
XX CC rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
XX CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases
XX CC such as inflammatory joint diseases (chronic arthritis), inflammatory
XX CC renal diseases and inflammatory bowel diseases and graft versus host and
XX CC transplant rejections. The present sequence is murine MC-1 antibody heavy
XX CC chain variable domain (VH) complementarity determining region 2 (CDR2)
XX CC peptide
XX
XX Sequence 19 AA;
SQ

Query Match 86.0%; Score 80; DB 5; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MIHPDSESTRYNQKFKD 17
|||:|||||
DB 2 MIHPDSESTRYNQKFKD 18

RESULT 44
ABUS6852
ID ABUS6852 standard; protein; 66 AA.
XX
XX ABUS6852;
XX
XX 04-APR-2003 (first entry)
XX
XX BoNT/A Hc binding antibody scTv VH region from 1D5 #1.
XX
XX Botulinum neurotoxin type A; BoNT/A; mouse; heavy chain variable region;
XX KM scFv; antibody; botulinum; antibacterial; single chain antibody; VH;
XX KM immunoglobulin.
XX
XX Mus sp.
XX OS
XX PN US2002155114-A1.
XX 24-OCT-2002.
XX PD 31-AUG-1998; 98US-00144886.
XX PF 31-AUG-1998; 98US-00144886.
XX PR 31-AUG-1998; 98US-00144886.
XX
XX (MARK/) MARKS J D.
XX PA

PA (AMER/) AMERSDORFER P.
 XX
 PI Marks JD, Amersdorfer P;
 XX
 XX WPI; 2003-182618/18.
 DR
 XX Novel antibody that specifically binds and neutralizes botulinum
 PT neurotoxin type A useful for neutralizing botulinum neurotoxin and
 PT treating botulism.
 XX
 PS Claim 6; Page 22; 31pp; English.
 XX
 XX The invention relates to an isolated antibody that specifically binds to
 CC an epitope specifically bound by an antibody expressed by a clone such as
 CC clone 825, C25, C39, 1C6 and clone 1F3, where the antibody binds to and
 CC neutralises botulinum neurotoxin type A (BoNT/A). Also included are a
 CC polypeptide comprising BoNT/A neutralising epitope comprising an epitope
 CC which is specifically bound by the antibody, where the polypeptide is not
 CC a full-length botulinum neurotoxin H C fragment and making an anti-BoNT/A
 CC antibody that neutralises BoNT/A (by contacting several antibodies with
 CC an epitope specifically bound by an antibody expressed by any of the
 CC novel clones and isolating an antibody that specifically binds to the
 CC epitope). The antibody is useful for neutralising a BoNT/A, by contacting
 CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
 CC chain variable region complementarity determining region) and with a
 CC second anti-BoNT/A antibody which comprises a VH CDR, where the second
 CC antibody binds to a different epitope than the first anti-BoNT/A
 CC antibody. The antibody is useful in the treatment of pathologies
 CC associated with botulinum neurotoxin poisoning, for rapid
 CC detection/diagnosis of botulism and in the detection and/or
 CC quantification of BoNT/A in a biological sample obtained from an organism
 CC which is indicative of a Clostridium botulinum infection of the organism.
 CC The present sequence is a heavy chain variable region (VH) of a single
 CC chain antibody (scFv) of the invention
 XX
 SQ Sequence 66 AA;
 XX
 Query Match 86.0%; Score 80; DB 6; Length 66;
 Best Local Similarity 88.2%; Pred. No. 7.1e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MIHPDSETRYNQKFKD 17
 |||||:|||||
 Db 50 MIHPNSETRLNOKFKD 66
 |||||:|||||
 RESULT 45
 AAE22192 ID AAE22192 standard; protein; 117 AA.
 XX
 AC AAE22192;
 XX
 XX 25-JUL-2002 (first entry)
 DT
 XX Murine MC-1 antibody heavy chain variable domain (VH) (1) #2.
 DE
 XX Chemokine construct; human immunodeficiency virus 1; allergic disease;
 KW skin disease; immunological disorder; autoimmune disease; psoriasis;
 KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
 KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
 KW inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine;
 KW MC-1 antibody; VH; heavy chain variable domain; chemokine receptor 5.
 XX
 OS Mus sp.
 XX
 XX WO200220615-A2.
 PN
 XX 14-MAR-2002.
 PD
 XX 10-SEP-2001; 2001WO-BP010433.
 PE
 XX 08-SEP-2000; 2000EP-00119694.
 XX
 PR 05-SEP-2001; 2001US-00948004.
 PR

XX
 PA (MICR-) MICROMET AG.
 XX
 XX Mack M, Schloendorff D, Spring M;
 PI
 XX WPI; 2002-362240/39.
 DR
 XX N-PSDB; MAD35251.
 DR
 XX Use of an antibody and/or chemokine construct that binds to a chemokine
 PT receptor, for eliminating cells latently infected with primate
 PT immunodeficiency virus, or treating, preventing and alleviating immune
 PT disorders.
 PT
 PS Claim 12; Page 50; 117pp; English.
 XX
 XX The invention relates to the use of an antibody and/or chemokine
 CC construct that binds a chemokine receptor for preparing a pharmaceutical
 CC composition for eliminating cells latently infected with a primate
 CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They
 CC are used in gene therapy and as vaccines. The antibody and/or chemokine
 CC construct is also used for preparing a pharmaceutical composition for
 CC treating, preventing and/or alleviating immunological disorders including
 CC autoimmune diseases (e.g. multiple sclerosis, type 1 diabetes and
 CC rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
 CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases
 CC such as inflammatory joint diseases (chronic arthritis), inflammatory
 CC renal diseases and inflammatory bowel diseases and graft versus host and
 CC transplant rejections. The present sequence is murine MC-1 antibody heavy
 CC chain variable domain (VH) (1). This antibody is specific for human
 CC chemokine receptor 5 (CCR5)
 CC
 XX
 SQ Sequence 117 AA;
 XX
 Query Match 86.0%; Score 80; DB 5; Length 117;
 Best Local Similarity 88.2%; Pred. No. 1.4e-05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MIHPDSETRYNQKFKD 17
 |||||:|||||
 Db 60 MIHPDSETRLNOKFKD 76
 |||||:|||||
 RESULT 46
 ADR38648 ID ADR38648 standard; peptide; 125 AA.
 XX
 XX ADR38648;
 AC
 XX 02-DEC-2004 (first entry)
 DT
 XX Mouse heavy chain variable region scFv seqid 50.
 DE
 XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KW heavy chain variable region; single chain antibody; scFv.
 XX
 OS Mus sp.
 XX
 XX US2004175385-A1.
 FN
 XX 09-SEP-2004.
 PD
 XX 01-AUG-2003; 2003US-00632706.
 PE
 XX 31-AUG-1998; 98US-00144886.
 PR
 XX 01-AUG-2002; 2002US-0400721P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Marks JD, Amersdorfer P;
 PI
 XX WPI; 2004-652009/63.
 DR

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.

PS Example 1; SEQ ID NO 50; 110pp; English.

The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A (BoNT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clones S25, C25, C39, 1C6, 3D12, B4, 1f3, huc5, Ar1, Ar2, WR1 (V), WR1 (T), 3-1-, 3-8-, 3-10 and ING1, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I), producing (I), and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BoNT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of a mouse heavy chain variable fragment anti-botulinum toxin gCFV.

Sequence 125 AA;

Query Match	86.0%	Score 80	DB 8	Length 125
Best Local Similarity	88.2%	Pred. No. 1.5e-05		
Matches 15; Conservative		1; Mismatches 1;	Indels 0;	Gaps 0;

```
QY      1 MIHPDSETRYNQKFKD 17
        ||||:|||||
Db      50 MIHPNSETRLNQKFKD 66
```

RESULT 47
AAE22191
ID AAE22191 standard; protein; 138 AA.

AC AAE22191;

DT 25-JUL-2002 (first entry)

DE Murine MC-1 antibody heavy chain variable domain (VH) (1) #1.

KM Chemokine construct; human immunodeficiency virus 1; allergic disease;
KM skin disease; immunological disorder; autoimmune disease; psoriasis;
KM multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
KM diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
KM inflammatory renal disease; HIV-1; transplant rejection; CCR5; murine
KM MC-1 antibody; VH; heavy chain variable domain; chemokine receptor 5.

OS Mus sp.

PN WO200220615-A2

PD 14-MAR-2002.

PF 10-SEP-2001; 2001WO-EP010433.

PR 08-SEP-2000; 2000EP-00119694.

XX

PA (MICR-) MICROMET AG.

Mack M, Schloendorff D, Spring M, PI.

DR WPI; 2002-362240/39.

XX 9

PT Use of an antibody and/or chemokine construct that binds to a chemokine
PT receptor, for eliminating cells latently infected with primate
PT immunodeficiency virus, or treating, preventing and alleviating immune
PT disorders.

PS Example 2; Page 50; 117pp; English.

CC The invention relates to the use of an antibody and/or chemokine
CC construct that binds a chemokine receptor for preparing a pharmaceutical
CC composition for eliminating cells latently infected with a primate
CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1). They
CC are used in gene therapy and as vaccines. The antibody and/or chemokine
CC construct is also used for preparing a pharmaceutical composition for
CC treating, preventing and/or alleviating immunological disorders including
CC autoimmune diseases (e.g. multiple sclerosis, type I diabetes and
CC rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases
CC such as inflammatory joint diseases (chronic arthritis), inflammatory
CC renal diseases and inflammatory bowel diseases and graft versus host and
CC transplant rejections. The present sequence is murine MC-1 antibody heavy
CC chain variable domain (VH) (1). This antibody is specific for human
CC chemokine receptor 5 (CCR5).

SQ Sequence 138 AA;

Query Match	86.0%	Score 80	DB 5	Length 138
Best Local Similarity	88.2%	Pred. No.	1.7e-05	
Matches 15; Conservative	0	Mismatches	2	Indels 0; Gaps 0

```
QY      1 MIHPDSETRYNQKFKD 17
        |||||
Db      69 MIHPDSETRLNQKFN 85
```

RESULT 48
AAE22193
ID AAE22193 standard; protein; 495 AA

AC AAE22193;

DT 25-JUL-2002 (first entry)

DE Murine CCR5xCD3 bispecific single chain antibody construct.

KM Chemokine construct; human immunodeficiency virus 1; allergic disease
KM skin disease; immunological disorder; autoimmune disease; psoriasis;
KM multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
KM diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
KM inflammatory renal disease; HIV-1; transplant rejection; CCR5xCD3;
KM antibody; chemokine receptor 5; CD3 antigen; chemetic; murine.
KM antibody; chemokine receptor 5; CD3 antigen; chemetic; murine.

W OS Mus sp.

Chimeric.

AA WO200220615-A2
PN

PD 14-MAR-2002.

MM 10-SEP-2001
PF

PR 08-SEP-2000; 2000EP-00119694

XX
XX-DEF 2001 200100 00000000

FILED - FIDUCIARIES, AND.
XX

PI	Mack M, Schloendorff D, Spring M;
XX	
DR	WP1: 2002-362240/39.
DR	N-PSDB; AAD35252.
XX	
PT	Use of an antibody and/or chemokine construct that binds to a chemokine
PT	receptor, for eliminating cells latently infected with primate
PT	immunodeficiency virus, or treating, preventing and alleviating immune
PT	disorders.
XX	
PS	Claim 29; Page 52; 117pd; English.
XX	
CC	The invention relates to the use of an antibody and/or chemokine
CC	construct that binds a chemokine receptor for preparing a pharmaceutical
CC	composition for eliminating cells latently infected with a primate
CC	immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They
CC	are used in gene therapy and as vaccines. The antibody and/or chemokine
CC	construct is also used for preparing a pharmacological composition for
CC	treating, preventing and/or alleviating immunological disorders including
CC	autoimmune diseases (e.g. multiple sclerosis, type I diabetes and
CC	rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
CC	inflammation, atopic dermatitis and psoriasis), inflammatory diseases
CC	such as inflammatory joint diseases (chronic arthritis), inflammatory
CC	renal diseases and inflammatory bowel diseases and graft versus host and
CC	transplant rejections. The present sequence is CCR5XCD3 bispecific single
CC	chain antibody construct. This antibody construct comprises light chain
CC	variable domain (VL) and heavy chain variable (VH) domains of murine MC-1
CC	antibody specific for human chemokine receptor 5 (CCR5) and VH and VL
CC	domains of an antibody specific for a CD3 antigen joined by a peptide
CC	linker
XX	
SQ	Sequence 495 AA;
	Query Match 86.0%; Score 80; DB 5; Length 495;
	Best Local Similarity 88.2%; Pred. No. 7.2e-05;
	Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Oy	1 MIHPSDSETRYNOKFKD 17
Db	172 MIHPSDSETRYLNQKFN 188
RESULT 49	
ADNR03390	ADNR03390 standard; peptide; 17 AA.
XX	
AC	ADNR03390;
XX	
DT	21-OCT-2004 (first entry)
XX	
DE	Humanised MHM24 CDR-H2 mutant peptide, H2.
XX	
KM	CD14 antibody; human immunodeficiency virus infection; HIV infection;
KM	rhinovirus infection; inflammatory skin disease; psoriasis;
KM	inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KM	adult respiratory distress syndrome; allergic disease; eczema; asthma;
KM	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KM	SLR; diabetes mellitus; Reynaud's syndrome; immunological disease;
KM	tuberculosis; sarcoidosis; polymyositis;
KM	chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KM	skin hypersensitivity disorder; poison ivy; poison oak;
KM	B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
KM	graft versus host disease; cancer; gene therapy;
KM	murine anti-human CD14 monoclonal antibody; MHM24; variable heavy chain;
KM	VH; murine; human; fusion protein; complementarity determining region;
KM	CDR; mutant; mutcin.
XX	
OS	Mus sp.
OS	Homo sapiens.
OS	Chimeric.
XX	
FN	US2004146507-A1.

```

PD      29-JUN-2004.
XX
PF      03-DEC-2003; 2003JUS-00727737.
XX
PR      27-NOV-1996; 96US-0031945P.
XX
PR      20-NOV-1997; 97US-00975329.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Jardieu PM, Presta LG;
XX
DR      WPI, 2004-552640/53.
XX
PT      New antibody mutant of a species-dependent antibody, useful for treating
PS      disease, allergic conditions, autoimmune diseases, or cancer.
XX
Example; SEQ ID NO 27; 54pp; English.
CC
CC      The present invention relates to an antibody mutant of a species-
CC      dependent antibody with beneficial properties. The invention is useful
CC      for treating and preventing infectious diseases such as human
CC      immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC      disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC      disease and ulcerative colitis, adult respiratory distress syndrome,
CC      allergic diseases such as eczema and asthma, autoimmune diseases such as
CC      rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC      mellitus, Reynaud's syndrome, immunological diseases such as
CC      tuberculosis, sarcoidosis, polyomyelitis and chronic obstructive
CC      disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC      disorders such as poison ivy and poison oak, B-cell malignancies such as
CC      chronic lymphocytic leukaemia and hairy cell leukemia, graft versus host
CC      disease and cancer. The invention is also useful in gene therapy. The
CC      present sequence is humanised murine anti-human CD1a monoclonal antibody
CC      (MHM24) CDR-H2 mutant peptide. This sequence is used in the
CC      exemplification of the invention.
SQ
Sequence 17 AA:
Query Match          82.8%; Score 77; DB 0; Length 17;
Beat Local Similarity 82.4%; Pred. No. 4.9e-06;
Matches   14; Conservative    2; Mismatches    1; Indels    0; Gaps    0.
QY              1 MIHPSDSETRYNOKFKD 17
               |||::|||:|||
DB              1 MIAPADAEETRYNOKFKD 17
RESULT 50
ADZ45355
ID      ADZ45355 standard; peptide; 17 AA.
XX
XX      AC      ADZ45355;
DE      30-JUN-2005 (first entry)
XX
XX      Murine factor IX directed antibody CDR2 SEQ ID NO 59.
KW      bippecific antibody; blood coagulation factor VIII; bleeding;
KW      fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
KW      factor VIII deficiency; von Willebrand's disease; hemostatic;
KW      immunostimulant; antibody engineering.
OS      Mus musculus.
PN      WO2005035756-A1.
PD      21-APR-2005.
PF      08-OCT-2004; 2004WO-JP014911.
PR      10-OCT-2003; 2003WO-JP013062.
PR      14-OCT-2003; 2003WO-JP013123.

```

XX (CHUS) CHUGAI SEIYAKU KK.
PA

XX Hattori K, Kojima T, Miyazaki T, Soeda T;
PI

XX WPI; 2005-315563/32.
DR

XX Novel bispecific antibody substituting for function of cofactor that
PT enhances enzyme reaction, and recognizing both enzyme and substrates of
PT enzyme, useful for treating hemophilia A.
XX

PS Disclosure; SEQ ID NO 59; 699p; Japanese.
XX

CC This invention describes a novel bispecific antibody which can act as a
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
CC the enzyme substrate. The antibody specifically binds to blood
CC coagulation factor VIII. The invention also describes a composition
CC comprising the antibody and a carrier, a kit useful in preventing and/or
CC treating bleeding associated with a disorder or from a disease caused by
CC bleeding. The composition includes blood coagulation factor VIII. The
CC antibody of the invention can be a blood-coagulation fibrinolysis related
CC factor including blood-coagulation factor VIII, blood coagulation factor
CC X, or blood-coagulation factor IX. The antibody comprises a complementary
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
CC antibody. The novel antibody or composition is useful for preventing
CC and/or treating a disease accompanying bleeding, or the disease resulting
CC from bleeding, where the disease accompanies bleeding or the disease
CC resulting from bleeding develops and/or progresses by an active reduction
CC or deletion of the blood coagulation factor VIII. The disease the
CC develops and/or progresses by an active reduction or deletion of the
CC blood coagulation factor VIII and/or activation blood coagulation factor
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
CC an acquired hemophilia A. This sequence represents a fragment of the
CC antibody described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 17 AA;
XX

Query Match 82.8%; Score 77; DB 9; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.9e-06;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 16
|||

DB 2 IHPSDSEARYNQKFK 16
|||

Search completed: January 17, 2006, 11:58:09
Job time : 113.379 secs

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:48:18 ; Search time 15.9697 Seconds
(without alignments)
102.424 Million cell updates/sec

Title: US-10-665-658-11

Perfect score: 93
Sequence: 1 MHIPDSETRYNQKFKD 17Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database :

PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	91.4	101	2	S42183
2	77	82.8	103	2	PH0986
3	77	82.8	117	1	HVMS3
4	74	79.6	98	2	PH1164
5	74	79.6	117	1	HVMS02
6	74	79.6	120	2	S25175
7	74	79.6	120	2	B22769
8	72	77.4	114	2	A49060
9	70	75.3	88	2	PH1161
10	70	75.3	108	2	S26316
11	70	75.3	110	2	S26317
12	70	75.3	111	2	S26463
13	70	75.3	122	2	S24287
14	68	73.1	54	2	PH1163
15	68	73.1	106	2	S26315
16	67	72.0	117	2	G45722
17	65	69.9	109	2	S26318
18	64	68.8	101	2	H37262
19	64	68.8	107	2	PH0987
20	61	65.6	69	2	D25150
21	61	65.6	87	2	PH1162
22	61	65.6	98	2	PH1154
23	61	65.6	98	2	PH1160
24	61	65.6	116	2	S53751
25	59	63.4	96	2	S17230
26	59	63.4	96	2	S17614
27	59	63.4	96	2	S17620
28	59	63.4	96	2	S17618
29	59	63.4	96	2	S17610

30	59	63.4	102	2	S26471	Ig heavy chain V r
31	59	63.4	106	2	PH1005	Ig heavy chain V r
32	59	63.4	109	2	PH1003	Ig heavy chain V r
33	59	63.4	117	2	PH0237	Ig heavy chain V r
34	59	63.4	117	2	PH0235	Ig heavy chain V r
35	59	63.4	120	2	S41394	Ig heavy chain V r
36	58	62.4	91	2	PH1004	Ig heavy chain V r
37	58	62.4	96	2	S17619	Ig heavy chain V r
38	58	62.4	96	2	S17611	Ig heavy chain V r
39	58	62.4	96	2	S17612	Ig heavy chain V r
40	58	62.4	96	2	S17606	Ig heavy chain V r
41	58	62.4	96	2	S17617	Ig heavy chain V r
42	58	62.4	96	2	S17607	Ig heavy chain V r
43	58	62.4	96	2	S17613	Ig heavy chain V r
44	58	62.4	96	2	S17602	Ig heavy chain V r
45	58	62.4	96	2	S17616	Ig heavy chain V r
46	58	62.4	117	2	S55541	Ig heavy chain V r
47	58	62.4	125	2	PH0100	Ig heavy chain V r
48	58	62.4	136	2	B47159	Ig heavy chain V r
49	57	61.3	102	2	PH1241	Ig heavy chain V r
50	57	61.3	104	2	S26466	Ig heavy chain V r
51	57	61.3	113	2	S55528	Ig heavy chain V r
52	57	61.3	113	2	S55532	Ig heavy chain V r
53	57	61.3	113	2	S55531	Ig heavy chain V r
54	57	61.3	117	1	HVMSA1	Ig heavy chain pre
55	56	60.2	122	2	S20643	Ig heavy chain V r
56	55	59.1	96	2	S17621	Ig heavy chain V r
57	55	59.1	102	2	PH1268	Ig heavy chain V-D
58	55	59.1	116	2	S09962	Ig heavy chain pre
59	55	59.1	140	2	S09216	Ig gamma chain V r
60	54	58.1	93	2	S42182	Ig gamma chain V r
61	54	58.1	94	2	S42177	Ig gamma chain V r
62	54	58.1	95	2	S42178	Ig gamma chain V r
63	54	58.1	97	2	S42181	Ig gamma chain V r
64	54	58.1	101	2	S42184	Ig gamma chain V r
65	54	58.1	101	2	S42179	Ig gamma chain V r
66	54	58.1	102	2	S42180	Ig gamma chain V r
67	54	58.1	113	2	S55533	Ig heavy chain V r
68	54	58.1	113	2	S55535	Ig heavy chain V r
69	54	58.1	140	2	S04575	Ig heavy chain pre
70	53	57.0	96	2	S17615	Ig heavy chain V r
71	53	57.0	101	2	PH0983	Ig heavy chain V r
72	53	57.0	101	2	PH0982	Ig heavy chain V r
73	53	57.0	104	2	PH0981	Ig heavy chain V r
74	53	57.0	109	2	PH0973	Ig heavy chain V r
75	53	57.0	112	2	PH0232	Ig heavy chain V r
76	53	57.0	118	2	PH0231	Ig heavy chain pre
77	53	57.0	119	2	A24672	Ig heavy chain pre
78	53	57.0	131	2	A27472	Ig heavy chain pre
79	53	57.0	135	2	A30577	Ig heavy chain pre
80	52	57.0	138	2	B32513	Ig heavy chain pre
81	52	55.9	86	2	A25150	Ig heavy chain V r
82	52	55.9	102	2	PH1234	Ig heavy chain V r
83	52	55.9	112	2	S09957	Ig heavy chain V-D
84	52	55.9	112	2	PH0980	Ig heavy chain V r
85	52	55.9	113	2	S55530	Ig heavy chain V r
86	52	55.9	113	2	PH0974	Ig heavy chain V r
87	52	55.9	115	2	A54378	Ig heavy chain V r
88	52	55.9	117	2	PH0234	Ig heavy chain V r
89	52	55.9	138	1	HVMS17	Ig heavy chain pre
90	51	54.8	66	2	H28833	Ig kappa chain V r
91	51	54.8	67	2	G28833	Ig kappa chain V r
92	51	54.8	89	2	G28833	Ig kappa chain V r
93	51	54.8	97	2	PH1155	Ig kappa chain V r
94	51	54.8	98	2	PH1254	Ig kappa chain V r
95	51	54.8	102	2	PH1254	Ig kappa chain V r
96	51	54.8	102	2	S42176	Ig heavy chain V r
97	51	54.8	107	2	PH0999	Ig heavy chain V r
98	51	54.8	108	2	PH0975	Ig heavy chain V r
99	51	54.8	108	2	PH0985	Ig heavy chain V r
100	51	54.8	109	2	PH0997	Ig heavy chain V r
101	51	54.8	111	2	PH0998	Ig heavy chain V r
102	51	54.8	114	2	PH0247	Ig heavy chain V r

103	51	54.8	120	1	MHMS15	Ig heavy chain V r
104	51	54.8	122	2	A27635	Ig heavy chain pre
105	51	54.8	127	2	PH1420	Ig heavy chain V r
106	51	54.8	246	2	S38950	Ig gamma chain - m
107	51	54.8	446	2	S40295	Ig gamma-2a chain
108	50	53.8	88	2	C25155	Ig heavy chain V r
109	50	53.8	88	2	E25155	Ig heavy chain V r
110	50	53.8	88	2	G25155	Ig heavy chain V r
111	50	53.8	88	2	F25155	Ig heavy chain V r
112	50	53.8	94	2	S42185	Ig gamma chain V r
113	50	53.8	98	2	PH1274	Ig heavy chain V r
114	50	53.8	98	2	S26907	Ig heavy chain V r
115	50	53.8	101	2	S12428	Ig heavy chain V r
116	50	53.8	101	2	S12424	Ig heavy chain V r
117	50	53.8	102	2	PH1266	Ig heavy chain V r
118	50	53.8	102	2	PH1279	Ig heavy chain V r
119	50	53.8	102	2	PH1281	Ig heavy chain V r
120	50	53.8	102	2	PH1277	Ig heavy chain V r
121	50	53.8	102	2	PH1244	Ig heavy chain V r
122	50	53.8	102	2	PH1267	Ig heavy chain V r
123	50	53.8	102	2	PH1272	Ig heavy chain V r
124	50	53.8	102	2	PH1282	Ig heavy chain V r
125	50	53.8	102	2	PH1248	Ig heavy chain V r
126	50	53.8	102	2	PH1280	Ig heavy chain V r
127	50	53.8	102	2	PH1258	Ig heavy chain V r
128	50	53.8	102	2	PH1264	Ig heavy chain V r
129	50	53.8	102	2	PH1259	Ig heavy chain V r
130	50	53.8	102	2	PH1273	Ig heavy chain V r
131	50	53.8	102	2	PH1249	Ig heavy chain V r
132	50	53.8	102	2	PH1271	Ig heavy chain V r
133	50	53.8	102	2	PH1278	Ig heavy chain V r
134	50	53.8	104	2	B36006	Ig heavy chain V r
135	50	53.8	105	2	PH0976	Ig heavy chain V r
136	50	53.8	112	2	S26473	Ig heavy chain V r
137	50	53.8	112	2	PH1428	Ig heavy chain V r
138	50	53.8	115	2	PH1557	Ig heavy chain V r
139	50	53.8	115	2	PL0238	Ig heavy chain V r
140	50	53.8	117	1	MHMS4E	Ig heavy chain V r
141	50	53.8	117	1	MHMSJ5	Ig heavy chain V r
142	50	53.8	117	2	A28846	Ig heavy chain pre
143	50	53.8	117	2	S19669	Ig heavy chain V r
144	50	53.8	117	2	S19670	Ig heavy chain V r
145	50	53.8	117	2	JC2269	PL7-6 antibody hea
146	50	53.8	118	1	MHMS38	Ig heavy chain V r
147	50	53.8	119	2	PL0086	Ig heavy chain V r
148	50	53.8	120	2	G28195	Ig heavy chain V r
149	50	53.8	123	2	PH1423	Ig heavy chain V r
150	50	53.8	123	2	S38492	Ig heavy chain - h
151	50	53.8	123	2	C36006	Ig heavy chain V r
152	50	53.8	123	2	S20646	Ig heavy chain V r
153	50	53.8	126	2	PH1416	Ig heavy chain V r
154	50	53.8	126	2	PH1419	Ig heavy chain V r
155	50	53.8	127	2	PH1414	Ig heavy chain V r
156	50	53.8	127	2	PH1409	Ig heavy chain V r
157	50	53.8	128	2	S16685	Ig heavy chain V r
158	50	53.8	128	2	I37267	Ig heavy chain V r
159	50	53.8	134	2	PH1422	Ig heavy chain V r
160	50	53.8	136	2	A49047	Ig heavy chain V r
161	50	53.8	136	2	PH1559	Ig heavy chain V r
162	50	53.8	138	2	S21810	Ig heavy chain V r
163	50	53.8	139	2	PH1558	Ig heavy chain V r
164	50	53.8	139	2	PS0024	Ig heavy chain pre
165	50	53.8	140	2	T01407	Ig heavy chain (my
166	49	52.7	86	2	S12580	Ig heavy chain V r
167	49	52.7	90	2	PH1159	Ig heavy chain V r
168	49	52.7	91	2	PL0242	Ig heavy chain V r
169	49	52.7	98	2	S17604	Ig heavy chain V r
170	49	52.7	98	2	A28572	Ig heavy chain V r
171	49	52.7	98	2	PH1156	Ig heavy chain V r
172	49	52.7	102	2	PH1247	Ig heavy chain V r
173	49	52.7	102	2	PH1263	Ig heavy chain V r
174	49	52.7	106	2	PH1002	Ig heavy chain V r
175	49	52.7	107	2	PL0240	Ig heavy chain V r
176	49	52.7	107	2	PL0243	Ig heavy chain V r
177	49	52.7	107	2	PL0241	Ig heavy chain V r
178	49	52.7	107	2	S26330	Ig heavy chain V r
179	49	52.7	109	2	PH1001	Ig heavy chain V r
180	49	52.7	112	2	PH0979	Ig heavy chain V r
181	49	52.7	114	2	PH1523	Ig heavy chain V r
182	49	52.7	114	2	PH1522	Ig heavy chain V r
183	49	52.7	114	2	S26319	Ig heavy chain V r
184	49	52.7	117	2	S03305	Ig heavy chain V r
185	49	52.7	118	2	S38565	Ig heavy chain V r
186	49	52.7	119	2	PH1505	Ig heavy chain V r
187	49	52.7	119	2	PH1517	Ig heavy chain V r
188	49	52.7	119	2	S09955	Ig heavy chain V-D
189	49	52.7	119	2	PH1502	Ig heavy chain V r
190	49	52.7	119	2	PH1521	Ig heavy chain V r
191	49	52.7	119	2	PH1500	Ig heavy chain V r
192	49	52.7	119	2	PH1504	Ig heavy chain V r
193	49	52.7	119	2	PH1520	Ig heavy chain V r
194	49	52.7	119	2	PH1512	Ig heavy chain V r
195	49	52.7	121	2	A26405	Ig heavy chain V r
196	49	52.7	122	2	S36276	Ig heavy chain V r
197	49	52.7	122	2	PH0887	Ig heavy chain V r
198	49	52.7	123	2	PH1413	Ig heavy chain pre
199	49	52.7	135	2	E50057	Ig heavy chain pre
200	49	52.7	137	2	F29380	Ig heavy chain pre
201	49	52.7	140	2	PH1482	Ig heavy chain V r
202	48	51.6	84	2	PH1487	Ig heavy chain V r
203	48	51.6	95	2	S26469	Ig heavy chain V r
204	48	51.6	98	2	PH1149	Ig heavy chain V r
205	48	51.6	117	2	S01822	Ig heavy chain V-D
206	48	51.6	117	2	B27563	Ig heavy chain V r
207	48	51.6	118	2	C30560	Ig heavy chain V r
208	48	51.6	118	2	S38717	Ig heavy chain V r
209	48	51.6	119	2	S36257	Ig heavy chain V r
210	48	51.6	119	2	E30562	Ig heavy chain V r
211	48	51.6	120	2	E35722	anti-glycoprotein
212	48	51.6	135	2	PH1493	Ig heavy chain V r
213	47	50.5	56	2	PH1158	Ig heavy chain V r
214	47	50.5	75	2	A25155	Ig heavy chain V r
215	47	50.5	76	2	PH1153	Ig heavy chain V r
216	47	50.5	80	2	S25050	Ig heavy chain V r
217	47	50.5	80	2	F28833	Ig kappa chain V r
218	47	50.5	90	2	PH1152	Ig heavy chain V r
219	47	50.5	94	2	PH0996	Ig heavy chain V r
220	47	50.5	94	2	PH1142	Ig heavy chain V r
221	47	50.5	96	2	PH1165	Ig heavy chain V r
222	47	50.5	97	2	S17603	Ig heavy chain V r
223	47	50.5	97	2	PH1137	Ig heavy chain V r
224	47	50.5	98	2	PH1138	Ig heavy chain V r
225	47	50.5	98	2	PH1106	Ig heavy chain V r
226	47	50.5	98	2	S26313	Ig heavy chain V r
227	47	50.5	98	2	S26312	Ig heavy chain V r
228	47	50.5	98	2	PH1125	Ig heavy chain V r
229	47	50.5	98	2	PH1134	Ig heavy chain V r
230	47	50.5	98	2	PH1105	Ig heavy chain V r
231	47	50.5	98	2	PH1126	Ig heavy chain V r
232	47	50.5	98	2	PH1128	Ig heavy chain V r
233	47	50.5	98	2	PH1108	Ig heavy chain V r
234	47	50.5	98	2	PH1119	Ig heavy chain V r
235	47	50.5	98	2	PH1114	Ig heavy chain V r
236	47	50.5	98	2	PH1151	Ig heavy chain V r
237	47	50.5	101	2	S26314	Ig heavy chain V r
238	47	50.5	101	2	S26310	Ig heavy chain V r
239	47	50.5	102	2	PH1252	Ig heavy chain V r
240	47	50.5	102	2	S25025	Ig heavy chain - m
241	47	50.5	102	2	S25091	Ig heavy chain V r
242	47	50.5	104	2	S25036	Ig heavy chain V r
243	47	50.5	106	2	S25038	Ig heavy chain V r
244	47	50.5	109	2	PH0989	Ig heavy chain V r
245	47	50.5	109	2	PH1094	Ig heavy chain V r
246	47	50.5	109	2	PH1096	Ig heavy chain V r
247	47	50.5	110	2	S25028	Ig heavy chain V r
248	47	50.5	110	2		

249	47	50.5	110	2	PH1000	Ig heavy chain V r	322	45	48.4	118	2	S37201	Ig heavy chain V r
250	47	50.5	110	2	PH0995	Ig heavy chain V r	323	45	48.4	119	2	F30502	Ig heavy chain V r
251	47	50.5	111	2	S25024	Ig heavy chain V r	324	45	48.4	120	2	F45722	anti-glycoprotein
252	47	50.5	111	2	S25033	Ig heavy chain V r	325	45	48.4	120	2	S09956	Ig heavy chain V-D
253	47	50.5	111	2	S25032	Ig heavy chain V r	326	45	48.4	120	2	A54256	Ig heavy chain V r
254	47	50.5	111	2	S25047	Ig heavy chain V r	327	45	48.4	126	2	PH1417	Ig heavy chain V r
255	47	50.5	111	2	S25055	Ig heavy chain V r	328	45	48.4	126	2	PH1418	Ig heavy chain V r
256	47	50.5	111	2	S25045	Ig heavy chain V r	329	45	48.4	133	2	PC1155	Ig heavy chain pre
257	47	50.5	111	2	S25054	Ig heavy chain V r	330	45	48.4	137	2	H32513	Ig heavy chain pre
258	47	50.5	111	2	S25048	Ig heavy chain V r	331	45	47.3	50	2	S26941	Ig heavy chain V r
259	47	50.5	111	2	S25052	Ig heavy chain V r	332	44	47.3	71	2	PH1167	Ig heavy chain V r
260	47	50.5	111	2	S25030	Ig heavy chain V r	333	44	47.3	96	2	S17608	Ig heavy chain V r
261	47	50.5	111	2	S25031	Ig heavy chain V r	334	44	47.3	98	2	PH1145	Ig heavy chain V r
262	47	50.5	111	2	PH0990	Ig heavy chain V r	335	44	47.3	98	2	PH1131	Ig heavy chain V r
263	47	50.5	111	2	PH0993	Ig heavy chain V r	336	44	47.3	99	2	D34964	Ig heavy chain V-V
264	47	50.5	111	2	PH0994	Ig heavy chain V r	337	44	47.3	102	2	PH1260	Ig heavy chain V r
265	47	50.5	111	2	PH0992	Ig heavy chain V r	338	44	47.3	114	4	A47271	nitrophenyl phosph
266	47	50.5	112	2	S25042	Ig heavy chain V r	339	44	47.3	116	2	S22558	Ig heavy chain V r
267	47	50.5	112	2	A30502	Ig heavy chain V r	340	44	47.3	116	2	S26309	Ig heavy chain V-D
268	47	50.5	113	2	S25044	Ig heavy chain V r	341	44	47.3	117	2	S09960	Ig heavy chain V a
269	47	50.5	113	2	S25041	Ig heavy chain V r	342	44	47.3	119	2	B53285	Ig heavy chain V r
270	47	50.5	115	2	C27563	Ig heavy chain V r	343	44	47.3	119	2	C30562	Ig heavy chain V r
271	47	50.5	116	2	I84704	gene VH104B protei	344	44	47.3	125	2	PH1410	Ig heavy chain V r
272	47	50.5	116	2	S55542	Ig heavy chain V r	345	44	47.3	127	2	PH1415	Ig heavy chain V r
273	47	50.5	117	1	HVMS23	Ig heavy chain pre	346	44	47.3	142	2	A32483	Ig heavy chain V r
274	47	50.5	117	1	HVMS45	Ig heavy chain pre	347	44	47.3	151	2	PL0011	Ig heavy chain pre
275	47	50.5	117	1	HVMS61	Ig heavy chain pre	348	44	47.3	474	1	G2MS11	Ig gamma-2b chain
276	47	50.5	117	1	HVMS84	Ig heavy chain pre	349	44	47.3	980	2	E71605	hypothetical prote
277	47	50.5	117	1	HVMSB4	Ig heavy chain pre	350	44	46.8	1268	2	G85154	hypothetical prote
278	47	50.5	117	1	HVMSB4	Ig heavy chain pre	351	43	46.2	76	2	B28572	Ig heavy chain V r
279	47	50.5	119	2	S25176	Ig heavy chain V r	352	43	46.2	77	2	S46465	Ig heavy chain V r
280	47	50.5	119	2	PL0089	Ig heavy chain V r	353	43	46.2	85	2	E37262	Ig heavy chain V r
281	47	50.5	119	2	PH1503	Ig heavy chain V r	354	43	46.2	98	2	S26909	Ig heavy chain V r
282	47	50.5	120	2	S31999	Ig heavy chain V r	355	43	46.2	98	2	B24754	Ig heavy chain V r
283	47	50.5	120	2	PD0008	Ig heavy chain V r	356	43	46.2	98	2	PH1111	Ig heavy chain V r
284	47	50.5	120	2	A49982	Ig heavy chain V r	357	43	46.2	98	2	PH1118	Ig heavy chain V r
285	47	50.5	122	2	PC4279	anti-SS-A/Ro 60K p	358	43	46.2	98	2	PH1129	Ig heavy chain V r
286	47	50.5	122	2	PC4280	anti-SS-A/Ro 60K p	359	43	46.2	102	2	PH1233	Ig heavy chain V r
287	47	50.5	123	2	B30560	Ig heavy chain V r	360	43	46.2	102	2	PH1491	Ig heavy chain V r
288	47	50.5	127	2	PH1411	Ig heavy chain V r	361	43	46.2	111	2	S25034	Ig heavy chain V r
289	47	50.5	131	2	S66537	Ig heavy chain V r	362	43	46.2	113	2	S55534	Ig heavy chain V r
290	47	50.5	131	2	PN0536	Ig heavy chain V r	363	43	46.2	117	2	S17586	Ig heavy chain V r
291	47	50.5	136	2	PL0077	Ig heavy chain pre	364	43	46.2	119	2	PH1518	Ig heavy chain V r
292	47	50.5	139	1	MHMS18	Ig heavy chain pre	365	43	46.2	119	2	PH1516	Ig heavy chain V r
293	47	50.5	139	2	A27609	Ig heavy chain pre	366	43	46.2	119	2	PH1519	Ig heavy chain V r
294	47	50.5	140	2	PH1483	Ig heavy chain V r	367	43	46.2	120	2	P28195	Ig heavy chain V r
295	47	50.5	141	2	PL0076	Ig heavy chain pre	368	43	46.2	122	2	S06825	Ig heavy chain V r
296	47	50.5	144	2	B30502	Ig heavy chain V r	369	43	46.2	122	2	S32185	Ig heavy chain V r
297	47	50.5	148	2	S29257	Ig heavy chain V r	370	43	46.2	123	2	G48677	Ig heavy chain V-D
298	47	50.5	287	4	PC4402	Ig gamma-2a chain	371	43	46.2	123	2	F48677	Ig heavy chain V r
299	47	50.5	469	2	S37483	Ig gamma-2a chain	372	43	46.2	126	2	PH1424	Ig heavy chain V r
300	46	49.5	72	2	C37263	Ig heavy chain V r	373	43	46.2	135	2	PH1494	Ig heavy chain V r
301	46	49.5	94	2	G32513	Ig heavy chain V r	374	43	46.2	138	2	PH0105	Ig heavy chain V r
302	46	49.5	94	2	PL0078	Ig heavy chain V r	375	43	46.2	140	2	PH1488	Ig heavy chain V r
303	46	49.5	96	2	H28195	Ig heavy chain V r	376	43	46.2	459	2	S06607	Ig heavy chain V r
304	46	49.5	98	2	PH1139	Ig heavy chain V r	377	43	46.2	503	2	B81858	Ig heavy chain pre
305	46	49.5	98	2	PH1124	Ig heavy chain V r	378	43	46.2	503	2	C81086	lyeYl-cRNA synthet
306	46	49.5	98	2	PH1157	Ig heavy chain V r	380	43	46.2	505	2	AT0108	hypothetical prote
307	46	49.5	102	2	B37263	Ig heavy chain V r	381	42	45.7	2911	2	T20566	hypothetical prote
308	46	49.5	108	2	PH0977	Ig heavy chain V r	382	42	45.2	98	2	S26920	Ig heavy chain V r
309	46	49.5	121	2	PL0281	Ig heavy chain V r	383	42	45.2	98	2	PH0877	Ig heavy chain V r
310	46	49.5	137	2	B29380	Ig heavy chain pre	384	42	45.2	98	2	S26911	Ig heavy chain V r
311	45	48.4	96	2	D25155	Ig heavy chain V r	385	42	45.2	98	2	PH1150	Ig heavy chain V r
312	45	48.4	98	2	S26913	Ig heavy chain V r	386	42	45.2	98	2	PH1147	Ig heavy chain V r
313	45	48.4	101	2	F37262	Ig heavy chain V r	387	42	45.2	98	2	PH1144	Ig heavy chain V r
314	45	48.4	102	2	PH1243	Ig heavy chain V r	388	42	45.2	102	2	PH1276	Ig heavy chain V r
315	45	48.4	102	2	PH1232	Ig heavy chain V r	389	42	45.2	102	2	PH1235	Ig heavy chain V r
316	45	48.4	102	2	PH1262	Ig heavy chain V r	390	42	45.2	108	2	PH0972	Ig heavy chain V r
317	45	48.4	105	2	PH1265	Ig heavy chain V r	391	42	45.2	111	2	S25040	Ig heavy chain V r
318	45	48.4	106	2	PH0978	Ig heavy chain V r	392	42	45.2	117	1	HVHDHC	Ig heavy chain pre
319	45	48.4	107	2	F32513	Ig heavy chain V r	393	42	45.2	117	2	S19966	Ig heavy chain V r
320	45	48.4	109	2	PH0971	Ig heavy chain V r	394	42	45.2	119	2	S19964	Ig heavy chain V r
321	45	48.4	109	2	PL0233	Ig heavy chain V r							

395	42	45.2	121	2	A21854	Ig heavy chain V r	468	40	43.0	751	2	T15403	hypothetical prote
396	42	45.2	127	2	PH1421	Ig heavy chain V r	469	40	43.0	815	2	T15402	hypothetical prote
397	42	45.2	127	2	S34014	Ig heavy chain V r	470	40	43.0	824	2	T44037	helicase [imported
398	42	45.2	128	2	A37267	Ig heavy chain V r	471	40	43.0	1033	2	F71256	conserved hypotnet
399	42	45.2	136	2	PL0208	Ig heavy chain pre	472	40	43.0	1054	2	S54473	78S3 protein - yea
400	42	45.2	137	2	PH1227	Ig heavy chain pre	473	40	43.0	1108	2	UC4037	alpha-mannosidase
401	42	45.2	138	2	S45249	Ig heavy chain pre	474	40	43.0	1607	2	T21982	hypothetical prote
402	42	45.2	150	2	PN0444	Ig heavy chain V r	475	39.5	42.5	326	2	C97090	lactate dehydrogen
403	42	45.2	197	2	C69779	NaD(P)H oxidoreduc	476	39	41.9	93	2	A37253	Ig heavy chain V r
404	42	45.2	288	2	S28690	Ig heavy chain VDU	477	39	41.9	110	2	PL0244	Ig heavy chain V r
405	42	45.2	342	2	T39545	hypothetical prote	478	39	41.9	112	2	PL0245	Ig heavy chain V r
406	42	45.2	402	2	A46495	IL-1 beta converta	479	39	41.9	113	2	E33936	Ig heavy chain V r
407	42	45.2	504	2	C86470	hypothetical prote	480	39	41.9	114	2	S20707	Ig heavy chain V r
408	42	45.2	588	2	T07085	probable lysine-tr	481	39	41.9	118	2	PL0200	anti-DNA autoantib
409	42	45.2	597	2	S43187	lysine-tRNA ligase	482	39	41.9	119	2	S45714	Ig heavy chain V r
410	42	45.2	652	2	AB1020	acetate-CoA ligase	483	39	41.9	126	2	PH1412	Ig heavy chain V r
411	42	45.2	722	2	D71607	VP845-like protein	484	39	41.9	132	2	PH1427	Ig heavy chain V r
412	42	45.2	1086	2	AH1290	cellulobiose-phospho	485	39	41.9	211	2	B95064	conserved hypotnet
413	42	45.2	1086	2	AF1662	hypothetical prote	486	39	41.9	211	2	D97931	conserved hypotnet
414	41	44.1	79	2	C97829	hypothetical prote	487	39	41.9	216	2	AF0789	phosphage p13 prote
415	41	44.1	86	2	S29544	Ig heavy chain V r	488	39	41.9	279	2	D86802	hypothetical prote
416	41	44.1	96	2	S17609	Ig heavy chain V r	489	39	41.9	362	2	T42689	hypothetical prote
417	41	44.1	98	2	S26921	Ig heavy chain V r	490	39	41.9	418	2	G71952	hypothetical prote
418	41	44.1	98	2	PH1429	Ig heavy chain V r	491	39	41.9	429	2	UC4656	rRNA endonuclease
419	41	44.1	101	2	S12431	Ig heavy chain V r	492	39	41.9	442	2	T39683	znuotin-like protei
420	41	44.1	101	2	I37262	Ig heavy chain V r	493	39	41.9	462	2	S12527	metalloproteinae
421	41	44.1	102	2	PH1275	Ig heavy chain V r	494	39	41.9	463	2	T48116	Ig gamma-2b chain
422	41	44.1	102	2	PH1238	Ig heavy chain V r	495	39	41.9	475	2	S01321	Ig gamma-2b chain
423	41	44.1	102	2	PH1240	Ig heavy chain V r	496	39	41.9	492	2	A55589	lysine-tRNA ligase
424	41	44.1	102	2	PH1490	Ig heavy chain V r	497	39	41.9	508	2	H75605	hypothetical prote
425	41	44.1	107	2	PH1013	Ig heavy chain V r	498	39	41.9	520	2	T37957	probable cytochrom
426	41	44.1	107	2	PH0984	Ig heavy chain V r	499	39	41.9	556	2	T32567	hypothetical prote
427	41	44.1	108	2	PH1012	Ig heavy chain V r	500	39	41.9	591	2	T21564	glycosyl hydrolase
428	41	44.1	111	2	S25051	Ig heavy chain V r	501	39	41.9	626	2	B95250	hypothetical prote
429	41	44.1	114	2	A27563	Ig heavy chain V r	502	39	41.9	626	2	B98115	hypothetical prote
430	41	44.1	115	2	PH1560	Ig heavy chain V r	503	39	41.9	1123	2	T30880	dynein heavy chain
431	41	44.1	116	2	S20645	Ig heavy chain V r	504	39	41.9	1627	2	A82109	two-component hydr
432	41	44.1	118	2	A24754	Ig heavy chain V r	505	38	40.9	2496	2	A71616	secreted protein p
433	41	44.1	119	2	PH0099	Ig heavy chain V r	506	38.5	41.4	105	2	S67941	Ig heavy chain var
434	41	44.1	122	2	PH1426	Ig heavy chain V-D	507	38.5	41.4	528	2	B96625	hypothetical prote
435	41	44.1	123	2	E46677	Ig heavy chain V-D	508	38	40.9	67	2	PH1146	Ig heavy chain V r
436	41	44.1	125	1	HVHUMO	Ig heavy chain V-I	509	38	40.9	90	2	PH1485	Ig heavy chain V r
437	41	44.1	126	2	S31930	Ig gamma chain pre	510	38	40.9	98	2	S26910	Ig heavy chain V r
438	41	44.1	128	2	C37267	Ig heavy chain V r	511	38	40.9	98	2	S26912	Ig heavy chain V r
439	41	44.1	137	2	PH1562	Ig heavy chain V r	512	38	40.9	98	2	S26938	Ig heavy chain V r
440	41	44.1	138	2	PH1564	Ig heavy chain V r	513	38	40.9	98	2	PH1141	Ig heavy chain V r
441	41	44.1	138	2	PH1565	Ig heavy chain V r	514	38	40.9	99	2	D37262	Ig heavy chain V r
442	41	44.1	140	1	HVMSG7	Ig heavy chain pre	515	38	40.9	102	2	PH1236	Ig heavy chain V r
443	41	44.1	140	2	PH1486	Ig heavy chain V r	516	38	40.9	104	2	S69899	Ig heavy chain V r
444	41	44.1	140	2	PH1499	Ig heavy chain V r	517	38	40.9	110	2	A32189	Ig heavy chain V r
445	41	44.1	140	2	PH1484	Ig heavy chain V r	518	38	40.9	117	1	HVHUS5	Ig heavy chain pre
446	41	44.1	144	2	PH1563	Ig heavy chain V r	519	38	40.9	117	2	S31680	Ig heavy chain V r
447	41	44.1	147	2	PH1561	Ig heavy chain V r	520	38	40.9	117	2	S18551	Ig heavy chain V r
448	41	44.1	147	2	PC4202	monoclonal antibod	521	38	40.9	117	2	S09961	Ig heavy chain V-D
449	41	44.1	1791	2	T02909	hypothetical prote	522	38	40.9	118	2	S36265	Ig heavy chain V r
450	40.5	43.5	239	2	AE0772	probable exported	523	38	40.9	118	2	PL0084	Ig heavy chain V r
451	40.5	43.5	239	2	T27079	hypothetical prote	524	38	40.9	120	2	S03471	Ig heavy chain V-D
452	40.5	43.5	239	2	T15795	hypothetical prote	525	38	40.9	122	2	S06823	Ig heavy chain V r
453	40.5	43.5	239	2	S29329	hypothetical prote	526	38	40.9	123	2	PH1403	Ig heavy chain V r
454	40.5	43.5	31	2	S22023	Ig mu chain - mous	527	38	40.9	125	2	S20639	Ig heavy chain V r
455	40	43.0	80	2	PH1166	Ig heavy chain V r	528	38	40.9	129	2	S46393	Ig heavy chain V r
456	40	43.0	98	2	PH1123	Ig heavy chain V r	529	38	40.9	131	2	S14390	tap2 protein - gar
457	40	43.0	111	2	PH0988	Ig heavy chain V r	530	38	40.9	135	2	S49530	anti-Sm antibody V
458	40	43.0	115	2	A56700	Ig heavy chain (an	531	38	40.9	140	2	PH1498	Ig heavy chain V r
459	40	43.0	131	2	PH1425	Ig heavy chain V r	532	38	40.9	171	2	S23625	Ig heavy chain V r
460	40	43.0	136	1	HVMSB1	Ig heavy chain pre	533	38	40.9	225	2	T03555	hypothetical prote
461	40	43.0	140	2	PH1489	Ig heavy chain pre	534	38	40.9	230	2	F95214	glycosyl transfera
462	40	43.0	202	1	HYRSR	ruberylsin (EC 3.4	535	38	40.9	243	2	E98078	conserved hypotnet
463	40	43.0	322	2	F75365	conserved hypotnet	536	38	40.9	246	2	JC1496	transcription fact
464	40	43.0	379	2	A37480	vermillion protein	537	38	40.9	271	2	T31304	2-hydroxypenta-2,4
465	40	43.0	483	2	T47974	hypothetical prote	538	38	40.9	303	2	H35068	apolipoprotein H-r
466	40	43.0	494	2	B86671	lysine-tRNA ligase	539	38	40.9	313	2	F72317	conserved hypotnet
467	40	43.0	679	2	G71615	phospholipase A2-1	540	38	40.9	349	2	T16872	hypothetical prote

541	38	40.9	353	2	D96596	hypothetical prote
542	38	40.9	378	2	A33271	manganese peroxidase
543	38	40.9	382	2	A32630	manganese peroxidase
544	38	40.9	433	2	G87948	protein W02D9.1 [i
545	38	40.9	449	2	S27098	pectate lyase (EC
546	38	40.9	453	2	B97738	outer membrane pro
547	38	40.9	456	2	H71733	intermediate filam
548	38	40.9	464	2	A56600	hypothetical prote
549	38	40.9	486	2	E64438	lysine-tRNA ligase
550	38	40.9	501	2	F71965	lysine-tRNA ligase
551	38	40.9	501	2	F64542	lysine-tRNA ligase
552	38	40.9	502	1	D83183	lysyl-tRNA synthet
553	38	40.9	501	2	D64110	lysine-tRNA ligase
554	38	40.9	503	2	T26114	hypothetical prote
555	38	40.9	505	2	S64837	hypothetical prote
556	38	40.9	510	2	S77380	lysine-tRNA ligase
557	38	40.9	531	2	T17212	hypothetical prote
558	38	40.9	591	1	SYBYKT	lysine-tRNA ligase
559	38	40.9	592	2	G69159	sensory transducti
560	38	40.9	597	2	G70403	lysine-tRNA ligase
561	38	40.9	642	2	T12113	transcription fact
562	38	40.9	824	2	T44222	probable helicase
563	38	40.9	876	2	F97688	leucyl-tRNA synthet
564	38	40.9	876	2	AC2914	leucyl-tRNA synthet
565	38	40.9	888	2	S23065	ufo protein - mous
566	38	40.9	894	1	A41527	protein-tyrosine k
567	38	40.9	942	2	C96760	probable sucrose s
568	38	40.9	942	2	S23251	protein-tyrosine k
569	38	40.9	963	2	B85055	hypothetical prote
570	38	40.9	976	2	S45738	pleiotropic drug r
571	38	40.9	1099	2	A59300	myosin-II - mouse
572	38	40.9	1157	2	T43258	pyruvate:ferredoxi
573	38	40.9	1157	2	T13158	adenylate cyclase
574	38	40.9	1444	1	ARKWPTM	genome polypeptide
575	38	40.9	2491	2	AS57036	tailin - slime mold
576	37.5	40.3	168	2	F71899	hypothetical prote
577	37.5	40.3	449	2	A45709	major early-transc
578	37.5	40.3	546	2	T26568	hypothetical prote
579	37.5	40.3	3433	1	S28381	utrophin - human
580	37	39.8	95	2	G37262	Ig heavy chain V r
581	37	39.8	98	2	PH1143	Ig heavy chain V r
582	37	39.8	101	2	F96950	uncharacterized sm
583	37	39.8	102	2	PH1237	Ig heavy chain V r
584	37	39.8	117	2	S18553	Ig heavy chain V r
585	37	39.8	117	2	S03289	Ig heavy chain pre
586	37	39.8	119	2	D30562	Ig heavy chain V r
587	37	39.8	119	2	S20640	Ig heavy chain V r
588	37	39.8	121	2	S19969	Ig heavy chain V r
589	37	39.8	123	2	S60067	Ig heavy chain V r
590	37	39.8	125	2	P85673	hypothetical prote
591	37	39.8	125	2	B90814	hypothetical prote
592	37	39.8	125	2	E64854	yeif protein precu
593	37	39.8	141	2	A39276	Ig heavy chain pre
594	37	39.8	163	2	D64077	SOL1 protein homol
595	37	39.8	176	2	T39438	probable ribosomal
596	37	39.8	216	2	E91016	alkylated DNA repa
597	37	39.8	216	2	G85860	DNA repair system
598	37	39.8	221	2	S49220	Ig gamma-1 chain -
599	37	39.8	239	2	T22573	hypothetical prote
600	37	39.8	264	2	E90500	lipase-protein 1i
601	37	39.8	307	2	E70082	glucose 1-dehydrog
602	37	39.8	354	2	A32231	B-cell differentia
603	37	39.8	357	2	D87563	4-hydroxyphenylpyr
604	37	39.8	359	2	A46509	B cell differentia
605	37	39.8	382	2	D89999	alanine racemase l
606	37	39.8	382	2	D96738	hypothetical prote
607	37	39.8	405	1	T03466	probable exonuclea
608	37	39.8	422	2	S69286	geranylgeranyl hyd
609	37	39.8	422	2	A35068	complement factor
610	37	39.8	455	2	H82881	cytosol aminopepti
611	37	39.8	459	2	A46372	immunophilin FKBP5
612	37	39.8	469	2	C86170	hypothetical prote
613	37	39.8	472	2	A60330	protein A precursor
614	37	39.8	614	1	SYECKT	lysine-tRNA ligase
615	37	39.8	615	1	SYECKU	lysine-tRNA ligase
616	37	39.8	616	1	AF0871	lysyl-tRNA synthet
617	37	39.8	617	2	F85944	lysine-tRNA synthet
618	37	39.8	618	2	B91099	lysine-tRNA synthet
619	37	39.8	619	2	G91257	lysine-tRNA synthet
620	37	39.8	620	1	B6108	lysine-tRNA ligase
621	37	39.8	621	1	D69884	conserved hypotnet
622	37	39.8	622	2	A82296	lysyl-tRNA synthet
623	37	39.8	623	2	A82236	phycoene dehydroge
624	37	39.8	624	1	RCKBAP	nif-specific regul
625	37	39.8	625	2	S15183	gas-vesicle operon
626	37	39.8	626	2	T08241	gas-vesicle operon
627	37	39.8	627	2	T50099	probable protein-c
628	37	39.8	628	2	S04845	Ig heavy chain pre
629	37	39.8	629	2	T08552	hypothetical prote
630	37	39.8	630	2	AC2932	GDBF family prote
631	37	39.8	631	2	H98349	photoreducer, m
632	37	39.8	632	2	T46236	hypothetical prote
633	37	39.8	633	2	E64046	mismatch repair pr
634	37	39.8	634	2	T06586	DNA-binding protei
635	37	39.8	635	2	S77547	ethylene response
636	37	39.8	636	2	A82515	conserved hypotnet
637	37	39.8	637	2	S64405	Mtcl protein - yea
638	37	39.8	638	2	AB2318	two-component hybr
639	37	39.8	639	2	C96620	protein T30E16.23
640	37	39.8	640	1	S31926	myosin IB heavy ch
641	37	39.8	641	2	T39663	paired amphipathic
642	37	39.8	642	1	NRM5H	complement factor
643	37	39.8	643	2	S55144	RRL1 protein - yea
644	37	39.8	644	2	T38774	myosin-3 heavy cha
645	37	39.8	645	2	T31679	bactitracin synthet
646	37	39.8	646	2	S33024	hypothetical prote
647	36.5	39.2	647	2	D75208	sugar abc transpor
648	36.5	39.2	648	1	AC2508	hypothetical prote
649	36.5	39.2	649	1	RNBYL2	DNA-directed DNA p
650	36.5	39.2	650	1	AS5875	xanthine dehydroge
651	36	38.7	651	2	H25114	T cell receptor V-
652	36	38.7	652	2	S57568	Ig heavy chain V r
653	36	38.7	653	2	PH1672	Ig heavy chain V r
654	36	38.7	654	2	S03482	Ig heavy chain V-D
655	36	38.7	655	2	B28814	Ig heavy chain V-D
656	36	38.7	656	2	JN0295	Ig heavy chain V r
657	36	38.7	657	2	S03077	Ig heavy chain V r
658	36	38.7	658	2	A30551	Ig heavy chain V r
659	36	38.7	659	2	PH1492	Ig heavy chain pre
660	36	38.7	660	2	S04576	hypothetical prote
661	36	38.7	661	2	T20697	Ig heavy chain V r
662	36	38.7	662	2	S31685	Ig heavy chain V r
663	36	38.7	663	2	F97003	probable transcrip
664	36	38.7	664	1	RSBY32	ribosomal protein
665	36	38.7	665	2	AR0259	probable phase-rel
666	36	38.7	666	2	S73343	hypothetical prote
667	36	38.7	667	2	UOQNT	ubiquitin precuro
668	36	38.7	668	2	XCSAS1	toxic shock syndro
669	36	38.7	669	2	T35717	hypothetical prote
670	36	38.7	670	2	G86368	hypothetical prote
671	36	38.7	671	2	A11983	hypothetical prote
672	36	38.7	672	2	S77176	cell-cell signalin
673	36	38.7	673	2	S42727	ornithine carbamoy
674	36	38.7	674	2	H24706	nifN protein - Azo
675	36	38.7	675	2	D85911	hypothetical prote
676	36	38.7	676	2	T47685	probable RNA bindi
677	36	38.7	677	2	JC3324	lim protein - huma
678	36	38.7	678	2	E71679	D-alanine-D-alanin
679	36	38.7	679	2	T45012	conserved hypotnet
680	36	38.7	680	2	S77598	cytochrome-c oxida
681	36	38.7	681	2	T00578	probable GDSL-moti
682	36	38.7	682	2	T21620	hypothetical prote
683	36	38.7	683	2	AB3233	replication protei
684	36	38.7	684	2	JC2579	manganese peroxidase
685	36	38.7	685	2	C91067	hypothetical prote
686	36	38.7	686	2	AD2191	hypothetical prote

687	36	38.7	446	2	D84683	hypothetical prote
688	36	38.7	501	2	C81339	probable phosphate
689	36	38.7	507	2	T50398	hypothetical serin
690	36	38.7	512	2	T37819	probable zinc met
691	36	38.7	523	2	S50479	26S proteasome reg
692	36	38.7	527	2	T51258	hypothetical prote
693	36	38.7	543	1	WZBEM5	gene 19 protein -
694	36	38.7	550	2	S65753	beta-fructofuran
695	36	38.7	550	2	A11163	flagellar basal-bo
696	36	38.7	550	2	A11522	hypothetical prote
697	36	38.7	570	2	T33320	hypothetical prote
698	36	38.7	571	2	T43456	hypothetical prote
699	36	38.7	581	2	B72221	hypothetical prote
700	36	38.7	615	2	PH0853	methyl-directed mi
701	36	38.7	615	2	B91272	enzyme in methyl-d
702	36	38.7	615	2	B86113	enzyme in methyl-d
703	36	38.7	618	2	AG1048	DNA mismatch repai
704	36	38.7	618	2	A33588	mismatch repair pr
705	36	38.7	635	2	AC0046	DNA mismatch repai
706	36	38.7	649	2	H84960	exoribonuclease II
707	36	38.7	653	2	A82334	DNA mismatch repai
708	36	38.7	655	2	A12556	hypothetical prote
709	36	38.7	660	2	AH2234	copper amine oxida
710	36	38.7	660	2	E90595	hypothetical prote
711	36	38.7	661	2	T51779	non-phototropic hy
712	36	38.7	707	1	A53530	protein kinase C (
713	36	38.7	773	1	ORRBG	secretory componen
714	36	38.7	778	2	B71164	probable beta-gala
715	36	38.7	793	2	S73662	probable lipoprote
716	36	38.7	794	2	S73877	probable lipoprote
717	36	38.7	815	2	H82137	biotin sulfoxide r
718	36	38.7	830	2	B44439	protein kinase (EC
719	36	38.7	856	2	A44439	protein kinase (EC
720	36	38.7	860	2	T28227	ORF MSY067 probabl
721	36	38.7	862	2	T01798	hypothetical prote
722	36	38.7	873	2	UC7079	homeobox protein z
723	36	38.7	873	2	JC4863	homeobox protein z
724	36	38.7	926	1	A41105	protein-tyrosine-p
725	36	38.7	1020	2	T18260	l-phosphatidylins
726	36	38.7	1042	2	H70203	isoleucine-tRNA li
727	36	38.7	1063	2	T00624	endo-1,4-beta-xyla
728	36	38.7	1369	2	T32338	hypothetical prote
729	36	38.7	2091	2	A97071	hypothetical prote
730	36	38.7	4868	2	B54161	ryanodine-binding
731	35.5	38.2	278	2	B83453	hypothetical prote
732	35.5	38.2	299	2	T37756	jun activation dom
733	35.5	38.2	359	2	T22731	hypothetical prote
734	35.5	38.2	451	2	T41877	ME53 ori139 - Bomb
735	35.5	38.2	464	2	T48339	hypothetical prote
736	35.5	38.2	479	2	S60924	hypothetical prote
737	35.5	38.2	498	2	H83793	hypothetical prote
738	35.5	38.2	531	2	B95180	hypothetical prote
739	35.5	38.2	531	2	F98047	hypothetical prote
740	35.5	38.2	609	2	F85078	probable transpos
741	35.5	38.2	663	2	F84490	probable TNP2-like
742	35.5	38.2	695	2	A13129	hypothetical prote
743	35.5	38.2	727	2	H98157	periplasmic alpha-
744	35.5	38.2	817	2	D85049	probable transpos
745	35.5	38.2	876	2	A89944	alanyl-tRNA syntase
746	35.5	38.2	1017	2	S62435	probable kinase h
747	35.5	38.2	1068	2	F84614	probable kinesin d
748	35.5	38.2	1074	2	G96504	probable Bn/Spm-11
749	35.5	38.2	1095	2	T43275	neubrain - rat
750	35.5	38.2	1157	1	S49247	paraspinal crysfa
751	35.5	38.2	1335	2	H86489	protein F27J15.14
752	35.5	38.2	1526	2	A96528	Ig heavy chain V r
753	35	37.6	90	2	S03306	Ig heavy chain V r
754	35	37.6	90	2	A90335	conserved hypochet
755	35	37.6	97	2	S16028	Ig heavy chain V r
756	35	37.6	98	2	S25918	Ig heavy chain V r
757	35	37.6	98	2	H47624	Ig heavy chain V-I
758	35	37.6	98	2	PH1122	Ig heavy chain V r
759	35	37.6	116	2	S22553	Ig heavy chain V r
760	760					
761	35	37.6	118	2	S25174	Ig heavy chain V r
762	35	37.6	123	2	D33548	Ig heavy chain V-1
763	35	37.6	130	2	B89793	hypothetical prote
764	35	37.6	132	2	S31596	Ig heavy chain V r
765	35	37.6	136	2	S31600	Ig heavy chain V r
766	35	37.6	137	1	G2MS43	Ig heavy chain pre
767	35	37.6	137	2	S68956	nucleoside-diphosp
768	35	37.6	141	2	F72466	probable nucleosid
769	35	37.6	147	2	S64252	probable membrane
770	35	37.6	155	2	S45342	galactose/lactose-
771	35	37.6	158	2	F82155	probable DNA repai
772	35	37.6	166	2	T50531	hypothetical prote
773	35	37.6	185	2	H86835	hypothetical prote
774	35	37.6	194	2	S59793	SKP1 protein - yea
775	35	37.6	195	2	T48945	hypothetical prote
776	35	37.6	199	2	T40870	very hypothetical
777	35	37.6	209	2	G70689	hypothetical prote
778	35	37.6	240	2	T04419	aleurone ribonucle
779	35	37.6	241	2	G86355	hypothetical prote
780	35	37.6	256	2	G82170	conserved hypotnet
781	35	37.6	261	2	T22120	hypothetical prote
782	35	37.6	265	2	AC1709	hydrolyase homolog
783	35	37.6	273	1	EDBE12	immediate-early pr
784	35	37.6	284	2	T42608	immediate-early pr
785	35	37.6	285	2	G86334	hypothetical prote
786	35	37.6	290	2	AG2216	hypothetical prote
787	35	37.6	303	2	E90602	hypothetical prote
788	35	37.6	305	2	A83340	hypothetical prote
789	35	37.6	329	2	T00873	hypothetical prote
790	35	37.6	332	2	T39391	meu14. RING zinc f
791	35	37.6	340	1	WMBEL1	latency-related pr
792	35	37.6	345	2	T02295	hypothetical prote
793	35	37.6	349	2	F83275	conserved hypotnet
794	35	37.6	355	2	T35025	probable DNA ligas
795	35	37.6	359	2	H84706	probable GDSF-meci
796	35	37.6	363	2	S04764	peroxidase (EC 1.1
797	35	37.6	363	2	AF2457	hypothetical prote
798	35	37.6	374	2	T77420	hypothetical prote
799	35	37.6	379	2	A49679	exo-alpha-sialidas
800	35	37.6	380	2	C71688	tail fiber protein
801	35	37.6	382	2	S13237	endo-alpha-sialidas
802	35	37.6	382	2	AC3055	succionglycan bios
803	35	37.6	385	2	UC7751	exo-alpha-sialidas
804	35	37.6	393	2	S49759	probable membrane
805	35	37.6	397	2	H86754	phage pi2 prote
806	35	37.6	401	2	T24381	hypothetical prote
807	35	37.6	405	2	H64408	hypothetical prote
808	35	37.6	413	2	A84620	similar to hookles
809	35	37.6	421	2	T35205	citrate synthase-1
810	35	37.6	422	2	T10655	hypothetical prote
811	35	37.6	423	2	T15350	hypothetical prote
812	35	37.6	436	2	B98231	exoh protein limpo
813	35	37.6	436	2	T14816	hypothetical prote
814	35	37.6	438	2	H71943	hypothetical prote
815	35	37.6	441	1	E70461	pmtA protein - Aqu
816	35	37.6	458	2	A43549	vimentin 1 - Afri
817	35	37.6	467	1	WZBB61	gene 61 protein -
818	35	37.6	470	2	C97032	Fe-S oxidoreductas
819	35	37.6	481	2	T38699	glucose-6-phosphat
820	35	37.6	481	2	S26698	alkaline proteinas
821	35	37.6	486	2	B84914	hypothetical prote
822	35	37.6	489	2	T34322	probable homoserin
823	35	37.6	489	2	F43715	probable oxysterol
824	35	37.6	490	2	T48189	cycochrome P450 II
825	35	37.6	506	2	B82721	lyeyl-tRNA syntnet
826	35	37.6	517	2	T49937	hypothetical prote
827	35	37.6	527	2	E72016	lysine-tRNA ligase
828	35	37.6	527	2	A86607	lyeyl tRNA syntnet
829	35	37.6	531	2	G84775	probable B2Fs fami
830	35	37.6	542	2	S57658	probable thioredox
831	35	37.6	558	2	S68447	origin recognition
832	35	37.6	560	2	AF1416	sucrose phosphoryl
			562	2	T15131	hypothetical prote

833	35	37.6	563	2	S59957	606	34.5	37.1	853	2	S74279	hypothetical prote
834	35	37.6	572	2	AC1200	907	34.5	37.1	965	2	AE2452	two-component hybr
835	35	37.6	572	2	AI1557	908	34.5	37.1	1003	2	AC9521	glycine dehydrogen
836	35	37.6	578	2	A34283	909	34.5	37.1	1123	2	AD2045	hypothetical prote
837	35	37.6	578	2	T03292	910	34.5	37.1	1844	2	S01956	hypothetical prote
838	35	37.6	594	2	B64018	911	34.5	37.1	1985	2	S31951	hypothetical prote
839	35	37.6	602	2	AG0155	912	34	36.6	70	2	H81379	30S ribosomal prot
840	35	37.6	611	2	S65472	913	34	36.6	73	2	B84901	hypothetical prote
841	35	37.6	616	1	I64056	914	34	36.6	80	2	G84773	hypothetical prote
842	35	37.6	625	1	A89844	915	34	36.6	82	2	A36025	Ig heavy chain V r
843	35	37.6	629	2	T14776	916	34	36.6	90	2	A60526	complement C3 - ax
844	35	37.6	632	2	T14776	917	34	36.6	91	2	SS2298	hypothetical prote
845	35	37.6	632	2	B88712	918	34	36.6	99	2	C37262	Ig heavy chain V r
846	35	37.6	635	1	A29358	918	34	36.6	99	2	C37262	Ig heavy chain V r
847	35	37.6	654	2	AB2932	919	34	36.6	104	2	PH1665	Ig heavy chain V r
848	35	37.6	654	2	D98350	920	34	36.6	111	2	S10222	hypothetical prote
849	35	37.6	658	2	T31958	921	34	36.6	114	2	PH1667	Ig heavy chain V r
849	35	37.6	666	2	C82932	922	34	36.6	118	2	PH1666	Ig heavy chain V r
850	35	37.6	687	2	F85188	923	34	36.6	119	1	AYMSJ5	Ig heavy chain V r
851	35	37.6	692	2	T20760	924	34	36.6	120	2	S46374	Ig kappa chain V-J
852	35	37.6	699	1	I54763	925	34	36.6	122	2	C49590	Ig heavy chain V r
853	35	37.6	709	2	T06557	926	34	36.6	122	2	E37267	Ig heavy chain V r
854	35	37.6	754	2	A87353	927	34	36.6	124	2	S40348	Ig kappa chain V-J
855	35	37.6	760	2	T20759	928	34	36.6	125	2	S68170	Ig heavy chain V r
856	35	37.6	761	2	C64813	929	34	36.6	125	2	G64076	ribosomal protein
857	35	37.6	761	2	G90728	930	34	36.6	129	2	T44056	glycoprotein gp82/
858	35	37.6	761	2	H85579	931	34	36.6	135	2	B32274	Ig heavy chain pre
859	35	37.6	774	2	T49573	932	34	36.6	137	2	G71915	hypothetical prote
860	35	37.6	776	2	T19532	933	34	36.6	143	1	KEMS	epsilon-casein pre
861	35	37.6	777	2	AD0982	934	34	36.6	161	2	T23912	hypothetical prote
862	35	37.6	778	2	T39047	935	34	36.6	170	2	T15991	hypothetical prote
863	35	37.6	779	2	E71825	936	34	36.6	178	2	S29594	Ig gamma chain (MM
864	35	37.6	794	2	S73328	937	34	36.6	181	2	D69990	hypothetical prote
865	35	37.6	798	2	T23539	938	34	36.6	191	2	H72767	hypothetical prote
866	35	37.6	825	1	H64083	939	34	36.6	191	2	AC2437	hypothetical prote
867	35	37.6	858	1	A42239	940	34	36.6	191	2	S76838	hypothetical prote
868	35	37.6	949	2	D84487	941	34	36.6	197	2	B34959	triacylglycerol li
869	35	37.6	954	2	AF2756	942	34	36.6	198	2	B89959	hypothetical prote
870	35	37.6	954	2	E97537	943	34	36.6	211	2	C97223	probable S-adenosy
871	35	37.6	964	2	S57379	944	34	36.6	211	2	T32976	hypothetical prote
872	35	37.6	1018	1	S73720	945	34	36.6	213	2	S35917	capsid protein VP1
873	35	37.6	1021	2	T40928	946	34	36.6	214	2	AG1276	hypothetical prote
874	35	37.6	1086	2	UC6079	947	34	36.6	214	2	AG1639	hypothetical prote
875	35	37.6	1109	2	S53601	948	34	36.6	216	1	BVCKRB	alpha protein - Bsc
876	35	37.6	1205	2	T27053	949	34	36.6	220	2	E84057	hypothetical prote
877	35	37.6	1235	2	AC1728	950	34	36.6	220	2	A72153	Q2L protein - vari
878	35	37.6	1287	2	S55954	951	34	36.6	220	2	T28457	hypothetical prote
879	35	37.6	1290	2	A36466	952	34	36.6	220	2	I36838	O2L protein - vari
880	35	37.6	1352	2	G84473	953	34	36.6	220	2	H83967	hypothetical prote
881	35	37.6	1462	1	B36182	954	34	36.6	224	1	A64055	Grp cyclonhydrolase
882	35	37.6	1509	2	B89985	955	34	36.6	224	2	S55081	hypothetical prote
883	35	37.6	1611	2	G84493	956	34	36.6	235	2	F75536	hypothetical prote
884	35	37.6	1631	1	SAZOK1	957	34	36.6	244	2	B90542	hypothetical prote
885	35	37.6	1639	2	S05603	958	34	36.6	256	2	D89769	hypothetical prote
886	35	37.6	1640	2	A24594	959	34	36.6	259	2	T09317	glycoprotein - hum
887	35	37.6	2672	2	A48126	960	34	36.6	263	2	T44415	tRNA pseudouridine
888	35	37.6	2957	2	T33152	961	34	36.6	266	2	T19191	hypothetical prote
889	35	37.6	2962	2	T19756	962	34	36.6	268	2	A56446	Ig heavy chain V r
890	35	37.6	3206	1	GNVSPV	963	34	36.6	271	2	D86767	hypothetical prote
891	35	37.6	3282	2	B82750	964	34	36.6	273	2	G69370	manganese-constan
892	35	37.6	3442	2	B82589	965	34	36.6	278	2	T19330	hypothetical prote
893	35	37.6	3455	2	B82519	966	34	36.6	278	2	C83019	conserved hypotet
894	34.5	37.1	137	2	C41287	967	34	36.6	292	2	T10106	chitinase (EC 3.2.
895	34.5	37.1	200	2	C83086	968	34	36.6	293	1	EDBERF	immediate-early pr
896	34.5	37.1	234	2	T07445	969	34	36.6	297	2	F70201	conserved hypotet
897	34.5	37.1	402	2	S32142	970	34	36.6	299	2	I37468	house keeping gene
898	34.5	37.1	425	2	T46698	971	34	36.6	299	2	C97118	uncharacterized co
899	34.5	37.1	515	2	G84492	972	34	36.6	310	2	UN0490	28k lipase precurs
900	34.5	37.1	559	2	S04531	973	34	36.6	321	2	E97741	D-alanine-D-alanin
901	34.5	37.1	664	2	T29011	974	34	36.6	328	2	B86030	probable dehydroge
902	34.5	37.1	729	2	S36605	975	34	36.6	328	2	C65154	probable 2-hydroxy
903	34.5	37.1	733	2	G84668	976	34	36.6	328	2	F91183	probable dehydroge
904	34.5	37.1	803	2	T00092	977	34	36.6	340	2	T42995	hypothetical prote
905	34.5	37.1	835	2	T35763	978	34	36.6	345	2	A97113	probable Fe-S-clus

979 34 36.6 347 2 B28653 fructose-bisphosph
980 34 36.6 350 2 T16385 hypothetical prote
981 34 36.6 361 2 B84827 probable GDSL-mot
982 34 36.6 363 2 T13926 mannopine biosynth
983 34 36.6 363 2 A34959 triacylglycerol li
984 34 36.6 364 2 S40097 hypothetical prote
985 34 36.6 373 2 D90032 translation elonga
986 34 36.6 374 2 T43829 hypothetical prote
987 34 36.6 377 2 T32798 translation elonga
988 34 36.6 379 2 A54961 sialidase, cytoel
989 34 36.6 380 1 S53307 alcohol dehydrogen
990 34 36.6 381 2 S40692 opsin rh2 - fruit
991 34 36.6 383 2 T02179 hypothetical prote
992 34 36.6 387 2 C86133 hypothetical prote
993 34 36.6 387 2 A98292 hypothetical prote
994 34 36.6 398 2 A45633 rhoptry-associated
995 34 36.6 401 2 T00162 integrase - Staphy
996 34 36.6 401 2 B87684 acyl-CoA dehydroge
997 34 36.6 403 2 B87513 acyl-CoA dehydroge
998 34 36.6 404 2 S71236 probable N-acetyl
999 34 36.6 404 2 S57178 2-nitropropane dio
1000 34 36.6 407 2 T51226 hypothetical prote

ALIGNMENTS

RESULT 1

S42183 Ig gamma chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C:Accession: S42183

R:Mo. J.A.; Bona, C.A.; Holmdahl, R.

Eur. J. Immunol. 23, 2503-2510, 1993

A>Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec

A:Reference number: S42176; MUID:94009207; PMID:7691608

A:Accession: S42183

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-101 <NOJ>

A:Cross-references: UNIPARC:UPI0000116565; EMBL:Z25455; NID:9407824; PIND:CAA80942.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 85; DB 2; Length 101;

Best Local Similarity 94.1%; Pred. No. 6.1e-07;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIHPSDETRYNQKFRD 17

DB 50 MIHPSDETRYNQKFRD 66

RESULT 2

PH0986 Ig heavy chain V region (clone 17s-c6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH0986

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A>Title: Both Igm and IgG anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH0986

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-103 <TIL>

A:Cross-references: UNIPARC:UPI0000176D06

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 77; DB 2; Length 103;

Best Local Similarity 93.3%; Pred. No. 1.3e-05;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 IHPDSETRYNQKFR 16

DB 51 IHPDSETRYNQKFR 65

RESULT 3

HVMS3

Ig heavy chain precursor V region (3) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004

C:Accession: A02031

R:Bochwell, A.L.M.; Paskind, M.; Rath, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D

Cell 24, 625-637, 1981

A>Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som

A:Reference number: A90809; MUID:81234548; PMID:6788376

A:Accession: A02031

A:Molecule type: DNA

A:Residues: 1-117 <BOT>

A:Cross-references: UNIPROT:P01749; UNIPARC:UPI0000024BF3

A>Note: the sequence was determined from the germline gene

1 (NPb antibodies)

C:Genetics:

A:Inserts: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (3) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 77; DB 1; Length 117;

Best Local Similarity 87.5%; Pred. No. 1.5e-05;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IHPDSETRYNQKFRD 17

DB 70 IHPDSETRYNQKFRD 85

RESULT 4

PH1164

Ig heavy chain V region (clone 37F.2A) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1164

R:Schltek, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A>Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A:Reference number: PH1105; MUID:92364545; PMID:1500855

A:Accession: PH1164

A:Molecule type: DNA

A:Residues: 1-98 <SCH>

A:Cross-references: UNIPARC:UPI0000176BC6

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 74; DB 2; Length 98;

Best Local Similarity 87.5%; Pred. No. 4e-05;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPDSETRYNQKFRD 17

DB 51 IHPDSETRYNQKFRD 66

RESULT 5
HMS02
Ig heavy chain precursor V region (102) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A02032
R:Bothwell, A.L.M.; Paekind, M.; Reith, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som
A:Reference number: A90809; MUID:81234548; PMID:6788376
A:Accession: A02032
A:Molecule type: DNA
A:Residues: 1-117 <BOT>
A:Cross-references: UNIPROT:P01750; UNIPARC:UPI000002705A
A>Note: the sequence was determined from the germline gene
A>Note: the germline gene, cloned from a library of strain C57BL/6 DNA, is one of a set
1 (NPb antibodies)
C:Genetics:
A:Introns: 16/1
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (102) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 74; DB 1; Length 117;
Best Local Similarity 86.7%; Pred. No. 4.8e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 16
|||||:|||||
Db 70 IHPSDSETRYNQKFK 84

RESULT 6
S25175
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S25175
R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
Submitted to the EMBL Data Library, July 1992
A:Description: Structure and binding properties of monoclonal antibodies to core histone
A:Reference number: S25174
A:Accession: S25175
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <MON>
A:Cross-references: UNIPARC:UPI00001160C2; EMBL:X67620; NID:951856; PIDN:CAA47878.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 74; DB 2; Length 120;
Best Local Similarity 87.5%; Pred. No. 5e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 17
|||||:|||||
Db 51 IHPSDSETRYNQKFK 66

RESULT 7
B22769
Ig heavy chain V region (B1-8.VI/V2) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C:Accession: B22769
R:Childrop, R.; Brugemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026; PMID:7188353
A:Accession: B22769

A:Molecule type: protein
A:Residues: 1-120 <DIR>
A:Cross-references: UNIPARC:UPI0000176B76
A>Note: the sequences of two spontaneously arising somatic variants, B1-8.VI and B1-8.V'
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 74; DB 2; Length 120;
Best Local Similarity 86.7%; Pred. No. 5e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 16
|||||:|||||
Db 51 IHPSDSETRYNQKFK 65

RESULT 8
A49060
Ig heavy chain V region, phenyl phosphonate hapten-specific catalytic monoclonal antibod
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C:Accession: A49060
R:Angelès, T.S.; Smith, R.G.; Darsley, M.J.; Sugawara, R.; Sanchez, R.I.; Kenten, J.;
Biochemistry 32, 12128-12135, 1993
A:Title: Isobzymes: structurally and mechanistically similar catalytic antibodies from
A:Reference number: A49060; MUID:94032348; PMID:8218291
A:Accession: A49060
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-114 <ANG>
A:Cross-references: UNIPARC:UPI0000176C1B
A:Experimental source: hybridoma cell
A>Note: sequence extracted from NCBI backbone (NCBIP:1140371)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 72; DB 2; Length 114;
Best Local Similarity 81.2%; Pred. No. 0.0001;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 17
|||||:|||||
Db 51 IHPSDSETRYNQKFK 66

RESULT 9
PH1161
Ig heavy chain V region (clone 13B.2A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1161
R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1161
A:Molecule type: DNA
A:Residues: 1-88 <SCH>
A:Cross-references: UNIPROT:Q924P9; UNIPARC:UPI0000176A3B
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-88/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 70; DB 2; Length 88;
Best Local Similarity 86.7%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 16
|||||:|||||

Db 43 IHPSDSTYNNQKFK 57

RESULT 10

Ig heavy chain V region - mouse

S26316

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C/Accession: S26316

R/Stark, S.B.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26316

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-108 <STA>

A/Cross-references: UNIPARC:UPI0000115F7E; EMBL:X59190; NID:952066; PIDN:CAA41900.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/2-85/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 70; DB 2; Length 108;

Best Local Similarity 76.5%; Pred. No. 0.00021;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MIHPSDSETRYNQKFKD 17

Db 37 MIDPSDSETRYNQKFRD 53

RESULT 11

S26317

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C/Accession: S26317

R/Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26317

A/Molecule type: mRNA

A/Residues: 1-110 <STA>

A/Cross-references: UNIPARC:UPI00001769A6; EMBL:X59186

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/4-87/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 70; DB 2; Length 110;

Best Local Similarity 76.5%; Pred. No. 0.00021;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MIHPSDSETRYNQKFKD 17

Db 39 MIDPSDSETRYNQKFRD 55

RESULT 12

S26463

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S26463

R/Kavaler, J.

submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S26463

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-111 <KAV>

A/Cross-references: UNIPARC:UPI0000115F67; EMBL:X59113; NID:951922; PIDN:CAA41839.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 70; DB 2; Length 111;

Best Local Similarity 81.2%; Pred. No. 0.00021;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 IHPSDSETRYNQKFKD 17

Db 43 IYPSDSTYNNQKFKD 58

RESULT 13

S24287

Ig heavy chain V region (J528/32) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000

C/Accession: S24287

R/Moncharmont, B.

submitted to the EMBL Data Library, September 1991

A/Description: Cloning and sequencing of the cDNA coding for the variable regions of the

A/Reference number: S24287

A/Accession: S24287

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-122 <MON>

A/Cross-references: UNIPARC:UPI0000116004; EMBL:X62706; NID:951669; PIDN:CAA44588.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 70; DB 2; Length 122;

Best Local Similarity 81.2%; Pred. No. 0.00023;

Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 IHPSDSETRYNQKFKD 17

Db 51 IYPSDSTYNNQKFKD 66

RESULT 14

PH1163

Ig heavy chain V region (clone 35F.2B) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PH1163

R/Schittek, B.; Rajewsky, K.

J. Exp. Med. 176, 427-438, 1992

A/Title: Natural occurrence and origin of somatically mutated memory B cells in mice.

A/Reference number: PH1105; MUID:92364545; PMID:1500855

A/Accession: PH1163

A/Molecule type: DNA

A/Residues: 1-54 <SCH>

A/Cross-references: UNIPARC:UPI0000176A40

A/Experimental source: B cell

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 73.1%; Score 68; DB 2; Length 54;

Best Local Similarity 86.7%; Pred. No. 0.00022;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 IHPSDSETRYNQKFK 16

Db 7 IDPSDSETRYNQKFK 21

RESULT 15

S26315

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C/Accession: S26315

```

R:Stark, S.E., Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; PMID:91341421; PMID:11908510
A:Accession: S26315
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <STD>
A:Cross-references: UNIPARC:UPI0000115F8B; EMBL:X59208; NID:952079; PIDN:CAA41918.1; PIR
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:2-85/Domain: immunoglobulin homology <IMM>

Query March 73.1% Score 68; DB 2; Length 106;
Best Local Similarity 81.2%; Pred. No. 0.00044;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOKFXD 17
db 38 IDPYDSETRYNOKFXD 53

```

```

RESULT 16
G45722
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 115) - mouse (I
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: G45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vassq
U. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; PMID:7677958
A:Accession: G45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-117 <SIM>
A:CROSS-references: UNIPARC:UPI0000176D42
A:Note: Sequence extracted from NCBI backbone (NCBI:120595)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 67; DB 2; Length 117;
Best Local Similarity 76.5%; Pred. No. 0.00071;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MHPSDSETRYQKPKD 17
:| ||||| |||||
DB 51 IIDPSDSETHYQIKPKD 67

```

```

RESULT 17
S26318
1g heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C:Accession: S26318
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26318
A:Molecule type: mRNA
A:Residues: 1-109 <STA>
A:Cross-references: UNIPARC:UPI00001769A7; EMBL:X59200
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/3-86/Domain: immunoglobulin homology <IMM>

```

Query Match	69.9%	Score 65;	DB 2;	Length 109;
Best Local Similarity	76.5%;	Pred. No. 0.0014;		
Matches 13; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0

```
QY      1 MIHPDSETRYNQKFKD 17
        |||:|||||
Db      38 MIDPSNSEYTLNQKFKD 54
```

RESULT 18
H37262
Ig heavy chain V region (2F8) - mouse (Fragment)
CSpecies: Mus musculus (house mouse)
CDate: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
CAccession: H37262
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A>Title: Common structural features among monoclonal antibodies binding the same antigen
A:Reference number: A38601; MUID:9115823; PMID:1703527
A:Accession: H37262
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-101 <COS-
A:Cross-References: UNIPARC:UPI0000115184; GB:57994; NID:9195273; PIDN:AAA63332.1; PID
A:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match	68.8%	Score 64	DB 2	Length 101
Best Local Similarity	75.0%	Pred. No.	0.0019	
Matches	12	Conservative	1	Mismatches 3
				Indels 0
				Gaps 0
Qy	2	IHPSDSETRYNQKFKD	17	
Db	43	IDPYDSETRHFNQKFKD	58	

RESULT 19
 PH0987
 Ig heavy chain V region (clone 163.47) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Sep-1993 #sequence_rev150 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PH0987
 R.Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A/Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A/Reference number: PH0971; PMID:92381444; PMID:1512540
 A/Accession: PH0987
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-107 <TIL>
 A/Cross-References: UNIPARC:UPI0000176D07
 A/Experimental source: B cell, strain [NZB x NZW]F1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 P.15-98/Domain: immunoglobulin homology <IMM>

	Query Match	68.8%	Score 64;	DB 2;	Length 107;
	Best Local Similarity	75.0%	Pred. No.	0.0021;	
	Matches	12;	Conservative	2;	Mismatches 2; Indels 0; Gaps 0
QY	2 IHPSDSTRYNOKFRD	17			
DB	51 ILPSDTRHYNOKFRN	66			

```

RESULT 20
D25150
Ig heavy chain V region (AC38 260.2) - mouse (Firegment)
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Aug-1996
C:Accession: D25150

```

EMBO J. 3, 517-523, 1984
A:Title: A V region determinant (idiotype) expressed at high frequency in B lymphocytes
A:Reference number: A91000; MUID:84182519; PMID:6201362
A:Accession: D25150

A:Molecule type: protein
A:Residues: 1-69 <DIL>
A:Cross-references: UNIPARC:UPI00001769E1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 65.6%; Score 61; DB 2; Length 69;
Best Local Similarity 80.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 16
| | | | | | | | | |
Db 39 IDPSDSTYTNQKFK 53

RESULT 21

PH1162

Ig heavy chain V region (clone 10C.2A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1162

R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1162

A:Molecule type: DNA
A:Residues: 1-87 <SCH>
A:Cross-references: UNIPROT:Q924P9; UNIPARC:UPI0000176A3F
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:6-87/Domain: immunoglobulin homology <IMM>

Query Match 65.6%; Score 61; DB 2; Length 87;
Best Local Similarity 80.0%; Pred. No. 0.0052;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 16
| | | | | | | | | |
Db 42 IDPSDSTYTNQKFK 56

RESULT 22

PH1154

Ig heavy chain V region (clone 45F.2B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1154

R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1154
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPARC:UPI0000115596
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.6%; Score 61; DB 2; Length 98;
Best Local Similarity 62.5%; Pred. No. 0.0059;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 IHPSDSETRYNQKFK 16
| | | | | | | | | |
Db 50 IHPNSGSTNYEKFK 65

RESULT 23

PH1160

Ig heavy chain V region (clone 7A.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C:Accession: PH1160

R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545; PMID:1500855
A:Accession: PH1160
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPROT:Q924P9; UNIPARC:UPI0000176BC5
A:Experimental source: B cell
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.6%; Score 61; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.0059;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 16
| | | | | | | | | |
Db 51 IDPSDSTYTNQKFK 65

RESULT 24

S53751

antibody Fab Jcl 103 heavy chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 31-Dec-2004
C:Accession: S53751

R:Pokkukul, P.R.; Bouchillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.
J. Mol. Biol. 243, 283-297, 1994
A:Title: Preparation, characterization and crystallization of an antibody Fab fragment C:
A:Reference number: S53750; MUID:95018269; PMID:7523684
A:Accession: S53751
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <POK>
A:Cross-references: UNIPROT:Q924P9; UNIPARC:UPI0000176DC3
C:Superfamily: immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.6%; Score 61; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 0.0071;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNQKFK 16
| | | | | | | | | |
Db 51 IDPSDSTYTNQKFK 65

RESULT 25

S17230

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17230

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phase display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17230
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <CLA>
A:Cross-references: UNIPARC:UPI0000176B6F
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 63.4%; Score 59; DB 2; Length 96;

Best Local Similarity 68.8%; Pred. No. 0.012;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
QY      2 IHPDSETRYNQKFKD 17
          |::| | | | | |
Db      44 INPSSGYTNYNQKFKD 59
```

RESULT 26

Ig heavy chain V region - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
 C/Accession: S17614
 R/Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
 Nature 352, 624-628, 1991
 A/Title: Making antibody fragments using phage display libraries.
 A/Reference number: S17230; PMID:91326098; PMID:1907718
 A/Accession: S17614
 A/Status: preliminary
 A/Status: preliminary
 A/Molecule type: nucleic acid
 A/Residues: 1-96 <C1A>
 A/Cross-references: UNIPARC:UP01000176E7C
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 ;8-91/Domain: immunoglobulin homology <IMM>

Query Match	63.4%	Score 59;	DB 2;	Length 96;
Best Local Similarity	68.8%	Pred. No. 0.012;		
Matches 11;	Conservative 1;	Mismatches 4;	Indels 0;	Gaps 0;

QY 2 IHPDSETRYNQKFKD 17
| : | | | | | | | |
Db 44 INPSSGYTNNQKFKD 59

RESULT 27

S17620
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C:Accession: S17620
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phase display libraries.
A:Reference number: S17230, PMID:91326058, PMID:1907718
A:Accession: S17620
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <C1A>
A:Cross-references: UNIPARC:UPI0000116E73
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:8-91/Domain: immunoglobulin homology <IM>

Query Match 63.4%; Score 59; DB 2; Length 96;
Best Local Similarity 68.8%; Pred. No. 0.012;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0.

QY	2	IHPDSETRYNQKFD	17
		:	
Db	44	INPSSGYTNYNQKFD	59

RESULT 26

157618
 Ig heavy chain V region - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 22-Nov-1993 #sequence,revision 10-Nov-1995 #ext_change 06-Jun-1997
 C.Accession: S17618
 R.Clackson, T.; Hoozenboom, H.R.; Griffiths, A.D.; Winter, G.
 Nature 352, 624-628, 1991
 A>Title: Making antibody fragments using phage display libraries.

A; Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17618
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <C1A>
A:Cross-references: UNIPARC:UPI0000176E72
A:Superfamily: Immunoglobulin V region; Immunoglobulin
C:Keywords: heterotetramer; immunoglobulin
P:8-51/Domain: Immunoglobulin homology <IMM>

Query Match	63.4%	Score 59;	DB 2;	Length 96;
Best Local Similarity	68.8%;	Pred. No. 0.012;		
Matches 11; Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0;

```
QY      2 IHPSDSETRYNQKFD 17
         | : | | | | | | |
Db      44 INPSSGYTNYNQKFD 59
```

RESULT 29

517610
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
 C:Accession: S17610
 R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
 Nature 352, 624-628, 1991
 A>Title: Making antibody fragments using phage display libraries.
 A:Reference number: S17230; M0ID:91326098; PMID:1907718
 A:Accession: S17610
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-96 <CLA>
 A:Cross-references: UNIPARC:UPI0000176E7D
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:8-91/Domain: immunoglobulin homology <IMM>

Query Match	63.4%	Score 59;	DB 2;	Length 96;
Best Local Similarity	68.8%	Pred. No. 0.012;		
Matches 11; Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0;

```

QY      2 IHPDSETRYNQKFD 17
          |::| | | | | |
Db      44 INPSSGYTNNQKFD 59

```

RESULT 30

Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26471
 R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26471
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-102 <KAV>
 A:Cross-references: UNIPARC:UPI000015F64; EMBL:X59110; NID:G51951; PIDN:CAA41836.1; PI
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 P:15-98/Domain: immunoglobulin homology <IMM>

Query Match	63.4%	Score 59	DB 2	Length 102
Best Local Similarity	68.8%	Pred. No. 0.013		
Matches 11; Conservative	1	Mismatches 4	Indels 0	Gaps 0

```

QY      2 IHPDSETRYNQKFKD 17
          | : || | || || || |
Db      51 INPSSGYTEYNQKFKD 66

```

```

RESULT 31
PH1005
Ig heavy chain V region (clone 202.54) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH1005
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH1005
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-106 <TIL>
A/Cross-references: UNIPARC:UPI0000176D15
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          63.4%; Score 59; DB 2; Length 106;
Best Local Similarity 68.8%; Pred. No. 0.014;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IHPDSETRYNQKFXD 17
   ||| |||||
Db 51 IYPGSDTNYNQKFXD 66

RESULT 32
PH1003
Ig heavy chain V region (clone 17s-c5) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PH1003
R/Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A/Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B
A/Reference number: PH0971; MUID:92381444; PMID:1512540
A/Accession: PH1003
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-109 <TIL>
A/Cross-references: UNIPARC:UPI0000176D14
A/Experimental source: B cell, strain [NZB x NZW]F1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          63.4%; Score 59; DB 2; Length 109;
Best Local Similarity 66.7%; Pred. No. 0.014;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 IHPDSETRYNQKFXD 16
   ||| |||||
Db 51 IYPGSDTNYNQKFXD 65

RESULT 33
PH0237
Ig heavy chain V region (anti-DNA, 1A11VH) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C/Accession: PH0237
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A/Reference number: PH0231; MUID:90111618; PMID:2104919
A/Accession: PH0237
A/Molecule type: mRNA
A/Residues: 1-117 <SHL>
A/Cross-references: UNIPARC:UPI0000176C59

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C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-49/Region: framework 2
F/50-66/Region: complementarity-determining 2
F/67-98/Region: framework 3
F/99-109/Region: complementarity-determining 3
F/110-117/Region: framework 4

Query Match          63.4%; Score 59; DB 2; Length 117;
Best Local Similarity 62.5%; Pred. No. 0.015;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IHPDSETRYNQKFXD 17
   ||| |||||
Db 51 IYPGSDTNYNQKFXD 66

RESULT 34
PH0235
Ig heavy chain V region (anti-DNA, 2F2VH and 4H6VH) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C/Accession: PH0235
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A/Reference number: PH0231; MUID:90111618; PMID:2104919
A/Accession: PH0235
A/Molecule type: mRNA
A/Residues: 1-117 <SHL>
A/Cross-references: UNIPARC:UPI0000176C5A
A/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-49/Region: framework 2
F/50-66/Region: complementarity-determining 2
F/67-98/Region: framework 3
F/99-109/Region: complementarity-determining 3
F/110-117/Region: framework 4

Query Match          63.4%; Score 59; DB 2; Length 117;
Best Local Similarity 62.5%; Pred. No. 0.015;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 IHPDSETRYNQKFXD 17
   ||| |||||
Db 51 IYPGSDTNYNQKFXD 66

RESULT 35
S41394
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C/Accession: S41394
R/Margartite, C.; Gilbert, D.; Brard, F.; Tron, F.
submitted to the EMBL Data Library, January 1994
A/Description: Structural characterization of an (NZB X NZW) F1 mouse-derived IGM anti-DN
A/Reference number: S41393
A/Accession: S41394
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-120 <MAR>
A/Cross-references: UNIPARC:UPI00001165E2; EMBL:Z29586; NID:G452354; PIDN:CAA82703.1; PI
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

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Query Match 63.4%; Score 59; DB 2; Length 120;
 Best Local Similarity 80.0%; Pred. No. 0.016;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPDSETRYNOXFK 16
 |||||
 Db 51 IDPSDSTYTYNOXFK 65

RESULT 36

PH1004

Ig heavy chain V region (clone 165.5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1004

R:Titman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1004

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-91 <TIL>

A:Cross-references: UNIPARC:UPI0000176ACD

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 62.4%; Score 58; DB 2; Length 91;
 Best Local Similarity 66.7%; Pred. No. 0.017;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPDSETRYNOXFK 16
 |||||
 Db 33 IYPGNSDTSYNOXFK 47

RESULT 37

S17619

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S17619

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17619

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <CIA>

A:Cross-references: UNIPARC:UPI0000176E78

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 58; DB 2; Length 96;
 Best Local Similarity 68.8%; Pred. No. 0.018;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPDSETRYNOXFKD 17
 |||||
 Db 44 INPSTGYTYNOXFKD 59

RESULT 38

S17611

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S17611

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17611

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <CIA>

A:Cross-references: UNIPARC:UPI0000176E77

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 58; DB 2; Length 96;
 Best Local Similarity 68.8%; Pred. No. 0.018;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPDSETRYNOXFKD 17
 |||||
 Db 44 INPSTGYTYNOXFKD 59

RESULT 39

S17612

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S17612

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17612

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <CIA>

A:Cross-references: UNIPARC:UPI0000176E70

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 58; DB 2; Length 96;
 Best Local Similarity 68.8%; Pred. No. 0.018;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPDSETRYNOXFKD 17
 |||||
 Db 44 INPSTGYTYNOXFKD 59

RESULT 40

S17606

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C:Accession: S17606

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17606

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <CIA>

A:Cross-references: UNIPARC:UPI0000176E74

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 62.4%; Score 58; DB 2; Length 96;
 Best Local Similarity 68.8%; Pred. No. 0.018;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPDSETRYNOXFKD 17
 |||||


```

C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55541
J:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes.
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55541
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <BOB>
A:Cross-references: UNIPARC:UPI00001161F8; EMBL:X82580; NID:9854286; PIDN:CAA57916.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match          62.4%; Score 58; DB 2; Length 117;
Best Local Similarity 66.7%; Pred. No. 0.023;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2  IHPDSETRYNOKFK 16
      |:|:|:|:|:|:|
      |:|:|:|:|:|:|
Db      50  IYPGNSDSTYNOKFK 64

RESULT 47
PH0100
Ig heavy chain V region (anti-cyclosporin B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C:Accession: PH0100
J:Schmiltner, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Koehler, H.P.; Quesniaux, V.F.J.; V
Mol. Immunol. 27, 1029-1038, 1990
A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A:Reference number: PH0087; MUID:91042649; PMID:2122240
A:Accession: PH0100
A:Molecule type: mRNA
A:Residues: 1-125 <SCH>
A:Cross-references: UNIPARC:UPI0000176B46
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:50-66/Region: complementarity-determining 2
F:99-112/Region: complementarity-determining 3

Query Match          62.4%; Score 58; DB 2; Length 125;
Best Local Similarity 64.7%; Pred. No. 0.024;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1  MIHPDSETRYNOKFKD 17
      |:|:|:|:|:|:|
      |:|:|:|:|:|:|
Db      50  LIIPSGCTYNOKFKD 66

RESULT 48
B47159
Ig heavy chain V region, anti-carcinogenic embryonic maid T84.66 antigen monoclonal anti-idiotyp
C:Species: Mus musculus (house mouse)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
C:Accession: B47159
J:Gaidar, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.
J. Biol. Chem. 268, 14138-14145, 1993
A:Title: Molecular characterization of a cloned idiotypic cascade containing a network a
A:Reference number: A47159; MUID:93300804; PMID:7686150
A:Accession: B47159
A:Status: preliminary
A:Molecule type: DNA; protein
A:Residues: 1-136 <GAI>
A:Cross-references: UNIPARC:UPI0000176C84
A:Experimental source: hybridoma 666.C4
A>Note: sequence inconsistent with the nucleotide translation

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A>Note: sequence extracted from NCBI backbone (NCBIN:134421, NCBIP:134422)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match          62.4%; Score 58; DB 2; Length 136;
Best Local Similarity 68.8%; Pred. No. 0.026;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 IHPSDSETRYNQKFKD 17
   ||| ||| ||| |||
Db 70 IDPYDSVTHYNQKFRD 85

RESULT 49
PH1241
Ig heavy chain V region (clone CLR10) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1241
R:Cal, J.; Humphries, C.; Richardson, A.; Tucker, P.W.
J. Exp. Med. 176, 1073-1081, 1992
A:Title: Extensive and selective mutation of a rearranged VHS gene in human B cell chronic
A:Reference number: PH1232; MUID:93018822; PMID:1402653
A:Accession: PH1241
A:Molecule type: mRNA
A:Residues: 1-102 <CA1>
A:Cross-references: UNIPARC:UPI0000176BC7
A:Experimental source: B cell chronic lymphocytic leukemia
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match          61.3%; Score 57; DB 2; Length 102;
Best Local Similarity 62.5%; Pred. No. 0.029;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 MIHPDSETRYNQKFK 16
   ||| ||| ||| |||
Db 54 IIVPSDSETRYSPSFQ 69

RESULT 50
S26466
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26466
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26466
A:Molecule type: mRNA
A>Status: preliminary
A:Cross-references: UNIPARC:UPI0000115F6A; EMBL:X59116; NID:951933; PIDN:CAA41842.1; PIR:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:3-86/Domain: immunoglobulin homology <IMM>

Query Match          61.3%; Score 57; DB 2; Length 104;
Best Local Similarity 60.0%; Pred. No. 0.029;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 IHPSDSETRYNQKFK 16
   ||| ||| ||| |||
Db 39 IYPGDSGSTRYNEKFK 53

Search completed: January 17, 2006, 12:05:42
Job time : 26.9697 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:47:28 : Search time 95.8182 Seconds
(without alignments)
125.174 Million cell updates/sec

Title: US-10-665-658-11

Perfect score: 93

Sequence: 1 MIHPDSEFRYNQKFD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	82.8	117	1 HV05_MOUSE	P01749 mus musculus
2	76	81.7	114	2 Q9JL81_MOUSE	Q9J181 mus musculus
3	76	81.7	486	2 Q5HRY6_MOUSE	Q5HRY6 mus musculus
4	74	79.6	117	1 HV06_MOUSE	P01750 mus musculus
5	62	65.6	143	2 Q91V67_MOUSE	Q91V67 mus musculus
6	61	65.6	143	2 Q924P9_MOUSE	Q924P9 mus musculus
7	61	65.6	143	2 Q504M7_MOUSE	Q504M7 mus musculus
8	60	64.5	117	2 Q4KML5_MOUSE	Q4KML5 mus musculus
9	59	63.4	117	2 Q921C6_MOUSE	Q921C6 mus musculus
10	58	62.4	470	2 Q71WK1_MOUSE	Q71WK1 mus musculus
11	57	61.3	117	1 HV52_MOUSE	P06327 mus musculus
12	57	61.3	119	2 Q9GYZ2_MOUSE	Q9GYZ2 mus musculus
13	57	61.3	481	2 Q91WT1_MOUSE	Q91WT1 mus musculus
14	56	60.2	110	2 Q9JL77_MOUSE	Q9J177 mus musculus
15	56	60.2	136	2 Q7PBE3_MOUSE	Q7PBE3 mus musculus
16	54	58.1	120	2 Q5F211_MOUSE	Q5F211 mus musculus
17	54	58.1	481	2 Q91WT3_MOUSE	Q91WT3 mus musculus
18	53	57.0	111	2 Q9D9B8_MOUSE	Q9D9B8 mus musculus
19	52	55.9	138	1 HV48_MOUSE	P03980 mus musculus
20	52	55.9	614	2 Q7MT66_MOUSE	Q7MT66 mus musculus
21	51	54.8	120	1 HV50_MOUSE	P06329 mus musculus
22	51	54.8	140	2 Q924P8_MOUSE	Q924P8 mus musculus
23	51	54.8	142	2 Q924Q1_MOUSE	Q924Q1 mus musculus
24	51	54.8	483	2 Q4VAB6_MOUSE	Q4VAB6 mus musculus
25	50.5	54.3	1078	2 Q6C172_YARLI	Q6C172 Yarrowia li
26	50	53.8	117	1 HV12_MOUSE	P01756 mus musculus
27	50	53.8	117	1 HV13_MOUSE	P01757 mus musculus
28	50	53.8	117	2 Q9QX69_MOUSE	Q9QX69 mus musculus
29	50	53.8	117	2 Q9QXFO_MOUSE	Q9QXFO mus musculus
30	50	53.8	118	1 HV51_MOUSE	P06330 mus musculus
31	50	53.8	118	2 Q921C4_MOUSE	Q921C4 mus musculus

32	50	53.8	123	2 Q6VJ1_MOUSE	Q6VJ1 mus musculus
33	50	53.8	134	2 Q65ZRE_MOUSE	Q65ZRE mus musculus
34	50	53.8	458	2 Q5BJZ2_RAT	Q5BJZ2 Rattus norv
35	50	53.8	468	2 Q505N9_MOUSE	Q505N9 mus musculus
36	50	53.8	475	2 Q5RE17_PONPY	Q5RE17 Pongo pygma
37	49	52.7	120	1 HV03_MOUSE	P01747 mus musculus
38	49	52.7	142	2 Q924Q2_MOUSE	Q924Q2 mus musculus
39	49	52.7	143	2 Q924Q0_MOUSE	Q924Q0 mus musculus
40	49	52.7	476	2 Q669X1_MOUSE	Q669X1 mus musculus
41	48	51.6	147	2 Q925S3_MOUSE	Q925S3 mus musculus
42	48	51.6	468	2 Q669W9_MOUSE	Q669W9 mus musculus
43	48	51.6	480	2 Q8K0Z4_MOUSE	Q8K0Z4 mus musculus
44	48	51.6	498	2 Q6N041_HUMAN	Q6N041 Homo sapien
45	47	50.5	109	2 Q9JL75_MOUSE	Q9J175 mus musculus
46	47	50.5	117	1 HV04_MOUSE	P01748 mus musculus
47	47	50.5	117	1 HV09_MOUSE	P01753 mus musculus
48	47	50.5	117	1 HV10_MOUSE	P01754 mus musculus
49	47	50.5	117	1 HV14_MOUSE	P01758 mus musculus
50	47	50.5	117	1 HV49_MOUSE	P06328 mus musculus
51	47	50.5	118	2 Q5R3X0_MOUSE	Q5R3X0 mus musculus
52	47	50.5	137	2 Q924R6_MOUSE	Q924R6 mus musculus
53	47	50.5	139	1 HV07_MOUSE	P01751 mus musculus
54	47	50.5	139	2 Q924R5_MOUSE	Q924R5 mus musculus
55	47	50.5	140	2 Q924R2_MOUSE	Q924R2 mus musculus
56	47	50.5	141	2 Q924Q4_MOUSE	Q924Q4 mus musculus
57	47	50.5	143	2 Q91VA2_MOUSE	Q91VA2 mus musculus
58	47	50.5	143	2 Q924R7_MOUSE	Q924R7 mus musculus
59	47	50.5	143	2 Q924Q5_MOUSE	Q924Q5 mus musculus
60	47	50.5	143	2 Q924R0_MOUSE	Q924R0 mus musculus
61	47	50.5	144	2 Q924B5_MOUSE	Q924B5 mus musculus
62	47	50.5	145	2 Q924P7_MOUSE	Q924P7 mus musculus
63	47	50.5	145	2 Q924Q6_MOUSE	Q924Q6 mus musculus
64	47	50.5	145	2 Q924Q7_MOUSE	Q924Q7 mus musculus
65	47	50.5	145	2 Q924Q9_MOUSE	Q924Q9 mus musculus
66	47	50.5	145	2 Q924R1_MOUSE	Q924R1 mus musculus
67	47	50.5	145	2 Q924R3_MOUSE	Q924R3 mus musculus
68	47	50.5	145	2 Q924R4_MOUSE	Q924R4 mus musculus
69	47	50.5	146	2 Q924Q8_MOUSE	Q924Q8 mus musculus
70	47	50.5	146	2 Q924Q3_MOUSE	Q924Q3 mus musculus
71	47	50.5	146	2 Q924R8_MOUSE	Q924R8 mus musculus
72	47	50.5	235	2 Q7RAC4_PLAYO	Q7RAC4 plaesmodium
73	47	50.5	247	2 Q7MUB4_PORGI	Q7MUB4 porphyromon
74	47	50.5	482	2 Q8K172_MOUSE	Q8K172 mus musculus
75	47	50.5	483	2 Q521S1_MOUSE	Q521S1 mus musculus
76	47	50.5	488	2 Q91WR1_MOUSE	Q91WR1 mus musculus
77	47	50.5	562	2 Q5WCC7_BACSK	Q5WCC7 bacillus cl
78	47	50.5	590	2 Q4Y9V8_MOUSE	Q4Y9V8 mus musculus
79	46.5	49.5	600	2 Q5NHG8_FRAT	Q5NHG8 francisella
80	46	49.5	110	2 Q9JL83_MOUSE	Q9J183 mus musculus
81	46	49.5	159	2 Q96QSO_HUMAN	Q96QSO homo sapien
82	46	49.5	170	2 Q925S2_MOUSE	Q925S2 mus musculus
83	46	49.5	454	2 Q4UKT7_RICFE	Q4UKT7 rickettsia
84	46	49.5	464	2 Q6RP95_MOUSE	Q6RP95 mus musculus
85	46	49.5	485	2 Q58B61_MOUSE	Q58B61 mus musculus
86	46	49.5	500	1 SYK_BOCBP	Q98965 buchnera ap
87	46	49.5	501	1 SYK_PASMP	P57822 pasteurella
88	46	49.5	503	2 Q6SSB0_MAMNM	Q6SSB0 mantheimia
89	46	49.5	781	2 Q6BSRO_DEBHA	Q6BSRO debaryomyce
90	46	49.5	1072	2 Q4MZJ7_THERPA	Q4MZJ7 thelteria p
91	46	48.4	288	2 Q561W9_BRARE	Q561W9 brachydanio
92	45	48.4	299	2 Q6P6V8_BRARE	Q6P6V8 brachydanio
93	45	48.4	330	2 Q6H487_ORYSA	Q6H487 oryza sativ
94	45	48.4	442	2 Q9RHTO_PSEFL	Q9RHTO pseudomonas
95	45	48.4	446	2 Q4KSP1_PSEFF5	Q4KSP1 pseudomonas
96	45	48.4	472	2 Q6R0J7_MOUSE	Q6R0J7 mus musculus
97	45	48.4	477	2 Q58B56_MOUSE	Q58B56 mus musculus
98	45	48.4	480	2 Q65ZL2_9MTRI	Q65ZL2 mus sp. fy/
99	45	48.4	580	2 Q69R56_ORYSA	Q69R56 oryza sativ
100	45	48.4	1082	2 Q568Y0_RAT	Q568Y0 rattus norv
101	44.5	47.8	168	2 Q6CJ82_XLULA	Q6CJ82 klyveromyc
102	44	47.3	185	2 Q8VDC9_MOUSE	Q8VDC9 mus musculus
103	44	47.3	202	2 Q6CK81_XLULA	Q6CK81 klyveromyc
104	44	47.3	202	2 Q7VOL9_PROMP	Q7VOL9 prochloroto

105	44	47.3	223	2	Q9E785	BRFV	Q9E785	bovine ephr	178	42	45.2	597	1	SYK	CRIGR	P37879	criceculus
106	44	47.3	363	2	Q7V3P6	PROXO	Q507h1	trypanosoma	179	42	45.2	597	1	SYK	HUMAN	Q51046	homo sapien
107	44	47.3	392	2	Q580H1	grrpmp	Q580f2	mus musculu	180	42	45.2	597	2	OSI1E4	GEBCJA	Q51046	gecko japon
108	44	47.3	488	2	Q8K0F7	MOUSE	Q60c10	methylococc	181	42	45.2	604	2	SYK	ORYZA	Q6f2u9	oryza sativ
109	44	47.3	496	2	Q60C10	METCA	Q60c10	methylococc	182	42	45.2	604	2	Q50Z24	ENTH1	Q50Z24	entamoeba h
110	44	47.3	503	2	Q6AMR7	DSBPS	Q6amr7	desulfotale	183	42	45.2	605	2	Q801R2	XENLA	Q801r2	xenopus lae
111	44	47.3	613	2	Q8VCX7	MOUSE	Q8vcx7	mus musculu	184	42	45.2	607	2	Q9W327	DROME	Q9W327	drosophila
112	44	47.3	743	2	Q6FTF8	CANGA	Q6ftf8	candida gla	185	42	45.2	622	2	Q8CFK5	MOUSE	Q8cfk5	mus musculu
113	44	47.3	784	2	Q655Z1	ORYSA	Q655z1	oryza sativ	186	42	45.2	624	2	Q8R2P8	MOUSE	Q8r2p8	mus musculu
114	44	47.3	784	2	Q655Z1	ORYSA	Q655z1	oryza sativ	187	42	45.2	625	2	Q8R2P3	HUMAN	Q8r2p3	homo sapien
115	44	47.3	1163	2	Q5FF30	DICDI	Q5ff30	dicytosteli	188	42	45.2	625	2	Q5RFG7	PONPY	Q5rfg7	pongo pygma
116	44	47.3	1383	2	Q816S9	PLAF7	Q816s9	plasmodium	189	42	45.2	626	2	Q5X1M7	RAT	Q5x1m7	rattus norv
117	44	47.3	1415	2	Q7YY94	CRYPV	Q7yy94	cryptospori	190	42	45.2	636	2	Q6CHB2	YARLI	Q6chb2	yarrowia li
118	44	47.3	1444	2	Q5CX05	CRYPV	Q5cx05	cryptospori	191	42	45.2	652	1	ACSA	SALTY	Q81k10	salmonella
119	44	47.3	2176	2	Q5KE09	CRYNE	Q5ke09	cryptococcu	192	42	45.2	652	1	ACSA	SALTY	Q81k10	salmonella
120	44	47.3	2218	2	Q5SPB3	CRYNE	Q5spb3	cryptococcu	193	42	45.2	652	2	Q5GVZ2	SALCH	Q5gvz2	salmonella
121	43.5	46.8	1268	2	Q23277	ARATH	Q23277	arabidopsis	194	42	45.2	652	2	Q5PU04	SALPA	Q5pu04	salmonella
122	43	46.2	268	2	Q7R975	PLAYO	Q7r975	plasmodium	195	42	45.2	706	2	Q81B14	PLAF7	Q81b14	plasmodium
123	43	46.2	282	2	Q7RRZ0	PLAYO	Q7rrz0	plasmodium	196	42	45.2	722	2	Q86243	PLAF7	Q86243	plasmodium
124	43	46.2	387	2	Q4NA58	PMICC	Q4na58	arthrobacte	197	42	45.2	870	2	Q5LFE1	BACFN	Q5lfe1	bacteroides
125	43	46.2	459	2	Q35376	PODAN	Q35376	podospora a	198	42	45.2	870	2	Q64W63	BACFR	Q64w63	bacteroides
126	43	46.2	473	2	Q41975	SRNAHJ	Q41975	staphylococ	199	42	45.2	1086	2	Q8Y6P9	LISMO	Q8y6p9	listeria mo
127	43	46.2	480	2	Q9DBL4	MOUSE	Q9db14	mus musculu	200	42	45.2	1086	2	Q92AT0	LISIN	Q92at0	listeria in
128	43	46.2	490	2	Q6SFG5	JBACT	Q6sfg5	uncultured	201	42	45.2	1151	2	Q6R7P1	9HERP	Q6r7p1	herpetid her
129	43	46.2	500	2	Q4RH75	TESTNG	Q4rh75	tetradodon n	202	42	45.2	1694	2	Q5RLX1	MUSDO	Q5rlx1	musca domes
130	43	46.2	502	2	Q6LUN2	PHOPR	Q6lun2	photobacter	203	42	45.2	1783	1	Y468	MYCSE	Q51Lk1	musca domes
131	43	46.2	503	2	SYK	NEIMA	Q91ct7	neisseria m	204	42	45.2	1787	2	Q5RLK3	MUSDO	Q5rlk3	muscoplasma
132	43	46.2	503	1	SYK	NEIMB	Q91yue	neisseria m	205	41.5	44.6	138	2	Q8KDM3	CHUTE	Q8kdm3	choloridum
133	43	46.2	503	2	Q5F6U2	NEIG1	Q5f6u2	neisseria g	206	41.5	44.6	825	2	Q832B8	ENTPA	Q832b8	enterococcu
134	43	46.2	504	1	SYK	PHOL	Q8thk5	yersinia pe	207	41.5	44.6	1082	2	Q6CN82	KUTLA	Q6cn82	kluyveromyc
135	43	46.2	505	1	SYK	YERPE	Q8thk5	yersinia pe	208	41	44.1	61	2	Q8KGP4	RHILLO	Q8kgp4	rhizodilum l
136	43	46.2	505	2	Q666T3	YERPS	Q666t3	yersinia pe	209	41	44.1	73	2	Q7P9P5	RICSI	Q7p9p5	ricektsia
137	43	46.2	505	2	Q6D945	BURPS	Q6d945	erwinia car	210	41	44.1	79	2	Q92GT7	RICCN	Q92gt7	rickettsia
138	43	46.2	508	2	Q63SN3	BURPS	Q63sn3	burkholderi	211	41	44.1	120	2	Q920B8	MOUSE	Q920b8	mus musculu
139	43	46.2	508	2	Q621Z9	BURMA	Q621z9	burkholderi	212	41	44.1	125	1	HY1F	HUMAN	P03326	homo sapien
140	43	46.2	645	2	Q8FNH5	COREF	Q8fnh5	corynebacte	213	41	44.1	140	1	HY02	MOUSE	P01746	mus musculu
141	43	46.2	926	2	Q7RBN7	PLAYO	Q7rbn7	plasmodium	214	41	44.1	146	2	Q57YX6	9TRYRP	Q57yx6	trypanosoma
142	43	46.2	953	2	Q4PDM8	TESTMA	Q4pdm8	usellago ma	215	41	44.1	221	2	Q5DE13	SCHJA	Q5de13	schistosoma
143	43	46.2	1792	2	Q4PCP7	USITMA	Q4pcp7	usellago ma	216	41	44.1	240	2	Q5OV21	IDILLO	Q5ov21	idionaria
144	43	46.2	1882	1	Y684	MYCEN	P75109	mycoplasma	217	41	44.1	257	2	Q754J1	ASHGO	Q754j1	ashbya gos
145	43	46.2	2075	2	Q9VXY2	DIROME	Q9vxy2	diosophila	218	41	44.1	266	2	Q720B3	STOCA	Q720b3	stomoxys ca
146	43	46.2	3589	2	Q6LFE3	PLAF7	Q6lfe3	plasmodium	219	41	44.1	303	2	Q51M02	MAGGR	Q51mq2	magnaporthe
147	42.5	45.7	2862	2	Q93442	CABEL	Q93442	caenonabati	220	41	44.1	308	2	Q9GSS9	SCHMA	Q9gss9	schistosoma
148	42.5	45.2	117	1	HY1B	HUMAN	P01743	homo sapien	221	41	44.1	315	2	Q4W4M5	BHRRU	Q4w4m5	ethiopia r
149	42	45.2	124	2	TEPC	CTACA	Q9u192	homo sapien	222	41	44.1	315	2	Q6VXC9	BHRRU	Q6vcx9	ethiopia r
150	42	45.2	185	2	TEPC	CTACA	Q9u192	homo sapien	223	41	44.1	315	2	Q5HA12	BHRRU	Q5ha12	ethiopia r
151	42	45.2	197	1	YD5Q	BACSU	P96674	bacillus su	224	41	44.1	332	2	Q8RD22	THETN	Q8rd22	thermanner
152	42	45.2	234	2	Q4N8T0	THEPA	Q4n8t0	theileria p	225	41	44.1	342	2	Q51VX7	MAGGR	Q51vx7	magnaporthe
153	42	45.2	238	2	Q9X4N5	BACFR	Q9x4n5	bacteroides	226	41	44.1	384	2	Q9TMM5	CYACA	Q9tm15	cyaniidum c
154	42	45.2	238	2	Q5LGG6	BACFN	Q5lgg6	bacteroides	227	41	44.1	386	2	Q6Z003	BRAFL	Q6z003	branchioleto
155	42	45.2	238	2	Q64TL1	BACFR	Q64tl1	bacteroides	228	41	44.1	426	2	Q9DDC9	MOUSE	Q9ddc9	mus musculu
156	42	45.2	242	2	Q9CM03	PASMU	Q9cm03	pasteurella	229	41	44.1	446	2	Q7P653	FUSNV	Q7p653	fusobacteri
157	42	45.2	242	2	Q8A9B0	BACTN	Q8a9b0	bacteroides	230	41	44.1	448	1	T11S	FUSNN	Q8thn5	fusobacteri
158	42	45.2	243	2	Q7TQM2	MOUSE	Q7tqm2	mus musculu	231	41	44.1	454	2	Q6BXE4	RICTY	Q6bxex	rickettsia
159	42	45.2	249	2	Q8JGU2	CHICK	Q8jgu2	gallus galli	232	41	44.1	456	2	Q6D6Z5	ERWCT	Q6d6z5	erwinia car
160	42	45.2	319	2	Q5Y0P9	HALMA	Q5y0p9	haloarcuila	233	41	44.1	474	2	Q8R3H6	MOUSE	Q8r3h6	mus musculu
161	42	45.2	342	2	Q42913	SCHPO	Q42913	schizosacch	234	41	44.1	481	2	Q8VCV5	MOUSE	Q8vcv5	mus musculu
162	42	45.2	401	2	Q7R569	GITLA	Q7r569	giardia lam	235	41	44.1	491	2	Q74AT0	GOSL	Q74at0	ghebacter s
163	42	45.2	402	1	CASPI	MOUSE	P29452	mus musculu	236	41	44.1	502	1	SYK	CHRYO	Q71z62	chromobacte
164	42	45.2	423	2	Q6ZT13	HUMAN	Q6zt13	homo sapien	237	41	44.1	550	2	Q94G00	SOLDE	Q94g00	solanum dem
165	42	45.2	463	2	Q991C4	MOUSE	Q991c4	mus musculu	238	41	44.1	626	2	Q4KE13	PEBFS	Q4ke13	pseudomonas
166	42	45.2	475	2	Q6PKN2	STRRA	Q6pkn2	nitzschia c	239	41	44.1	728	2	Q88GUV	PEBPK	Q88guv	pseudomonas
167	42	45.2	489	2	Q8VCKA	MOUSE	Q8vckx4	mus musculu	240	41	44.1	747	2	Q4KC24	PEBFS	Q4kc24	pseudomonas
168	42	45.2	504	2	Q9S9Z1	ARATH	Q9s9z1	arabidopsis	241	41	44.1	769	2	Q565A4	9TRYRP	Q565a4	9tryrmp
169	42	45.2	545	2	Q4S1B5	TESTNG	Q4s1b5	tetradodon n	242	41	44.1	777	2	Q8CMW9	STABP	Q8cmw9	staphylococ
170	42	45.2	565	2	Q7Q3G2	ANOGA	Q7q3g2	anopheles g	243	41	44.1	826	2	Q8RPE5	LEBPN	Q8rpe5	legionella
171	42	45.2	574	2	Q8SXM8	DROME	Q8sxm8	drosophila	244	41	44.1	826	2	Q5X069	LEBPN	Q5x069	legionella
172	42	45.2	578	2	Q6NVLA	XENTR	Q6nvla	xenopus tro	245	41	44.1	826	2	Q5X8S6	LEBPA	Q5x8s6	legionella
173	42	45.2	588	1	SYK	LIGES	Q43176	lycopersico	246	41	44.1	868	2	Q6AKU5	DSBPS	Q6ak15	desulfotale
174	42	45.2	590	1	Q5ZKP8	CHICK	Q5zkm1	mus musculu	247	41	44.1	911	2	Q5RK42	CRYNE	Q5rk42	cryptococcu
175	42	45.2	595	2	SYK	MOUSE	Q8c1v4	mus musculu	248	41	44.1	955	2	Q55W52	CRYNE	Q55w52	cryptococcu
176	42	45.2	595	2	Q8C1V4	MOUSE	Q8c1v4	mus musculu	249	41	44.1	1020	2	Q6S195	BOTCI	Q6s195	botrytis ci
177	42	45.2	595	2	Q8C292	_MOUSE	Q8c292	mus musculu	250	41	44.1	1020	2	Q6S195	_BOTCI	Q6s195	botrytis ci

251	41	44.1	1055	2	059X70 CANAL	059x70 candida alb	324	40	43.0	594	2	09JF66_9POXY	09Jf66 ectromella
252	41	44.1	1055	2	059XB8 CANAL	059xb8 candida alb	325	40	43.0	598	2	060J03_CABER	060j03 caenornabdi
253	41	44.1	1275	1	CE152_HUMAN	0949b8 homo sapien	326	40	43.0	598	2	073HN9_WOLPM	073hn9 wolbachia p
254	41	44.1	1345	2	0813P5_PLAF7	0813p9 plasmodium	327	40	43.0	608	2	073FM2_WOLPM	073fm2 wolbachia p
255	41	44.1	1465	2	0675V9_9RUC	0675v9 oligopleura	328	40	43.0	627	2	04HOM3_CAMUP	04hom3 campylobact
256	41	44.1	1911	2	09SUDI_ARYTH	09sud1 arabiidopsis	329	40	43.0	628	2	05GSP0_WOLTR	05gsp0 wolbachia s
257	41	44.1	1812	2	081I53_PLAF7	081i53 plasmodium	330	40	43.0	630	2	0527D5_MAGGR	0527d5 magnaportie
258	40.5	43.5	1227	2	05PLU1_SALPA	05plu1 salmonella	331	40	43.0	633	2	06BPD4_ORYSA	06bpd4 oryza sativ
259	40.5	43.5	239	2	057ML8_SALCH	057ml8 salmonella	332	40	43.0	679	2	096176_PLAF7	096176 plasmodium
260	40.5	43.5	239	2	0825B8_SALTI	0825e8 salmonella	333	40	43.0	680	2	006764_MYCFE	006764 mycoplasma
261	40.5	43.5	386	2	09XXQ7_CABEL	09xxq7 caenornabdi	334	40	43.0	680	2	05FPP4_EHRRG	05fpp4 ethiellia r
262	40.5	43.5	450	2	08B9C3_NPYRO	08b9c3 rachiidiplusia	335	40	43.0	689	2	05HBW2_EHRRW	05hbw2 ethiellia r
263	40.5	43.5	679	2	061KX9_CABER	061k9 caenornabdi	336	40	43.0	754	2	04HM09_GIBZB	04hm09 human herpe
264	40.5	43.5	686	1	A4_CABEL	010551 caenornabdi	337	40	43.0	824	1	HELI_HHVEU	0785m2 human herpe
265	40.5	43.5	897	2	041865_MAIZE	041865 zea mays (m	338	40	43.0	824	2	0785M2_9BETA	057139_9BETA
266	40	43.0	31	2	05R3T6_MOUSE	05r3t6 mus musculu	339	40	43.0	824	2	057139_9BETA	057139 human herpe
267	40	43.0	104	2	06ESU6_ORYSA	06esu6 oryza sativ	340	40	43.0	868	2	08MOT1_CABEL	08mot1 caenornabdi
268	40	43.0	121	2	08CGS2_MOUSE	08cgs2 mus musculu	341	40	43.0	871	2	075JX3_DICDI	075jx3 dictyostei
269	40	43.0	136	1	HV15_MOUSE	P01759 mus musculu	342	40	43.0	915	1	DNJ5_CABEL	061f46 caenornabdi
270	40	43.0	155	2	091T16_LSDV	091t16 lumpy skin	343	40	43.0	915	1	DNJ5_CABEL	061f46 caenornabdi
271	40	43.0	162	2	04UGZ3_THERA	04ugz3 theileria a	344	40	43.0	919	2	06NFT0_CORDI	06nft0 corynebacte
272	40	43.0	172	2	04N8N9_TREPA	04n8n9 theileria p	345	40	43.0	970	2	05LFD5_9CAUD	05lfd5 lactobacill
273	40	43.0	177	2	090789_DROSI	09u789 drosophila	346	40	43.0	988	2	06BT63_DBSHA	06btf63 debaryomye
274	40	43.0	178	2	086G88_DROSI	086g88 drosophila	347	40	43.0	1014	2	083955_TREPA	083955 saccharomye
275	40	43.0	178	2	086G89_DROSI	086gh9 drosophila	348	40	43.0	1022	2	083955_TREPA	083955 leptonema p
276	40	43.0	178	2	086G11_DROSI	086g11 drosophila	349	40	43.0	1054	2	06B1W2_YEAST	06b1w2 saccharomye
277	40	43.0	178	2	086G11_DROSI	086g11 drosophila	350	40	43.0	1108	1	MAN2_DROME	091h5 homo sapien
278	40	43.0	178	2	091W64_DROSI	091w64 drosophila	351	40	43.0	1164	2	09H155_HUMAN	09h155 leishmania
279	40	43.0	202	1	HR72_CRORU	P20897 croctalius ru	352	40	43.0	1303	2	04Q364_LBIMA	04u01 theileria a
280	40	43.0	204	2	09W7D1_ORYIA	09w7d1 oryzae lat	353	40	43.0	1430	2	04U0A1_TREAN	06u061 caenornabdi
281	40	43.0	232	2	065FX2_BACLD	065fx2 bacillus ii	354	40	43.0	1449	2	060U69_CABBR	020187 caenornabdi
282	40	43.0	243	2	07RVH8_NBUICR	07rvh8 neurospora	355	40	43.0	1607	2	020187_CABEL	081j16 caenornabdi
283	40	43.0	251	2	04SGY1_TETNG	04sgy1 tetradodium n	356	40	43.0	2111	2	081J16_PLAF7	081j16 dictyostei
284	40	43.0	262	2	07RB12_PLAYO	07rb12 plasmodium	357	40	43.0	2123	2	08U9S7_DICDI	055f68 dictyostei
285	40	43.0	318	2	05BEK3_EMENT	05bek3 aspergillus	358	40	43.0	2123	2	05SF68_DICDI	048yvo tetradod n
286	40	43.0	321	2	091MW5_ORYSA	091mw5 oryza sativ	359	40	43.0	3085	2	04SYVO_TETNG	04s196 tetradod n
287	40	43.0	322	1	TRMB_DBIRA	09trf6 delnecoccc	360	40	43.0	98	2	04SYVO_TETNG	04s196 tetradod n
288	40	43.0	338	2	088Z62_LACPL	088z62 lactobacill	361	40	42.5	162	2	04XSA5_PLACH	04xsa5 plasmodium
289	40	43.0	350	2	06EB21_CAMJE	06eb21 campylobact	362	39.5	42.5	251	2	04Z2F0_PLABE	04z2f0 plasmodium
290	40	43.0	350	2	082Z20_ENTPA	082z20 enterococcu	363	39.5	42.5	326	2	097IUY_CIOAB	097iuy clostridium
291	40	43.0	358	2	05EBE0_PROMA	05ep60 campylobact	364	39.5	42.5	326	2	076XU2_9CAUD	076xj2 enterobacte
292	40	43.0	358	2	07VE18_PROMA	07ve18 prochloroco	365	39.5	42.5	620	2	076XU2_9CAUD	076xj2 enterobacte
293	40	43.0	352	2	05CR60_CRYPV	05cr60 cryptospori	366	39	41.9	59	2	072MX9_BACCI	072mx9 neurospora
294	40	43.0	352	2	054SW8_DICDI	054sw8 dictyostei	367	39	41.9	83	2	07S7U8_NBUICR	07s7u8 neurospora
295	40	43.0	362	2	094PT8_ARYTH	094pt8 arabiidopsis	368	39	41.9	144	1	06S461_BURPS	06s461 photobacter
296	40	43.0	369	2	05CDP7_CRIPV	05cdp7 cryptospori	369	39	41.9	153	2	R66_PHOPR	06hnx6 debaryomye
297	40	43.0	369	2	07UA68_SYNDX	07ua68 synchococc	370	39	41.9	157	2	06H8A6_ORYSA	06h8a6 oryza sativ
298	40	43.0	379	1	VERM_DROME	P20351 drosophila	371	39	41.9	176	2	04UCD7_SULAC	04jcd7 sulfolobus
299	40	43.0	379	2	024630_DROSI	024630 drosophila	372	39	41.9	180	2	05IEG3_SALSA	05ieg3 salmo salar
300	40	43.0	379	2	09NGA5_DROYA	09nga5 drosophila	373	39	41.9	182	2	06PSY9_CANGA	06psy9 candida gla
301	40	43.0	380	2	017440_DROAN	017440 drosophila	374	39	41.9	207	2	065P85_BACLD	065p85 bacillus ii
302	40	43.0	380	2	017441_9D1PT	017441 drosophila	375	39	41.9	211	1	TRMB_STREN	067h06 streptococc
303	40	43.0	389	2	093NK1_PSEBY	093nk1 pseudomonas	376	39	41.9	211	1	TRMB_STREN	067h06 streptococc
304	40	43.0	389	2	04ZTR80_PSEBY	04ztr80 pseudomonas	377	39	41.9	213	1	TRMB_STREN	067h06 streptococc
305	40	43.0	389	2	08Y240_RALSQ	08y240 raletonia s	378	39	41.9	213	1	ALKB_SALTY	057m88 salmonella
306	40	43.0	400	2	09F6748_PSSSY	09f678 pseudomonas	379	39	41.9	216	2	05P138_SALCH	05p138 salmonella
307	40	43.0	407	2	04UWX2_CORXK	04jwx2 corynebacte	380	39	41.9	216	2	05P138_SALCH	05p138 salmonella
308	40	43.0	425	2	04LHDI_9BDRK	04lhd1 burkholderi	381	39	41.9	216	2	082566_SALTI	082566 homo sapien
309	40	43.0	448	2	08VLP5_YERUR	08vlp5 yerlinda ru	382	39	41.9	216	2	082566_SALTI	082566 homo sapien
310	40	43.0	467	2	050Q15_ENTHI	05oq15 entamoeba h	383	39	41.9	244	2	0652C8_HOWAN	0652c8 magnaportie
311	40	43.0	470	2	05BCS0_EMENT	05bcs0 aspergillus	384	39	41.9	269	2	0522S0_MAGGR	0522s0 magnaportie
312	40	43.0	483	2	09M356_ARYTH	09m356 arabiidopsis	385	39	41.9	279	2	09AZV5_9CAUD	09azv5 laccococcus
313	40	43.0	492	2	061YK4_CABER	061k4 caenornabdi	386	39	41.9	279	2	09CFP5_LACTA	09cfp5 laccococcus
314	40	43.0	494	1	SYK_LACTA	09c117 laccococcus	387	39	41.9	295	2	05TVO6_ANGCA	05tvo6 anopheles g
315	40	43.0	499	1	YLII_MYCHO	P43055 mycoplasma	388	39	41.9	299	2	083B48_COXBU	083b48 coxiellia bu
316	40	43.0	503	2	05QYV9_IDILO	05qyv9 idiomatina	389	39	41.9	304	2	07RBN1_PLAYO	07rhn1 plasmodium
317	40	43.0	513	2	06CT16_KLULA	06ct16 kluyveromyi	390	39	41.9	311	2	08Z247_PYRAE	08z247 pyrobaculum
318	40	43.0	526	2	05L545_KLULB	05l545 chlamydomyc	391	39	41.9	316	2	086MF4_CABEL	086mf4 caenornabdi
319	40	43.0	540	2	06BS60_DBSHA	06bs60 debaryomye	392	39	41.9	317	2	08F248_LBPIIC	08f248 leptonema p
320	40	43.0	540	2	0716H5_PLUTO	07t6h5 sugarcane y	393	39	41.9	317	2	072T92_LBPIIC	072t92 leptonema p
321	40	43.0	553	2	07RHP2_PLAYO	07rhp2 plasmodium	394	39	41.9	335	2	0619H4_CABER	0619h4 caenornabdi
322	40	43.0	560	2	088N04_PSEBK	088n04 pseudomonas	395	39	41.9	336	2	020515_CABEL	020515 caenornabdi
323	40	43.0	594	2	07QIM8_ANGCA	07qim8 anopheles g	396	39	41.9	345	2	08DXA7_STRAS	08dxa7 streptococc

397	39	41.9	345	2	Q8E330_STRA3	Q8E330 streptococc	470	38.5	41.4	350	2	Q4HHV8_CAMCO	Q4hhv8 campylobact
398	39	41.9	362	2	Q9UW3_HUMAN	Q9uiw3 homo sapien	471	38.5	41.4	352	2	Q8IEB3_PLAF7	Q8ieb3 plasmodium
399	39	41.9	362	2	Q61202_CAENBR	Q61202 caenorhabdi	472	38.5	41.4	429	2	Q87X17_PSESM	Q87x17 psestomas
400	39	41.9	372	2	Q4KS96_GYTRU	Q4ks96 orange-spot	473	38.5	41.4	431	1	TRPB2_SULTO	Q970n1 sulfolobus
401	39	41.9	374	2	Q6CMF4_KUTULA	Q6cmf4 kluyveromyc	474	38.5	41.4	528	2	Q9ZUJ3_ARATH	Q9zu13 arabidopsis
402	39	41.9	396	2	Q94K49_ARATH	Q94k49 arabidopsis	475	38.5	41.4	536	2	Q4LA08_STAHJ	Q4la08 staphylococ
403	39	41.9	397	2	Q4J1S1_AZOVI	Q4j1s1 azotobacter	476	38.5	41.4	633	2	Q88Y21_LACPL	Q88y21 lactobacilli
404	39	41.9	398	2	Q4ZM31_PSESP	Q4zm31 pseudomonas	477	38.5	41.4	728	2	Q88GP3_PSEPF	Q88gp3 pseudomonas
405	39	41.9	398	2	Q88CO3_PSEPK	Q88co3 pseudomonas	478	38.5	41.4	957	2	Q4K7P3_PSEF5	Q4k7p3 pseudomonas
406	39	41.9	398	2	Q88AH8_PSESM	Q88ah8 pseudomonas	479	38.5	41.4	1306	2	Q4Y229_PLACH	Q4y229 plasmodium
407	39	41.9	401	2	Q5AAJ0_CANAL	Q5aaj0 candida alb	480	38	40.9	36	2	Q28J16_CAPHI	Q28j16 capra hircu
408	39	41.9	414	2	Q5WB8_BACSK	Q5wb8 bacillus cl	481	38	40.9	40	2	Q4YRS9_PLABE	Q4yrs9 plasmodium
409	39	41.9	418	1	Y285_HELPJ	Q9zmf0 helicobacte	482	38	40.9	80	2	Q5UE80_PPROT	Q5ue80 uncultured
410	39	41.9	429	1	MTA1_RUEBE	P94147 ruegeria ge	483	38	40.9	112	2	Q9CQD9_MOUSE	Q9cqd9 m mus muscu
411	39	41.9	435	2	Q553O5_DICDI	P95395 dictyostellei	484	38	40.9	113	2	Q556G8_DICDI	Q556g8 dictyostellei
412	39	41.9	442	1	YO1I_SGHPO	O9Y718 schizosacch	485	38	40.9	114	2	Q5R3X1_MOUSE	Q5r3x1 mus musculu
413	39	41.9	448	2	Q6DDJ3_ERWCT	Q6dj3g erwina car	486	38	40.9	117	1	HYIG_HUMAN	Q93083 homo sapien
414	39	41.9	458	2	Q5QVP4_IDILO	Q5qvp4 idiomarina	487	38	40.9	128	2	Q4GZG9_PANPA	Q4gzg9 pan paniscu
415	39	41.9	462	1	PRTF_ERWCH	P23598 erwina chr	488	38	40.9	128	2	Q4GZG8_PANTR	Q4gzg8 pan troglod
416	39	41.9	462	1	OSD1L2_ERWCH	Q9a1w3 arabidopsis	489	38	40.9	129	1	Y2262_CHLTE	Q8kaa4 chlorobium
417	39	41.9	463	2	Q9MIW3_ARATH	P41255 thermus the	490	38	40.9	131	1	TAP2_ANTMA	P24609 antirrhinum
418	39	41.9	492	1	SYK_THETR	P41255 thermus the	491	38	40.9	135	2	Q8IEB2_PLAF7	Q8ieb2 plasmodium
419	39	41.9	492	2	Q5SUG7_THETR	O5EJ97 thermus the	492	38	40.9	143	2	Q4S6D8_TETNG	Q4s6d8 tetraodon n
420	39	41.9	493	2	Q7ZJT9_THET2	O5EJ97 thermus the	493	38	40.9	155	2	Q9IMT2_LSDV	Q9imc2 lumpy skin
421	39	41.9	493	2	Q7UR15_RHOBA	O7U715 rhodospirill	494	38	40.9	160	2	Q4HOQ0_PANPA	Q4hoq0 pan paniscu
422	39	41.9	508	2	Q9RZ44_DEIRA	O9Y244 denococcus	495	38	40.9	160	2	Q4HOP6_PAPAN	Q4hop6 papio anubi
423	39	41.9	511	1	SYK_CHLTE	O8cm7 chlorococcu	496	38	40.9	161	2	Q5Z112_CHICK	O5z112 gallus gall
424	39	41.9	518	2	Q7S7F6_GLOIA	O7S7F6 glomerella	497	38	40.9	161	2	Q9INE3_PPRIC	Q9ine3 foot-and-mo
425	39	41.9	530	2	Q4Z793_COLTR	O4Z793 colletotric	498	38	40.9	165	2	Q9INE4_PPRIC	Q9ine4 foot-and-mo
426	39	41.9	544	2	Q98G48_RHILLO	O98g48 rhizobium l	499	38	40.9	165	2	Q9INE5_PPRIC	Q9ine5 foot-and-mo
427	39	41.9	555	2	Q826W1_STRAW	O826w1 streptomyce	500	38	40.9	165	2	Q9INE7_PPRIC	Q9ine7 foot-and-mo
428	39	41.9	556	2	Q44400_CABEL	O44400 caenorhabdi	501	38	40.9	165	2	Q9INE8_PPRIC	Q9ine8 foot-and-mo
429	39	41.9	560	2	Q6CMW7_KULUA	Q6cmw7 kluyveromyc	502	38	40.9	165	2	Q91NE8_PPRIC	Q91ne8 foot-and-mo
430	39	41.9	560	2	Q5AKX8_CANAL	O5akx8 candida alb	503	38	40.9	174	2	Q91NO7_PPRIC	Q91no7 foot-and-mo
431	39	41.9	574	2	Q960G7_DROME	O960g7 drosophila	504	38	40.9	191	1	ARPC2_MOUSE	Q9c9v6 mus musculu
432	39	41.9	591	2	Q93641_CAENL	Q93641 caenorhabdi	505	38	40.9	192	2	Q6T246_PPRACH	Q6t246 planerocoe
433	39	41.9	593	2	Q8N328_HUMAN	O8n328 homo sapien	506	38	40.9	193	2	Q6T247_PPRACH	Q6t247 planerocoe
434	39	41.9	593	2	Q5WOM0_HUMAN	O5wom0 homo sapien	507	38	40.9	196	1	SOH1_ARATH	O8yhd1 arabidopsis
435	39	41.9	621	2	Q5BVR6_SCHJA	O5bvr6 schistosoma	508	38	40.9	199	2	Q8CH24_MOUSE	Q8ch24 mus musculu
436	39	41.9	626	2	Q8CY65_STRPB6	O8cy65 streptococc	509	38	40.9	200	2	Q9BXV5_HUMAN	Q9bxv5 homo sapien
437	39	41.9	626	2	Q97NB1_STRPB	O97nb1 streptococc	510	38	40.9	213	2	Q9DJ64_PPRIC	Q9dj64 foot-and-mo
438	39	41.9	626	2	Q4HLZ1_CAMLA	Q4hlz1 campylobact	511	38	40.9	225	2	Q68118_RHOCA	Q68118 rhodobacter
439	39	41.9	701	2	Q4V265_BACFZ	Q4v265 bacillus ce	512	38	40.9	230	2	Q97P06_STRPB	Q97p06 streptococ
440	39	41.9	704	2	Q4R4A3_MACFA	Q4r4a3 macacia fasc	513	38	40.9	230	2	Q88859_MOUSE	Q88859 mus musculu
441	39	41.9	711	2	Q9VP36_DROME	O9vp36 drosophila	514	38	40.9	232	1	6PGL_ACTAC	P70715 actinobacill
442	39	41.9	740	2	Q57V64_9TRYP	O57v64 trypanosoma	515	38	40.9	243	2	Q8DNLS_STRR6	Q8dnls streptococc
443	39	41.9	825	2	Q89J14_BRAJA	O89j14 bradyrhizob	516	38	40.9	246	1	TFAM_HUMAN	Q00059 homo sapien
444	39	41.9	859	2	Q7RNM2_PLAYO	Q7rnm2 plasmodium	517	38	40.9	246	2	Q6LES8_HUMAN	Q6les8 homo sapien
445	39	41.9	919	2	Q6BUI9_DEBHA	Q6bui9 debaryomyce	518	38	40.9	246	2	Q5UOC6_HUMAN	Q5uoc6 homo sapien
446	39	41.9	1061	2	Q6PIH0_HUMAN	Q6pih0 homo sapien	519	38	40.9	248	2	Q5QMG7_IDILO	Q5qmg7 idiomarina
447	39	41.9	1065	2	Q5OZFI_ENTHI	Q5ozfi entamoeba h	520	38	40.9	250	2	Q4LJ79_9BURK	Q4lj79 burkholderi
448	39	41.9	1084	2	Q71YU0_LISMF	Q71yu0 listeria mo	521	38	40.9	267	2	Q7RLM1_PLAYO	Q7rlm1 plasmodium
449	39	41.9	1123	2	Q27809_TRIGR	Q27809 tritaneusces	522	38	40.9	267	2	Q7RLM5_PLAYO	Q7rlm5 plasmodium
450	39	41.9	1137	2	Q4UGR0_THEAN	Q4ugr0 theileria a	523	38	40.9	267	2	Q5UP87_MIMIV	Q5up87 mimivirus
451	39	41.9	1241	2	Q874N2_KLUDE	Q874n2 kluyveromyc	524	38	40.9	271	2	Q66012_SPHAR	Q66012 spillingmona
452	39	41.9	1253	2	Q5YFZ9_9VIRU	Q5yfz9 rock bream	525	38	40.9	276	2	Q4FZG5_MOUSE	Q4fzg5 mus musculu
453	39	41.9	1442	2	Q7NGZ7_GLOVI	Q7ngz7 gloeobacter	526	38	40.9	296	2	Q7RMZ1_PLAYO	Q7rmz1 plasmodium
454	39	41.9	1512	2	Q4UD96_THEAN	Q4ud96 theileria a	527	38	40.9	300	1	ARPC2_HUMAN	Q51144 homo sapien
455	39	41.9	1621	2	Q4X2X5_PLACH	Q4x2x5 plasmodium	528	38	40.9	300	1	ARPC2_PONPY	Q55525 pongo pygma
456	39	41.9	1629	2	Q8YUC4_ANASP	Q8yuc4 anabaena sp	529	38	40.9	300	2	Q53R19_HUMAN	Q53r19 homo sapien
457	39	41.9	1697	2	Q4UHB3_THEAN	Q4uhb3 theileria a	530	38	40.9	303	2	Q61405_MOUSE	Q61405 mus musculu
458	39	41.9	1819	2	Q4OJG4_LEIMA	Q4ojg4 leishmania a	531	38	40.9	306	2	Q6AON6_DESPS	Q6aon6 desulfofatale
459	39	41.9	2083	2	Q7PWC2_ANOGA	Q7pwc2 anopheles g	532	38	40.9	313	1	TRMB_THEMEA	Q9x027 thermotoga
460	39	41.9	2508	2	Q96175_PLAF7	Q96175 plasmodium	533	38	40.9	315	2	Q65ZV9_BORGA	Q65zv9 borrelia ga
461	39	41.9	5251	2	Q811D4_PLAF7	Q811d4 plasmodium	534	38	40.9	316	2	Q6ZFW2_ORYSA	Q6zfw2 oryza sativ
462	39	41.9	81	2	Q5L2M0_GEOXA	Q5l2m0 geobacillus	535	38	40.9	332	2	Q4LDF6_MOUSE	Q4ldf6 mus musculu
463	38.5	41.4	109	2	Q8FTZ7_CORBF	Q8ftz7 corynebacte	536	38	40.9	345	2	Q8WD19_ANOTR	Q8wd19 anolis tran
464	38.5	41.4	135	2	Q8KGO1_RHILLO	Q8kgo1 rhizobium l	537	38	40.9	353	2	Q9ZVU1_ARATH	Q9zv1 arabidopsis
465	38.5	41.4	240	2	Q6NBE3_CORDI	Q6nef3 corynebacte	538	38	40.9	357	2	Q5B7O3_EMENT	Q5b7q3 aspergillus
466	38.5	41.4	306	2	Q6D508_ERMCT	Q6d508 erwina car	539	38	40.9	365	2	Q6CVH6_KULUA	Q6cvh6 kluyveromyc
467	38.5	41.4	308	2	Q8F247_LEPIN	Q8f247 leptospira	540	38	40.9	374	2	Q8KAK1_CHLTE	Q8kak1 chlorobium
468	38.5	41.4	308	2	Q72T93_LEPIC	Q72t93 leptospira	541	38	40.9	376	2	Q559H4_DICDI	Q559h4 dictyostellei
469	38.5	41.4	346	2	Q4RSJ9_TETNG	Q4rsj9 tetraodon n	542	38	40.9	377	2	Q8NKX8_PAPHY	Q8nkx8 planerocoe

543	38	40.9	377	2	QBRAB0	Thermapne	616	38	40.9	600	2	QAN420	Therpa	Qan420	theileria p
544	38	40.9	378	1	PEM1	Phach	617	38	40.9	601	2	Q51G25	ENTHI	Q51g25	entamoeba h
545	38	40.9	378	1	Q22472	CAEEL	618	38	40.9	602	2	Q6DHB6	BRARE	Q6dHB6	brachydanio
546	38	40.9	382	1	PEM4	Phach	619	38	40.9	605	2	Q7ZWY9	XENLA	Q7zwY9	xenopus lae
547	38	40.9	382	2	Q12170	PhACH	620	38	40.9	620	2	Q8EKX1	SHEON	Q8ekX1	shewanella
548	38	40.9	386	2	Q4HK82	CAMLA	621	38	40.9	627	2	Q6ST21	STRGN	Q6st21	streptococ
549	38	40.9	387	2	Q815W8	PLAF7	622	38	40.9	630	2	Q4VAL3	MOUSE	Q4val3	mus musculu
550	38	40.9	398	2	Q6C8P7	YARLI	623	38	40.9	642	2	Q04235	VICPA	Q04235	vicia faba
551	38	40.9	405	2	Q6CTOI	KULIA	624	38	40.9	656	2	Q6AWM2	ORYSA	Q6aWm2	oryza sativ
552	38	40.9	405	2	Q61YP2	CAEBR	625	38	40.9	660	2	Q8CX55	LEPIN	Q8cx55	leptospira
553	38	40.9	405	2	Q7NXT7	CHRBV	626	38	40.9	660	2	Q8CX55	LEPIN	Q8cx55	leptospira
554	38	40.9	417	2	Q51O10	MAGGR	627	38	40.9	670	2	Q72GR2	THET2	Q72gr2	thermus the
555	38	40.9	422	2	Q86AN7	DICDI	628	38	40.9	670	2	Q6NMW4	MOUSE	Q6nmW4	mus musculu
556	38	40.9	428	1	SYD	THEBAC	629	38	40.9	671	2	Q7RKE1	PLAYO	Q7rke1	clostridium
557	38	40.9	428	1	Q9NTU6	HUMAN	630	38	40.9	674	1	MOTL	GLOPE	Q415D3	glibbrella
558	38	40.9	428	2	Q5NV77	HUMAN	631	38	40.9	678	1	Q415D3	GIBZE	Q415D3	glibbrella
559	38	40.9	428	2	Q6UW63	HUMAN	632	38	40.9	678	1	Q415D3	GIBZE	Q415D3	glibbrella
560	38	40.9	440	1	VRN2	ARATH	633	38	40.9	693	2	Q81UT7	CIOIN	Q81ut7	ctona infes
561	38	40.9	448	2	Q4USQ3	XANCP	634	38	40.9	696	2	Q9Y138	DRYME	Q9Y138	dtrosophila
562	38	40.9	448	2	Q8BPW0	XANCP	635	38	40.9	702	2	Q7XVP9	ORYSA	Q7xvp9	oryza sativ
563	38	40.9	449	1	PEL59	LYCPS	636	38	40.9	708	2	Q6PJR8	HUMAN	Q6pJr8	homo sapien
564	38	40.9	453	2	Q7PB44	RICSI	637	38	40.9	711	2	Q6KAL9	MOUSE	Q6kAl9	mus musculu
565	38	40.9	453	2	Q921W4	RICCN	638	38	40.9	712	2	Q9V6G3	DROME	Q9v6G3	dtrosophila
566	38	40.9	456	2	Q9ZDV0	RICPR	639	38	40.9	720	2	Q81BHI	PLAF7	Q81bh1	plasmodium
567	38	40.9	459	2	Q9B8T8	AVALA	640	38	40.9	725	2	Q8CCF8	MOUSE	Q8ccf8	mus musculu
568	38	40.9	460	1	ANGL3	HUMAN	641	38	40.9	755	2	Q41EN6	GIBZE	Q41en6	glibbrella
569	38	40.9	460	1	IFE	BRILA	642	38	40.9	767	2	Q8U3U2	PYRPU	Q8u3U2	pyrococcus
570	38	40.9	464	1	Q06920	YEAST	643	38	40.9	772	2	Q8BUD7	DEBHA	Q8bud7	debaromyce
571	38	40.9	469	2	Q821S9	STRAW	644	38	40.9	774	2	Q8RCR3	ECOL6	Q8rcr3	escherichia
572	38	40.9	472	2	Q5FVP3	RAT	645	38	40.9	785	2	Q6CXK1	KULIA	Q6cxk1	kluyveromyc
573	38	40.9	475	2	Q6FW51	CANGA	646	38	40.9	805	2	Q7PB65	FUSON	Q7pb65	fluebadactei
574	38	40.9	481	2	Q21798	CABEL	647	38	40.9	822	2	Q8ECV1	SHEON	Q8ecv1	shewanella
575	38	40.9	484	2	Y1110	METIA	648	38	40.9	824	1	HELI	HV62	Q4YU53	plasmodium
576	38	40.9	486	1	Q601Z2	CAEBR	649	38	40.9	829	2	Q7BMT3	PLAYO	Q7bmt3	plasmodium
577	38	40.9	489	2	Q8BU29	OCBIR	650	38	40.9	830	2	Q51G23	BACFN	Q51g23	bacteroides
578	38	40.9	489	2	Q8BU29	OCBIR	651	38	40.9	845	2	Q64WX9	BACFR	Q64wx9	bacteroides
579	38	40.9	500	1	SYK	PSBPK	652	38	40.9	845	2	Q6K973	ORYSA	Q6k973	oryza sativ
580	38	40.9	500	1	SYK	PSBPM	653	38	40.9	846	2	Q53KJ0	ORYSA	Q53kJ0	oryza sativ
581	38	40.9	500	2	Q9BRV0	HUMAN	654	38	40.9	868	2	SYL	AGRTS	Q6PE80	mus musculu
582	38	40.9	500	2	Q4ZMW0	PSSEY	655	38	40.9	876	1	Q6PE80	MOUSE	Q6pe80	mus musculu
583	38	40.9	500	2	Q41XP3	AZCVI	656	38	40.9	879	2	Q8V199	RAT	Q8v199	ratu mus
584	38	40.9	500	2	Q4KHL4	PSSEV	657	38	40.9	887	1	UFO	HUMAN	P30530	homo sapien
585	38	40.9	501	1	SYK	HELPU	658	38	40.9	887	1	UFO	HUMAN	P30530	homo sapien
586	38	40.9	501	1	SYK	HELPU	659	38	40.9	888	1	UFO	HUMAN	P30530	homo sapien
587	38	40.9	501	1	SYK	PSBPA	660	38	40.9	888	1	UFO	HUMAN	P30530	homo sapien
588	38	40.9	502	1	SYK	HABIN	661	38	40.9	888	1	UFO	HUMAN	P30530	homo sapien
589	38	40.9	502	2	Q4Q0L8	HABE18	662	38	40.9	889	2	Q5SD43	DICDI	Q5sd43	dictyosteli
590	38	40.9	503	1	PR12	CAEEL	663	38	40.9	894	2	Q8N512	HUMAN	Q8n512	homo sapien
591	38	40.9	503	1	BRE2	YEAST	664	38	40.9	901	2	Q47F1	USTMA	Q47f1	ustellago ma
592	38	40.9	505	1	SYK	XANCP	665	38	40.9	908	2	Q5UUA8	ENTHI	Q5uua8	entamoeba h
593	38	40.9	505	1	SYK	XANCP	666	38	40.9	931	2	Q9FX32	ARATH	Q9fx32	arabidopsi
594	38	40.9	505	2	Q4UD84	XANCP	667	38	40.9	944	2	Q6CQ04	KULIA	Q6cq04	kluyveromyc
595	38	40.9	510	1	SYK	STNY3	668	38	40.9	944	2	Q6CQ04	KULIA	Q6cq04	kluyveromyc
596	38	40.9	511	2	Q91332	9CGAMA	669	38	40.9	960	2	Q8BKVA	PSBPK	Q8bkV4	pseudomonas
597	38	40.9	528	2	Q5GYU5	XANOR	670	38	40.9	961	2	Q8A065	BACTN	Q8a065	bacteroides
598	38	40.9	537	2	Q6OXU0	CAEBR	671	38	40.9	963	2	Q9XEP6	ARATH	Q9xeP6	arabidopsi
599	38	40.9	542	2	Q9P903	SACKL	672	38	40.9	965	2	Q4PEB7	USTMA	Q4peB7	ustellago ma
600	38	40.9	542	2	Q51EL3	ENTHI	673	38	40.9	965	2	Q4KIV9	PSBPA	Q4kiv9	pseudomonas
601	38	40.9	551	2	Q54TY4	DICDI	674	38	40.9	976	1	PRR3	YEAST	Q33200	saccharomyc
602	38	40.9	560	2	Q5KVT9	CRYNE	675	38	40.9	976	1	Q6B1E6	YEAST	Q6b1E6	saccharomyc
603	38	40.9	560	2	Q5KVT9	CRYNE	676	38	40.9	988	2	Q54KM7	DICDI	Q54km7	dictyosteli
604	38	40.9	567	2	Q69WN4	ORYSA	677	38	40.9	994	2	Q9HHB9	HUMAN	Q9hhB9	homo sapien
605	38	40.9	568	2	Q81B54	PLAF7	678	38	40.9	1047	2	Q9HC39	HUMAN	Q9hc39	homo sapien
606	38	40.9	572	2	Q6B1D1	DEBHA	679	38	40.9	1047	2	Q4UG73	THKAN	Q4ug73	thellieria a
607	38	40.9	575	2	Q7QF68	ANOGA	680	38	40.9	1055	2	Q5SG65	DICDI	Q5sg65	dictyosteli
608	38	40.9	577	2	Q6DRH3	BRARE	681	38	40.9	1058	1	GEM14	HUMAN	P57678	homo sapien
609	38	40.9	589	2	Q750C0	ASHGO	682	38	40.9	1058	1	Q8WUM5	HUMAN	Q8wum5	homo sapien
610	38	40.9	589	2	Q7O1V7	ANOGA	683	38	40.9	1083	1	Q55T89	CRYNE	Q55t89	cryptococcu
611	38	40.9	589	2	Q5LT76	SILPO	684	38	40.9	1098	1	MWOLF	HUMAN	Q00160	homo sapien
612	38	40.9	590	1	SYK	YEAST	685	38	40.9	1098	1	Q811E7	MOUSE	Q811e7	mus musculu
613	38	40.9	592	2	Q6FM07	CANGA	686	38	40.9	1098	2	Q8CG29	MOUSE	Q8cg29	mus musculu
614	38	40.9	592	2	Q26557	METTH	687	38	40.9	1098	2	Q8CG29	MOUSE	Q8cg29	mus musculu
615	38	40.9	597	1	SYK	AQDAE	688	38	40.9	1099	1	MWOLF	MOUSE	P70248	mus musculu

689	38	40.9	1105	2	Q6ZN19_HUMAN	Q6zn19	homo sapien	762	37	39.8	140	2	Q8C925_MOUSE	Q8c925	mus musculus
690	38	40.9	1111	2	Q73104_WOLPMP	Q73104	homo sapien	763	37	39.8	146	2	Q5AAH0_CANAL	Q5aah0	candida alb
691	38	40.9	1143	2	Q4LE34_HUMAN	Q4le34	homo sapien	764	37	39.8	147	2	Q897D1_CLOTE	Q897d1	clostridium
692	38	40.9	1150	2	Q6RH56_DEBHA	Q6rh56	debrayomce	765	37	39.8	147	2	Q94XU3_CROUN	Q94xu3	cretalus un
693	38	40.9	1152	2	Q98F27_RHITO	Q98f27	rhizobium l	766	37	39.8	152	2	Q9MPC5_BRTVU	Q9mpc5	beta vulgar
694	38	40.9	1157	2	Q27088_TRIVA	Q27088	trichomonas	767	37	39.8	153	2	Q9P988_CANTR	Q9p988	candida tro
695	38	40.9	1157	2	Q4KY23_TRIVA	Q4ky23	trichomonas	768	37	39.8	153	2	Q9Y735_CANTR	Q9y735	candida tro
696	38	40.9	1188	2	Q66KF3_XENLTA	Q66kf3	xenopus lae	769	37	39.8	160	2	Q8R0P0_BACCE	Q8r0p0	brachydanio
697	38	40.9	1285	2	Q7PT50_ANOGA	Q7pt50	anopheles g	770	37	39.8	167	2	Q731Q0_WOLPMP	Q731q0	wolbachia p
698	38	40.9	1307	2	Q9YW60_DROME	Q9yw60	drosophila	771	37	39.8	173	2	Q4R468_MACFA	Q4r468	macaca fasc
699	38	40.9	1329	2	Q77247_DROME	Q77247	drosophila	772	37	39.8	176	2	Q60091_SCHPO	Q60091	schizosacch
700	38	40.9	1339	2	Q6CEK4_XENLTA	Q6cek4	yarrowia li	773	37	39.8	176	2	Q87N04_VIBPA	Q87n04	vibrio para
701	38	40.9	1358	2	Q6PA47_XENLTA	Q6pa47	xenopus lae	774	37	39.8	180	2	Q4IS44_AZOVI	Q4is44	azotobacter
702	38	40.9	1455	2	Q81JQ4_PLAFY	Q81jq4	plasmodium	775	37	39.8	182	2	Q5IER6_SALSA	Q5ier6	salmo salar
703	38	40.9	1508	2	Q7RHFS_PLAFY	Q7rhfs	plasmodium	776	37	39.8	182	2	Q5IER6_SALSA	Q5ier6	salmo salar
704	38	40.9	1575	2	Q615N5_CABBR	Q615n5	caenorhabdi	777	37	39.8	183	2	Q5X6D7_LEGPA	Q5x6d7	legionella
705	38	40.9	1596	2	Q553P2_DICDI	Q553p2	dictyosteli	778	37	39.8	185	2	Q5QW44_IDILLO	Q5qw44	idionella
706	38	40.9	1844	1	P0LR_TTYMA	P20128	turnip yell	779	37	39.8	192	2	Q9FIT9_NARAT	Q9fit9	arabidopsis
707	38	40.9	1844	2	Q56254_TYMW	Q56254	turnip yell	780	37	39.8	195	2	Q504CS_BRARE	Q504cs	brachydanio
708	38	40.9	1975	2	Q84MV2_ORYSA	Q84mv2	oryza sativ	781	37	39.8	197	2	Q6K3M2_ORYSA	Q6k3m2	oryza sativ
709	38	40.9	1989	2	Q6DN89_BRARE	Q6dn89	brachydanio	782	37	39.8	197	2	Q5ZMW7_LEGPH	Q5zwm7	legionella
710	38	40.9	2160	2	Q7PFA2_ORYSA	Q7faa2	oryza sativ	783	37	39.8	197	2	Q9Z213_STRPY	Q9z213	streptococ
711	38	40.9	2348	2	Q4UCQ9_THRYAN	Q4ucq9	theliera a	784	37	39.8	197	2	Q7CN32_STRPY	Q7cn32	streptococ
712	38	40.9	2457	2	Q54ZN9_DICDI	Q54zn9	dictyosteli	785	37	39.8	204	2	Q9W7D2_ORYLA	Q9w7d2	oryzias lat
713	38	40.9	2457	2	Q76N06_DICDI	Q76n06	dictyosteli	786	37	39.8	209	2	Q4FWD8_LEITMA	Q4fwd8	leishmania
714	38	40.9	2464	2	Q54FX1_DICDI	Q54fx1	dictyosteli	787	37	39.8	209	2	Q8DU89_STRMU	Q8du89	streptococ
715	38	40.9	2492	1	TALA_DICDI	P54633	dictyosteli	788	37	39.8	209	2	Q9W7D0_ORYLA	Q9w7d0	oryzias lat
716	38	40.9	2921	2	Q5WNK5_CABBR	Q5wnk5	caenorhabdi	789	37	39.8	212	2	Q73J71_TREDE	Q73j71	treponema d
717	38	40.9	3127	2	Q81DA0_PLAF7	Q81da0	plasmodium	790	37	39.8	212	2	Q8Y1D6_RALSO	Q8y1d6	raistonia s
718	38	40.9	3190	2	Q4X0G8_ASPFU	Q4x0g8	aspergillus	791	37	39.8	213	2	Q9PT05_ORYLA	Q9pt05	oryzias lat
719	38	40.9	3300	2	Q4N127_THRPA	Q4n127	theliera p	792	37	39.8	214	2	Q6U0V8_CABBR	Q6u0v8	caenorhabdi
720	38	40.9	3781	2	Q9V1S5_DROME	Q9v1s5	drosophila	793	37	39.8	214	2	Q9NF11_CABEL	Q9nf11	caenorhabdi
721	38	40.9	4841	2	Q41BN6_GIBZE	Q41bn6	gibberella	794	37	39.8	216	2	Q8PFQ3_ECOL6	Q8pfq3	escherichia
722	38	40.9	5157	2	Q01133_MERAN	Q01133	metarhizium	795	37	39.8	216	2	Q83Q08_SHIFL	Q83q08	shigella fl
723	37.5	40.3	58	2	Q5ZK94_NARAT	Q5zk94	arabidopsis	796	37	39.8	216	2	Q8XE43_ECO57	Q8xe43	escherichia
724	37.5	40.3	168	2	Q9ZL78_HELPU	Q9zl78	helicobacte	797	37	39.8	218	2	Q4Y6D6_PLACH	Q4y6d6	plasmodium
725	37.5	40.3	173	2	Q5CSG5_CRYPV	Q5csg5	cryptospori	798	37	39.8	223	2	Q4XKS2_GEOXA	Q4xks2	geobacillus
726	37.5	40.3	173	2	Q5CN10_CRYTHO	Q5cn10	cryptospori	799	37	39.8	226	2	Q9MF33_SHEXA	Q9mf33	sheella b
727	37.5	40.3	191	2	Q7XHH6_ORYSA	Q7xhh6	oryza sativ	800	37	39.8	226	2	Q5ZNV0_VYTRU	Q5znv0	cotelea con
728	37.5	40.3	191	2	Q8S5R5_ORYSA	Q8s5r5	oryza sativ	801	37	39.8	232	1	6PGL_HAEIN	6Pgl	haeini
729	37.5	40.3	288	2	Q4WZ56_THRPA	Q4wz56	theliera p	802	37	39.8	233	2	Q5IKS2_GNEOP	Q5iks2	gneop
730	37.5	40.3	294	1	ERTS_MYCNO	Q6k1b3	mycoplasma	803	37	39.8	239	1	NHNM_CABEL	NHnm	caenorhabdi
731	37.5	40.3	443	2	Q7T0P6_XENLTA	Q7t0p6	xenopus lae	804	37	39.8	239	2	Q61F50_CABBR	Q61f50	caenorhabdi
732	37.5	40.3	449	1	ME53_NPVAA	Q04719	autographa	805	37	39.8	245	2	Q4QW22_HAE18	Q4qw22	hae18
733	37.5	40.3	496	2	Q61K03_CABBR	Q61k03	caenorhabdi	806	37	39.8	246	2	Q6ANG7_DESPS	Q6ang7	desp
734	37.5	40.3	513	2	Q5FHE7_BHRBG	Q5fhe7	ehlichia r	807	37	39.8	248	2	Q4UE12_THRYAN	Q4ue12	theliera a
735	37.5	40.3	513	2	Q5HB06_BHRBW	Q5hb06	ehlichia r	808	37	39.8	256	2	Q5O0H9_PESBY	Q5o0h9	pseudomonas
736	37.5	40.3	530	2	Q61Q18_CABBR	Q61q18	caenorhabdi	809	37	39.8	264	2	Q97U62_SUTSO	Q97u62	sutisobus
737	37.5	40.3	546	2	Q9U2P8_CABEL	Q9u2p8	caenothabdi	810	37	39.8	267	2	Q4X6S6_PLACH	Q4x6s6	plasmodium
738	37.5	40.3	576	2	Q88XD8_LACPL	Q88xd8	lactobacilli	811	37	39.8	269	2	Q5A6R4_CANAL	Q5a6r4	candida alb
739	37.5	40.3	758	2	Q8R2M2_MOUSE	Q8r2m2	mus musculu	812	37	39.8	269	2	Q5AFU7_CANAL	Q5afu7	candida alb
740	37.5	40.3	1418	2	Q4WE14_ASPFU	Q4we14	aspergillus	813	37	39.8	272	2	Q5FMW8_LACAC	Q5fmw8	lactobacilli
741	37.5	40.3	1883	2	Q4WE14_BRARE	Q4we14	brachydanio	814	37	39.8	275	2	Q61DW4_CABBR	Q61dw4	caenorhabdi
742	37.5	40.3	3338	2	Q5GQW5_GCAUD	Q5gqw5	bacteriopho	815	37	39.8	276	2	Q5DD10_SCHTA	Q5dd10	schistosoma
743	37.5	40.3	3433	1	UTRO_HUMAN	P46939	homo sapien	816	37	39.8	277	2	Q8CXH8_MOUSE	Q8cxh8	mus musculu
744	37.5	40.3	3433	1	UTRO_HUMAN	Q5a257	homo sapien	817	37	39.8	298	2	Q54XT8_DICDI	Q54xt8	dictyosteli
745	37	39.8	77	2	Q7ULM5_RHOBA	Q7ulm5	rhodospirell	818	37	39.8	299	2	Q6GL82_XENTR	Q6gl82	xenopus tro
746	37	39.8	77	2	Q9JRK4_9LACT	Q9jrk4	lactococcus	819	37	39.8	301	2	Q8EXJ3_MYCPE	Q8exj3	mycoplasma
747	37	39.8	83	1	Q7R083_LACTIA	Q7r083	lactococcus	820	37	39.8	304	2	Q640B5_USYMA	Q640b5	usiliago ma
748	37	39.8	83	1	RS27_HOMAN	P55833	homonys ame	821	37	39.8	306	2	Q4PSS9_USYMA	Q4pss9	usiliago ma
749	37	39.8	84	2	Q8MU65_9RIVA	Q8mue6	chlamys far	822	37	39.8	310	2	Q8GZM8_VITVI	Q8gzm8	vitib vinitif
750	37	39.8	94	2	Q87SM9_VIBPA	Q87sm9	vibrio para	823	37	39.8	313	2	Q8AWA3_BRARE	Q8awa3	brachydanio
751	37	39.8	99	2	Q70097_STRMU	Q70097	streptococ	824	37	39.8	314	2	Q415Q7_GIBZE	Q415q7	gibberella
752	37	39.8	101	2	Q97LY7_CLOAB	Q97ly7	clostridium	825	37	39.8	318	2	Q4PEZ4_USYMA	Q4pez4	usiliago ma
753	37	39.8	112	2	Q8JTX3_LSDV	Q8jtx3	lumpy skin	826	37	39.8	318	2	Q8BS58_MOUSE	Q8bs58	mus musculu
754	37	39.8	112	2	Q91MY4_LSDV	Q91my4	lumpy skin	827	37	39.8	320	2	Q4K0S7_STRPN	Q4k0s7	streptococ
755	37	39.8	112	2	Q91T30_LSDV	Q91t30	lumpy skin	828	37	39.8	322	2	Q6FVD7_CANGA	Q6fvd7	candida gla
756	37	39.8	114	2	Q8UJ16_LSDV	Q8uj16	lumpy skin	829	37	39.8	325	2	Q61M9_ORYSA	Q61m9	oryza sativ
757	37	39.8	116	1	RS6_IDILO	Q5GY01	idiomaria	830	37	39.8	334	2	Q4JMK7_9BACT	Q4jmk7	uncultured
758	37	39.8	125	1	YCFL_BCOLI	P75446	escherichia	831	37	39.8	335	2	Q6PG29_BRARE	Q6pg29	brachydanio
759	37	39.8	125	2	Q8FIN5_ECOL6	Q8fins	escherichia	832	37	39.8	341	2	Q63BH8_BACCE	Q63bh8	baecillus ce
760	37	39.8	125	2	Q8X8G7_ECO57	Q8x8g7	escherichia	833	37	39.8	343	2	Q81QNT_BACAN	Q81qnt	baecillus an
761	37	39.8	131	2	Q4T8Q6_TETNG	Q4t8q6	tetrinodon n	834	37	39.8	343	2			

835	37	39.8	345	2	Q81YA7 BACAN	Q81YA7 bacillus an	908	37	39.8	505	2	Q5PLJ0 SALPA	Q5PLJ0 salmonella
836	37	39.8	354	1	CD72 MOUSE	P21855 mus musculus	909	37	39.8	506	1	SYK BORBR	Q7WK46 bordetella
837	37	39.8	354	2	Q9AL57 CAMJE	Q9AL57 campylobact	910	37	39.8	506	1	SYK BORP	Q7WK46 bordetella
838	37	39.8	355	2	Q8HX42 SALS	Q8HX42 salmo. salar	911	37	39.8	506	1	SYK BORP	Q7WK46 bordetella
839	37	39.8	356	2	Q3Z291 BACSU	Q3Z291 bacillus su	912	37	39.8	509	1	YMCB BACSU	Q31778 bacillus su
840	37	39.8	357	2	Q620G5 CABBR	Q620G5 caenorhabdi	913	37	39.8	509	2	Q8R018 MOUSE	Q8R018 mus musculu
841	37	39.8	357	2	Q9A5B7 CAUCR	Q9A5B7 callobacter	914	37	39.8	510	1	SYK VIBCH	Q9RU60 vibrio chol
842	37	39.8	359	2	Q5CM04 CRYHO	Q5CM04 cryptospori	915	37	39.8	510	1	SYK VIBVU	Q8QED9 vibrio vuln
843	37	39.8	365	2	Q4N3V5 THEPA	Q4N3V5 theileria p	916	37	39.8	510	2	SYK VIBVY	Q7EMPE vibrio vuln
844	37	39.8	373	2	Q8G797 BIFLO	Q8G797 bifidobacte	917	37	39.8	511	2	Q6ERS5 ORYSA	Q6ERS5 oryza sativ
845	37	39.8	380	2	Q4IAL8 GIBZE	Q4IAL8 gibberella	918	37	39.8	511	2	Q8IKT8 PLAF7	Q8IKT8 plasmodium
846	37	39.8	382	1	ALR1 STRAN	P63479 staphylococ	919	37	39.8	512	2	Q9HPD8 HALSA	Q9HPD8 halobacteri
847	37	39.8	382	1	ALR1 STRAN	P63480 staphylococ	920	37	39.8	515	2	Q8AK72 DESPS	Q8AK72 desulfofate
848	37	39.8	382	1	ALR1 STRAS	Q63479 staphylococ	921	37	39.8	516	2	Q8S263 DROME	Q8S263 drosophila
849	37	39.8	382	1	ALR1 STRAS	Q6G7N9 staphylococ	922	37	39.8	516	2	Q9VC88 DROME	Q9VC88 drosophila
850	37	39.8	382	1	ALR1 STRAN	Q9Z6H5 staphylococ	923	37	39.8	516	2	Q4YSNO PLABE	Q4YSNO plasmodium
851	37	39.8	382	1	ALR1 STRAN	P63481 staphylococ	924	37	39.8	516	2	Q4XYB8 PLACH	Q4XYB8 plasmodium
852	37	39.8	388	2	Q5HED1 STRAC	Q5HED1 staphylococ	925	37	39.8	518	2	Q6N030 HOMAN	Q6N030 homo sapien
853	37	39.8	388	2	Q9FN10 ARATY	Q9FN10 arabidopsis	926	37	39.8	524	1	NIFA_KLEBX	NIFA_KLEBX klebsiella
854	37	39.8	389	2	Q6F7M0 ACIAD	Q6F7M0 acinetobact	927	37	39.8	524	1	NIFA_KLEBX	NIFA_KLEBX klebsiella
855	37	39.8	390	2	Q8TRP02 METAC	Q8TRP02 methanosarc	928	37	39.8	532	2	Q5CN04 CRYHO	Q5CN04 cryptospori
856	37	39.8	391	2	Q4UB29 THEAN	Q4UB29 theileria a	929	37	39.8	532	2	Q6EMX0 ARATY	Q6EMX0 arabidopsis
857	37	39.8	391	2	Q8A2G6 BACTN	Q8A2G6 bacteroides	930	37	39.8	532	2	Q6EMX0 ARATY	Q6EMX0 arabidopsis
858	37	39.8	393	2	Q41749 GIBZE	Q41749 gibberella	931	37	39.8	536	1	FLPI1_SCHPO	FLPI1_SCHPO schizosacch
859	37	39.8	396	2	Q9D5K4 MOUSE	Q9D5K4 mus musculu	932	37	39.8	537	2	Q57UC0 STRYP	Q57UC0 trypanosoma
860	37	39.8	398	2	Q4K4A3 PSBFS	Q4K4A3 pseudomonas	933	37	39.8	546	2	Q54FR7 DICDI	Q54FR7 dictyosteli
861	37	39.8	402	2	Q4TMY4 CORJK	Q4TMY4 corynebacte	934	37	39.8	553	2	Q4HXC6 GIBZE	Q4HXC6 gibberella
862	37	39.8	403	2	Q6BYT5 DEBHA	Q6BYT5 debaryomyce	935	37	39.8	554	2	Q9SZR2 ARATY	Q9SZR2 arabidopsis
863	37	39.8	405	1	CHLP_SYNY3	Q68033 rhodobacter	936	37	39.8	559	2	Q8CER2 CRYPV	Q8CER2 cryptospori
864	37	39.8	407	1	SBCD_RHOCA	Q68033 rhodobacter	937	37	39.8	560	2	Q8CER2 CRYPV	Q8CER2 cryptospori
865	37	39.8	411	2	Q7S3B8 NEUCR	Q7S3B8 neuropsora	938	37	39.8	562	2	Q59U49 CANAL	Q59U49 candida alb
866	37	39.8	421	2	Q6S578 STRMU	Q6S578 streptococc	939	37	39.8	567	2	Q934W3 SALT1	Q934W3 salmonella
867	37	39.8	421	2	Q7BRU3 STRMU	Q7BRU3 streptococc	940	37	39.8	574	2	Q8OMN6 COMPX	Q8OMN6 combox viru
868	37	39.8	421	2	Q8BDS4 STRMU	Q8BDS4 streptococc	941	37	39.8	576	2	Q5N189 PRATY	Q5N189 franciella
869	37	39.8	427	2	Q84089 ORYSA	Q84089 oryza sativ	942	37	39.8	579	2	Q7RTT7 PLAYO	Q7RTT7 plasmodium
870	37	39.8	432	2	Q4Z345 PLABE	Q4Z345 plasmodium	943	37	39.8	583	2	Q8IDB6 PLAF7	Q8IDB6 plasmodium
871	37	39.8	436	2	Q5ZLZ8 CHICK	Q5ZLZ8 gallus gall	944	37	39.8	586	2	Q7RNE2 PLAYO	Q7RNE2 plasmodium
872	37	39.8	451	2	Q756M3 ASHGO	Q756M3 ashbya gosb	945	37	39.8	587	2	Q416S5 GIBZE	Q416S5 gibberella
873	37	39.8	451	2	Q81572 PLAF7	Q81572 plasmodium	946	37	39.8	589	2	Q8UBF5 AGRT5	Q8UBF5 agrobacteri
874	37	39.8	451	2	Q61407 MOUSE	Q61407 mus musculu	947	37	39.8	590	2	Q6N313 RHOPA	Q6N313 rhodopseudo
875	37	39.8	455	2	Q9PEY3 UREBP	Q9PEY3 ureaplasma	948	37	39.8	599	1	Q5A4E0 CANAL	Q5A4E0 candida alb
876	37	39.8	456	2	Q6FV58 CANCA	Q6FV58 candida gla	949	37	39.8	599	1	Q5A4E0 CANAL	Q5A4E0 candida alb
877	37	39.8	458	1	FKBP4_HUMAN	Q02190 homo sapien	950	37	39.8	603	2	Q9SCR0 ARATY	Q9SCR0 arabidopsis
878	37	39.8	459	2	Q7YWB5 ANOGA	Q7YWB5 anopheles g	951	37	39.8	613	2	Q5DW98 PER	Q5DW98 perleuella
879	37	39.8	463	2	Q8PTM3 METMA	Q8PTM3 methanosarc	952	37	39.8	617	1	Q9AM87 GUITH	Q9AM87 guillardia
880	37	39.8	468	2	Q6FUB2 MOUSE	Q6FUB2 mus musculu	953	37	39.8	627	2	Q9MAL0 ARATY	Q9MAL0 arabidopsis
881	37	39.8	468	2	Q7OC02 ANOGA	Q7OC02 anopheles g	954	37	39.8	627	2	Q9MAL0 ARATY	Q9MAL0 arabidopsis
882	37	39.8	469	2	Q9ZWB4 ARATY	Q9ZWB4 arabidopsis	955	37	39.8	629	1	Q4QPH7_HAE18	Q4QPH7 haemophilus
883	37	39.8	472	2	Q6BRH5 DEBHA	Q6BRH5 debaryomyce	956	37	39.8	632	2	Q4QPH7_HAE18	Q4QPH7 haemophilus
884	37	39.8	472	2	Q6BOD7 DEBHA	Q6BOD7 debaryomyce	957	37	39.8	632	2	Q4QPH7_HAE18	Q4QPH7 haemophilus
885	37	39.8	475	2	Q6SK98 ORYSA	Q6SK98 oryza sativ	958	37	39.8	633	2	Q4QPH7_HAE18	Q4QPH7 haemophilus
886	37	39.8	483	2	Q4YIN6 PLACH	Q4YIN6 plasmodium	959	37	39.8	649	2	Q8MA30_HUMAN	Q8MA30 homo sapien
887	37	39.8	488	2	Q4XPI1 PLACH	Q4XPI1 plasmodium	960	37	39.8	651	2	Q6D065 ERKCT	Q6D065 erynia car
888	37	39.8	490	1	TAS3_TREDE	P18164 treponema d	961	37	39.8	655	2	Q9C919 ARATY	Q9C919 arabidopsis
889	37	39.8	493	2	Q6CAH3 YARLI	Q6CAH3 yarrowia li	962	37	39.8	658	2	Q4FXR6 LEIMA	Q4FXR6 leishmania
890	37	39.8	493	2	Q4WYQ4 ASPRU	Q4WYQ4 aspergillus	963	37	39.8	660	2	Q8NHV4_HUMAN	Q8NHV4 homo sapien
891	37	39.8	498	1	SYK_RHIME	Q87821 rhizobium m	964	37	39.8	663	2	Q5CH98 CRYHO	Q5CH98 cryptospori
892	37	39.8	500	2	Q7YTC4_SACCO	Q7YTC4 saccharomyce	965	37	39.8	678	2	Q87D04_NEUCR	Q87D04 neuropsora
893	37	39.8	500	2	Q73S69 MYCPA	Q73S69 mycobacteri	966	37	39.8	679	2	Q8CW15 STRMU	Q8CW15 streptococ
894	37	39.8	501	2	Q27038 THEPA	Q27038 theileria p	967	37	39.8	686	2	Q9V979 DROME	Q9V979 drosophila
895	37	39.8	501	2	Q5E7P8 THEPA	Q5E7P8 vibrio fisci	968	37	39.8	687	2	Q5J3R19 ORYSA	Q5J3R19 oryza sativ
896	37	39.8	504	1	SYK1_SALTY	Q08457 escherichia	969	37	39.8	695	2	Q9Z414 NEIME	Q9Z414 neisseria m
897	37	39.8	504	1	SYK1_SALTY	Q08457 escherichia	970	37	39.8	721	2	Q8M9S0_PERIC	Q8M9S0 perikantus
898	37	39.8	504	1	SYK1_SALTY	Q08457 escherichia	971	37	39.8	742	2	Q6BRB3 DEBHA	Q6BRB3 debaryomyce
899	37	39.8	504	1	SYK1_SALTY	Q08457 escherichia	972	37	39.8	751	2	Q410M2 GIBZE	Q410M2 gibberella
900	37	39.8	504	1	SYK1_SALTY	Q08457 escherichia	973	37	39.8	751	2	Q410M2 GIBZE	Q410M2 gibberella
901	37	39.8	504	1	SYK1_SALTY	Q08457 escherichia	974	37	39.8	755	2	Q9NED3_CANGA	Q9NED3 candida gla
902	37	39.8	504	1	SYK1_SALTY	Q08457 escherichia	975	37	39.8	794	2	Q6FLK9 CANCA	Q6FLK9 candida gla
903	37	39.8	504	1	SYK1_SALTY	Q08457 escherichia	976	37	39.8	817	2	Q5E138 VIBF1	Q5E138 vibrio fisci
904	37	39.8	504	1	SYK1_SALTY	Q08457 escherichia	977	37	39.8	834	2	Q73XK6_TREDE	Q73XK6 treponema d
905	37	39.8	505	2	Q7XSH3 CITRER	Q7XSH3 citrobacter	978	37	39.8	838	1	HS74L_MOUSE	HS74L mus musculu
906	37	39.8	505	2	Q7XSH3 CITRER	Q7XSH3 citrobacter	979	37	39.8	844	2	P73363_STYV3	P73363 synechocyst
907	37	39.8	505	2	Q57K76_SALCH	Q57K76 salmonella	980	37	39.8	846	2	Q53U26_STREX	Q53U26 streptomyce

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981 37 39.8 848 2 Q84H05_HELIPY Q84H05 helicobacte
982 37 39.8 853 2 Q5XG17_XENTR Q5XG17 xenopus tro
983 37 39.8 855 2 Q4MOV5_ASPFU Q4MOV5 aspergillus
984 37 39.8 867 2 Q6BTV1_DBBHA Q6BTV1 debaryomyce
985 37 39.8 868 2 Q879X4_XYLFT Q879X4 xyella fas
986 37 39.8 868 2 Q9PA07_XYLFA Q9PA07 xyella fas
987 37 39.8 872 2 Q5SP54_BRARE Q5SP54 brachydanio
988 37 39.8 903 2 Q5VN31_ORYSA Q5VN31 oryza sativ
989 37 39.8 909 2 Q4MMP3_BACCE Q4MMP3 bacillus ce
990 37 39.8 909 2 Q81A44_BACCR Q81A44 bacillus ce
991 37 39.8 910 2 Q732X8_BACCI Q732X8 bacillus ce
992 37 39.8 911 2 Q81W18_BACAN Q81W18 bacillus an
993 37 39.8 911 2 Q6HF62_BACHK Q6HF62 bacillus th
994 37 39.8 914 2 Q636S9_BACCB Q636S9 bacillus ce
995 37 39.8 914 2 Q61GL2_CAEBR Q61GL2 caenorhabdi
996 37 39.8 922 2 Q54DZ9_DICDI Q54DZ9 dictyostei
997 37 39.8 929 2 Q426A4_PLABE Q426A4 plasmodium
998 37 39.8 933 2 Q583Y9_9TRYP Q583Y9 trypanosoma
999 37 39.8 933 2 Q691I1_ORYSA Q691I1 oryza sativ
1000 37 39.8 934 2 Q691O7_ORYSA Q691O7 oryza sativ

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ALIGNMENTS

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RESULT 1
HV05_MOUSE
ID HV05_MOUSE STANDARD; PRT; 117 AA.
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 3 precursor.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Boehmell A.L.M., Paekind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: This germline gene belongs to a set of closely
CC related genes that could encode V regions of Npb antibodies.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J00536; AAA38605.1; -, Genomic_DNA.
CC PIR; A02031; HVMS3.
CC PDB; 1AI4; X-ray; H=20-117.
CC SMR; P01749; 20-117.
CC Ensemble; ENSMUSG0000060210; Mus musculus.
CC MGI; MGI:96486; Igh-VJ558.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT REGION 20 117 Ig heavy chain V region 3.
FT REGION 50 54 Framework-1.
FT REGION 55 68 Complementarity-determining-1.

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FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13016 MW; 427C661CS3975EDC CRC64;
Query Match 82.8%; Score 77; DB 1; Length 117;
Best Local Similarity 87.5%; Pred. No. 0.00016;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 IHPDSETRVNOXKFD 17
Db 70 IYPSDSETRVNOXKFD 85

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RESULT 2

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ID Q9UL81_MOUSE PRELIMINARY; PRT; 114 AA.
AC Q9UL81;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206025; AAF69323.1; -, mRNA.
DR HSSP; P01751; INOB.
DR SMR; Q9UL81; 2-114.
DR Ensemble; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT FT 114 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

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Query Match 81.7%; Score 76; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 0.00023;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 MIHPDSETRVNOXKFD 17
Db 42 MIDPSDSETRVNOXKFD 58

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RESULT 3

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ID Q5HZY6_MOUSE PRELIMINARY; PRT; 486 AA.
AC Q5HZY6;
DT 10-MAY-2005 (TRENBLREL. 30, Created)
DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLREL. 30, Last annotation update)
DE LOC544903 protein.
GN Name=LOC544903;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muiridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Morley P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC088837; AAH88837.1; -; mRNA.
DR GO; GO:0003823; Functional binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 486 AA; 52867 MW; FB3538650D53624B CRC64;

Query Match 81.7%; Score 76; DB 2; Length 486;
Best Local Similarity 82.4%; Pred. No. 0.0011;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOKFKD 17
DB 69 MHPSDSESRDPOKFKD 85

RESULT 4
HY06 MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Botwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;

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RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: This germline gene belongs to a set of closely
CC related genes that could encode V regions of NpB antibodies.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A02032; HVM502.
DR PDB; 1QNZ; NMR; H=21-117.
DR Ensembl; ENSMUSG0000062849; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 102.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD651FCA8C CRC64;

Query Match 79.6%; Score 74; DB 1; Length 117;
Best Local Similarity 86.7%; Pred. No. 0.0005;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOKFK 16
DB 70 IHPSDSETRYNOKFK 84

RESULT 5
Q91V67_MOUSE PRELIMINARY; PRT; 143 AA.
ID Q91V67;
AC Q91V67;
DC 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RL Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069912; BAB63928.1; -; mRNA.
DR EMBL; AB069914; BAB63930.1; -; mRNA.
DR PIR; S26744; S26744.
DR HSSP; P01751; IAGW.
DR SMR; Q91V67; 1-129.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG LIKE; 1.
DR NON_TER 1 143
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44EFEBF CRC64;

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Query Match          66.7%; Score 62; DB 2; Length 143;
Best Local Similarity 75.0%; Pred. No. 0.057;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 MHPDSETRYNOXFK 16
       : ||||| |||||
Db       50 VIDPSDYTYNOXFK 65

RESULT 6
0924P9 MOUSE PRELIMINARY; PRT; 143 AA.
ID 0924P9;
AC 0924P9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE V303-D-J-C mu protein (Fragment).
GN Name=V303-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX [1]

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6;
RL Kozono Y., Kozono H., Azuma T.;
   Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
   [2]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=7523684;
RA Pokkuluri P.R., Bouthillier F., Li Y., Kuderova A., Lee J., Cygler M.;
   "Preparation, characterization and crystallization of an antibody Fab
   fragment that recognizes RNA. Crystal structures of native Fab and
   RT three Fab-monomononucleotide complexes.";
   RT J. Mol. Biol. 243:283-297(1994).
   RL EMBL, AB069916; BAB63932.1; -; mRNA.
   DR PIR: PH1160; PH1160.
   DR PIR: PH1161; PH1161.
   DR PIR: PH1162; PH1162.
   DR PIR: SS3751; SS3751.
   DR HSSP: P01751; 1A6W.
   DR Ensembl; ENSMUSG00000061773; Mus musculus.
   DR InterPro; IPR007110; IG-like.
   DR InterPro; IPR003596; IG_v.
   DR SMART; SM00406; IGV, 1.
   DR PROSITE; PSS0835; IG_LIKE; 1.
   DR NON_TER 1
   FT NON_TER 143
   SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;

Query Match          65.6%; Score 61; DB 2; Length 143;
Best Local Similarity 80.0%; Pred. No. 0.083;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 IHPDSETRYNOXFK 16
       : ||||| |||||
Db       51 IDPSDYTYNOXFK 65

RESULT 7
0504M7 MOUSE PRELIMINARY; PRT; 616 AA.
ID 0504M7;
AC 0504M7;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshynski S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettleman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
   "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences.";
   RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
   [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RC NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
   [2]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=7523684;
RA Pokkuluri P.R., Bouthillier F., Li Y., Kuderova A., Lee J., Cygler M.;
   "Preparation, characterization and crystallization of an antibody Fab
   fragment that recognizes RNA. Crystal structures of native Fab and
   RT three Fab-monomononucleotide complexes.";
   RT J. Mol. Biol. 243:283-297(1994).
   RL EMBL, AB069916; BAB63932.1; -; mRNA.
   DR InterPro; IPR003599; IG.
   DR InterPro; IPR007110; IG-like.
   DR InterPro; IPR003597; IG_CL.
   DR InterPro; IPR003066; IG_MHC.
   DR InterPro; IPR003596; IG_v.
   DR PIR: PF07654; CI-sect; 4.
   DR SMART; SM00409; IG; 2.
   DR SMART; SM00407; IGC1; 4.
   DR SMART; SM00406; IGV; 1.
   DR PROSITE; PSS0835; IG_LIKE; 5.
   DR PROSITE; PSS0290; IG_MHC; UNKNOWN_3.
   KW Hypothetical protein.
   SQ SEQUENCE 616 AA; 67919 MW; 0FF4532BCD596A52 CRC64;

Query Match          65.6%; Score 61; DB 2; Length 616;
Best Local Similarity 80.0%; Pred. No. 0.4;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 IHPDSETRYNOXFK 16
       : ||||| |||||
Db       70 IDPSDYTYNOXFK 84

RESULT 8
04KMUS MOUSE PRELIMINARY; PRT; 617 AA.
ID 04KMUS;
AC 04KMUS;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX [1]

RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshynski S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettleman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
   "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences.";
   RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
   [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RC NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
   [2]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=7523684;
RA Pokkuluri P.R., Bouthillier F., Li Y., Kuderova A., Lee J., Cygler M.;
   "Preparation, characterization and crystallization of an antibody Fab
   fragment that recognizes RNA. Crystal structures of native Fab and
   RT three Fab-monomononucleotide complexes.";
   RT J. Mol. Biol. 243:283-297(1994).
   RL EMBL, AB069916; BAB63932.1; -; mRNA.
   DR InterPro; IPR003599; IG.
   DR InterPro; IPR007110; IG-like.
   DR InterPro; IPR003597; IG_CL.
   DR InterPro; IPR003066; IG_MHC.
   DR InterPro; IPR003596; IG_v.
   DR PIR: PF07654; CI-sect; 4.
   DR SMART; SM00409; IG; 2.
   DR SMART; SM00407; IGC1; 4.
   DR SMART; SM00406; IGV; 1.
   DR PROSITE; PSS0835; IG_LIKE; 5.
   DR PROSITE; PSS0290; IG_MHC; UNKNOWN_3.
   KW Hypothetical protein.
   SQ SEQUENCE 616 AA; 67919 MW; 0FF4532BCD596A52 CRC64;

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek A.M., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC098504; AAH98504.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 617 AA; 68520 MW; BCFZAECS7CD3D12 CRC64;
 QY Query Match 64.5%; Score 60; DB 2; Length 617;
 Best Local Similarity 62.5%; Pred. No. 0.59;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Db 70 VNPSSGYTKNQKFKD 85
 2 HHPDSETRYNOKFKD 17
 :|||:|||||:
 Db VNPSSGYTKNQKFKD 85
 RESULT 9
 0921C6_MOUSE PRELIMINARY; PRT; 117 AA.
 ID 0921C6_MOUSE PRELIMINARY; PRT; 117 AA.
 AC 0921C6;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Anti-porcine VCAm mab 2A2 heavy chain variable region (Fragment).
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Balb/c;
 MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
 RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Matie L.A., Evans M.J.,
 RT "Humanized porcine VCAm-specific monoclonal antibodies with chimeric
 RT IgG2/G4 constant regions block human leukocyte binding to porcine
 RT endothelial cells";
 RL Mol. Immunol. 34:441-452(1997).
 DR EMBL; U78799; AAD00291.1; -; mRNA.
 DR HSSP; P01820; IGTV.
 DR SMR; 0921C6; 1-116.
 DR Ensemble; ENSMUSG00000021155; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGv_1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 117 AA; 13122 MW; 4F65E193AFB77E5B CRC64;
 QY Query Match 63.4%; Score 59; DB 2; Length 117;
 Best Local Similarity 64.7%; Pred. No. 0.14;
 Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHPDSETRYNOKFKD 17
 :|||:|||||:
 Db 50 MIDPDSSEVKLNQRLKD 66
 RESULT 10
 077MK1_MOUSE PRELIMINARY; PRT; 470 AA.
 ID 077MK1_MOUSE PRELIMINARY; PRT; 470 AA.
 AC 077MK1;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
 DE Hypothetical protein A1324046.
 GN Name=A1324046;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC098504; AAH98504.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 617 AA; 68520 MW; BCFZAECS7CD3D12 CRC64;
 QY Query Match 62.4%; Score 58; DB 2; Length 470;
 Best Local Similarity 56.2%; Pred. No. 0.93;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 1 MHPDSETRYNOKFK 16
 :|||:|||||:

Db 69 LVNPSNGDTSYNOKFK 84

RESULT 11
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Last Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;
RX Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT untranscribed VH gene segments";
RT Cell 40:271-281 (1985).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, M13787; AAA8499.1; -; mRNA.
DR PIR: A02029; HVMSA1.
DR HSSP: P01820; 1G7J.
DR SMR: P06327; 20-117.
DR InterPro: IPR007110; Ig-1-like.
DR InterPro: IPR003596; Ig_V.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region VH558 A1/A4.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC13856DFC9D CRC64;

Query Match 61.3%; Score 57; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 0.3; Indels 0; Gaps 0;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPDSETRYNOKFK 16
DB 70 IYPGDSITKYNKFK 84

RESULT 12
Q9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q9GYZ2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song X.T., Peng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF282622; AAC01452.1; -; mRNA.
DR HSSP: P01751; 1A6W.
DR SMR: Q9GYZ2; 1-119.
DR InterPro: IPR007110; Ig-1-like.
DR InterPro: IPR003596; Ig_V.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1 119
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 61.3%; Score 57; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.31;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPDSETRYNOKFKD 17
DB 51 INPSRGYTNYNOKFKD 66

RESULT 13
Q91WT1_MOUSE PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; PubMed=1477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadiri T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013490; AAH13490.1; -; mRNA.
DR HSSP: P01751; 1A6W.
DR Ensembl: ENSMUSG0000021155; Mus musculus.
DR GO: 0003823; F:antigen binding; IEA.

DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS50835; IG_MHC; UNKNOWN_2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 61.3%; Score 57; DB 2; Length 481;
 Best Local Similarity 60.0%; Pred. No. 1.4;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDETRYNOKFK 16
 DB 70 IYPGDNTRYNEKFK 84

RESULT 14
 Q9JL77_MOUSE PRELIMINARY; PRT; 110 AA.

AC Q9JL77;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RX NUCLEOTIDE SEQUENCE.
 RC STRAIN=DBA/2;
 RX MEDLINE=20448942; PubMed=10992488;
 RX DOI=10.1126/IAF.68.10.5803-5808.2000;
 RA Walkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Cell-dependent antibody response to the dominant epitope of
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808(2000).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 RT nonmutated germ-line genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
 DR EMBL; AF206029; AAF69327.1; -, mRNA.
 DR PIR; F33932; F33932.
 DR HSSP; P01751; INOB.
 DR SMR; Q9JL77; 1-110.
 DR ENSEMBL; ENSMUSG0000021155; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 110 AA; 12138 MW; 2ED881F5862C9AF CRC64;

Query Match 60.2%; Score 56; DB 2; Length 110;
 Best Local Similarity 60.0%; Pred. No. 0.41;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPSDETRYNOKFK 16
 DB 43 IHPSGHTYNEKFK 57

RESULT 15
 Q7TPE3_MOUSE PRELIMINARY; PRT; 136 AA.

AC Q7TPE3;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE V23-D-J-IgG1 protein (Fragment).
 GN Name=V23-D-J-IgG1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]

Query Match 60.2%; Score 56; DB 2; Length 136;
 Best Local Similarity 60.0%; Pred. No. 0.52;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPSDETRYNOKFK 16
 DB 48 IYPSGDNTRYNEKFK 62

RESULT 16
 Q5F211_MOUSE PRELIMINARY; PRT; 120 AA.
 AC Q5F211;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Gamma heavy chain variable region (Fragment).
 GN Name=IgG1 anti-TSI VH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Erlandsen A., Holm P., Ullen A., Stigbrand T., Sundstrom B.B.;
 RT "Studies of the interactions between the anticytokerafin 8 monoclonal
 RT antibody TSI, its antigen and its anti-idiotypic antibody alphaTsi.";
 RN J. Mol. Recognit. 16:157-163(2003).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RA Erlandsen A.,
 Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB884574; CA156336.1; -, mRNA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.

```
FT  NON TER      1      1
FT  NON TER      120     120
SQ  SEQUENCE      120 AA; 13087 MW; 4A6013141AB87BE2 CRC64;

Query Match
Best Local Similarity 58.1%; Score 54; DB 2; Length 120;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      2  IHPDSETRYNOXPK 16
Db      51  IYPGNGDTSTYNOXPK 65

RESULT 17
Q91WT3_MOUSE PRELIMINARY; PRT; 481 AA.
ID  Q91WT3_MOUSE PRELIMINARY; PRT; 481 AA.
AC  Q91WT3;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE  01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE  Igh-VJ558 protein.
DE  Igh-VJ558 protein.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=FVB/N; TISSUE=Colon;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Uedl T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA  Bosaik S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butlerfield Y.S.N., Krzywinski M.L., Skalski U., Smalins D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences."
RT  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=FVB/N; TISSUE=Colon;
RA  Strauberg R.;
RL  Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR  EMBL; BC013488; AAH13488.1; -, mRNA.
DR  HSPB1; P01751; IAGW.
DR  MGI; MGI:96486; Igh-VJ558.
DR  GO; GO:0003823; F:antigen binding; IEA.
DR  InterPro; IPR007110; I9-like.
DR  InterPro; IPR003597; I9_C1.
DR  InterPro; IPR003006; I9_MHC.
DR  InterPro; IPR003596; I9_V.
DR  Pfam; PF07654; C1-bec; 2.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS00835; I9_LIKE; 4.
DR  PROSITE; PS00290; I9_MHC; UNKNOWN_2.
KW  immunoglobulin domain.
SQ  SEQUENCE 481 AA; 52023 MW; 4EBB5C253038B718 CRC64;
```

```
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  IHPDSETRYNOXPK 16
Db      70  IDPFDSTYNOXPK 84

RESULT 18
Q9D9B8_MOUSE PRELIMINARY; PRT; 111 AA.
ID  Q9D9B8_MOUSE PRELIMINARY; PRT; 111 AA.
AC  Q9D9B8;
DT  01-JUN-2001 (TREMBLrel. 17, Created)
DT  01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE  01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE  Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE  library, clone:1700110J1 product:immunoglobulin heavy chain 6 (heavy
DE  chain of Igm), full insert sequence.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC  Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Testis;
RX  MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA  Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA  Aikawa T., Hara A., Fukunishi Y., Kono H., Aochi J., Fukuda S.,
RA  Aizawa K., Iawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA  Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA  Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA  Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
RA  Schiml L.M., Staib F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA  Sakai K., Okido T., Furuno M., Adono H., Baldarelli R., Bersh G.,
RA  Blakey J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA  Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
RA  Guerinich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereys P.,
RA  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,
RA  Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA  Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
RA  Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA  Hayashizaki Y.;
RT  "Functional annotation of a full-length mouse cDNA collection."
RT  Nature 409:685-690 (2001).
RN  [3]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Testis;
RA  The FANTOM Consortium;
RA  the RIKEN Genome Exploration Research Group Phase I & II Team;
RT  "Analysis of the mouse transcriptome based on functional annotation of
RT  60,770 full-length cDNAs."
RT  Nature 420:563-573 (2002).
RN  [4]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Testis;
RX  MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA  Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA  Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT  "Normalization and subtraction of cap-trapper-selected cDNAs to
RT  prepare full-length cDNA libraries for rapid discovery of new genes."
RT  Genome Res. 10:1617-1630 (2000).
RN  [5]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=C57BL/6J; TISSUE=Testis;
```

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RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shihata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ichii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasahagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsushita S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Furumishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ichii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shihata K., Shihata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007163; BB24877.1; -, mRNA.
DR HSSP; P01820; IG70.
DR SMR; Q9D988; 7-106.
DR Ensembl; ENSMUSG00000063520; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;

Query Match 57.0%; Score 53; DB 2; Length 111;
Best Local Similarity 60.0%; Pred. No. 1.3;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPSDSTRYNOKFK 16
DB 57 IYRGDGTWNGKFK 71

RESULT 19
HY48 MOUSE STANDARD; PRT; 138 AA.
AC P03960;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an Igd-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
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CC use as long as its content is in no way modified and this statement is not
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CC -----
DR PIR; A02033; HWMST7.
DR HSSP; P01751; 1A6V.
DR SMR; P03960; 20-138.
DR Ensembl; ENSMUSG00000063737; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 Ig heavy chain V region TEPC 1017.
FT REGION 21 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT REGION 118 127 Complementarity-determining-3.
FT REGION 128 138 Framework-4.
FT DISULFID 41 115 By similarity.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 55.9%; Score 52; DB 1; Length 138;
Best Local Similarity 50.0%; Pred. No. 2.4;
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDSTRYNOKFKD 17
DB 70 INPNDGRSNYNEKFKN 85

RESULT 20
Q7TMT6 MOUSE PRELIMINARY; PRT; 614 AA.
ID Q7TMT6_MOUSE PRELIMINARY;
AC Q7TMT6;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE MGCG0843 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange S.J.,
RA Raha S.S., Lounellano N.A., Peters G.J., Abramson R.D., Gunaratne P.H.,
RA Bosak S.A., McBryan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalski W., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;

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RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAH53409.1; -, mRNA.
DR HSSP; P01820; 1G7J.
DR Ensembl; ENSMUSG00000054328; Mus musculus.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 614 AA; 67747 MW; 839BAF3BD124F89 CRC64;

Query Match 55.9%; Score 52; DB 2; Length 614;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 IHPDSETRYNQKFK 16
Db 70 VFPDGDITNYNKKF 84

RESULT 21
HVS0_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotype) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J. 3:517-523(1984).

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CC PIR; A02037; MEMS15.
DR HSSP; P01751; 1A6W.
DR SMR; P06329; 1-120.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 98 V segment.
FT REGION 99 105 D segment.
FT REGION 106 120 U segment.
FT DISULFD 22 96 By similarity.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 91453F426F09834 CRC64;

Query Match 54.8%; Score 51; DB 1; Length 120;
Best Local Similarity 60.0%; Pred. No. 3;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 IHPDSETRYNQKFK 16
Db 51 INPSNGGTNYNKKF 65

RESULT 22
O924P8_MOUSE PRELIMINARY; PRT; 140 AA.
AC O924P8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN Name=AB069917; Synonyms=V23-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=315311;
RA Corbet S., Hirm M., Roth C., These J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
DR EMBL; AB069917; BAB63933.1; -, mRNA.
DR PIR; I28833; I28833.
DR PIR; PH156; PH156.
DR HSSP; P01751; 1A6W.
DR SMR; O924P8; 1-126.
DR MGI; MGI:3576502; AB069917.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1 1
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15392 MW; 904C80C82548C936 CRC64;

Query Match 54.8%; Score 51; DB 2; Length 140;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 IHPDSETRYNQKFK 16
Db 51 INPSNGGTNYNKKF 65

RESULT 23
O924Q1_MOUSE PRELIMINARY; PRT; 142 AA.
AC O924Q1;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE V23-D-J-C mu protein (Fragment).
GN Name=AB069917; Synonyms=V23-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;

DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0016820; F:hydrolase activity acting on acid anhydrid. . .; IEA.
 DR GO; GO:0006812; F:cation transport; IEA.
 DR GO; GO:0008152; F:metabolism; IEA.
 DR GO; GO:0015992; P:proton transport; IEA.
 DR InterPro; IPR006414; ATPase-IIID_KNA.
 DR InterPro; IPR001757; ATPase_EI-E2.
 DR InterPro; IPR006068; Cation_ATPase_C.
 DR InterPro; IPR004014; Cation_ATPase_N.
 DR InterPro; IPR005834; Denal_like_hydro.
 DR InterPro; IPR008250; EI-E2_ATPase_reg.
 DR InterPro; IPR000695; H_ATPase.
 DR Pfam; PF00689; Cation_ATPase_C; 1.
 DR Pfam; PF00690; Cation_ATPase_N; 1.
 DR Pfam; PF00122; EI-E2_ATPase; 1.
 DR Pfam; PF00702; Hydrolase; 1.
 DR PRINTS; PR00119; CATATPASE.
 DR PRINTS; PR00120; HATPASE.
 DR TIGRFAMs; TIGR01523; ATPase-IIID_K-Na; 1.
 DR TIGRFAMs; TIGR01494; ATPase_P-type; 4.
 DR PROSITE; PS00154; ATPASE_EI-E2; UNKNOWN_1.
 DR ATP-binding; Complete proteome; Hydrolase; Nucleotide-binding;
 KW Transmembrane.
 SQ SEQUENCE 1078 AA; 118400 MW; A3F3B87D836D628E CRC64;

Query Match 54.3%; Score 50.5; DB 2; Length 1078;
 Best Local Similarity 68.8%; Pred. No. 39;
 Matches 11; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

OY 2 IHPSDSTRYNQKFK 17
 :|||:|||||
 Db 955 MHP-DSETPYQVFKD 969

RESULT 26
 ID HV12_MOUSE STANDARD; PRT; 117 AA.
 AC P01756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region MOPC 104E.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridea; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 OX [1]
 RP PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 RX MEDLINE=83075344; PubMed=6816276;
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains.";
 RL Biochemistry 21:5415-5424(1982).
 CC -!- MISCELLANEOUS: The sequence of the light chain of this Igm myeloma
 CC protein has also been determined.
 CC -!- MISCELLANEOUS: This protein binds dextran.
 CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC PIR; A02039; MEMS4E.
 DR HSSP; P01751; INOB.
 DR SMR; P01756; 1-117.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT DOMAIN 1 116 Ig-like.
 FT CARBOHYD 55 55 N-linked (GlcNAc. . .) (complex).
 FT DISULFID 22 96 By similarity.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 13025 MW; 292E2AF4BE447E41 CRC64;

DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT DOMAIN 1 116 Ig-like.
 FT CARBOHYD 55 55 N-linked (GlcNAc. . .) (complex).
 FT DISULFID 22 96 By similarity.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACEABE447E41 CRC64;

Query Match 53.8%; Score 50; DB 1; Length 117;
 Best Local Similarity 60.0%; Pred. No. 4.2;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 IHPSDSTRYNQKFK 16
 :|||:|||||
 Db 51 INPNNGSTYNQKFK 65

RESULT 27
 ID HV13_MOUSE STANDARD; PRT; 117 AA.
 AC P01757;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region J558.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridea; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 OX [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain V-region gene segments.";
 RL Nature 283:35-40(1980).
 CC -!- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also
 CC bind dextran differ from that shown at 1-7 positions, many of
 CC which occur in the D and J segments.
 CC -!- MISCELLANEOUS: This protein binds dextran.
 CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC PIR; A26242; MEMSJ5.
 DR HSSP; P01751; INOB.
 DR SMR; P01757; 1-117.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT DOMAIN 1 116 Ig-like.
 FT DISULFID 22 96 By similarity.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 13025 MW; 292E2AF4BE447E41 CRC64;

Query Match 53.8%; Score 50; DB 1; Length 117;
 Best Local Similarity 60.0%; Pred. No. 4.2;
 Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 IHPSDSTRYNQKFK 16
 :|||:|||||
 Db 51 INPNNGSTYNQKFK 65


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RESULT 28
O9QX9_MOUSE PRELIMINARY; PRT; 117 AA.
ID O9QX9_MOUSE PRELIMINARY; PRT; 117 AA.
AC O9QX9_MOUSE PRELIMINARY; PRT; 117 AA.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Immunoglobulin heavy chain V-D-J region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RA Clemens A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
DR EMBL; AJ225174; CAB65237.1; -, mRNA.
DR PIR; F33932; F33932.
DR HSSP; P01751; 1NOB.
DR SMR; O9QX9; 1-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 13000 MW; CDDE2AF84D49734 CRC64;
SQ
Query Match 53.8%; Score 50; DB 2; Length 117;
Best Local Similarity 60.0%; Pred. No. 4.2;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 IHPSDETRYNQKFK 16
Db 51 INPNNGTSTYNQKFK 65

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DR SMR; O9QX9; 1-117.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 117 117
FT NON_TER 117 117
FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;
SQ
Query Match 53.8%; Score 50; DB 2; Length 117;
Best Local Similarity 60.0%; Pred. No. 4.2;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 IHPSDETRYNQKFK 16
Db 51 INPNNGTSTYNQKFK 65

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RESULT 30
HV51_MOUSE STANDARD; PRT; 118 AA.
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RX PubMed=6201362;
RA Dildrop R., Boveris U., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes."
RL EMBO J. 3:517-523 (1984).
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR PIR; A02040; MEMS38.
DR HSSP; P01751; 1NOB.
DR SMR; P06330; 1-118.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 98 V segment.
FT REGION 99 104 D segment.
FT REGION 105 118 J segment.
FT DISULFID 22 96 By similarity.
FT NON_TER 118 118
FT SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
SQ
Query Match 53.8%; Score 50; DB 1; Length 118;
Best Local Similarity 60.0%; Pred. No. 4.3;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 IHPSDETRYNQKFK 16
Db 51 INPNNGTSTYNQKFK 65

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RESULT 31
O9Z1C4_MOUSE PRELIMINARY; PRT; 118 AA.
ID O9Z1C4_MOUSE PRELIMINARY; PRT; 118 AA.

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AC Q921C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-porcine VCAM mAb 3F4 heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c;
RX MEDLINE=97450619; PubMed=9307060; DOI=10.1016/S0161-5890(97)00042-4;
RA Mueller J.P., Gianni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matris B.A., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Mol. Immunol. 34:441-452(1997).
DR EMBL; U78801; AAD00293.1; -, mRNA.
DR HSP; P01751; INOB.
DR Q921C4; 1-118.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90BEC559D31EC4FC CRC64;

Query Match 53.8%; Score 50; DB 2; Length 118;
Best Local Similarity 53.3%; Pred. No. 4.3;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOKFK 16
DB 51 IYPGDDTSYTKFR 65

RESULT 32
Q5BUI1 MOUSE PRELIMINARY; PRT; 123 AA.
ID Q5BUI1
AC Q5BUI1
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-DNA heavy chain (Fragment).
GN Name=J558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CD3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59154; AAB02916.1; -, mRNA.
DR HSP; P01751; INOB.
DR SMR; Q5BUI1; 1-123.
DR Ensembl; ENSMUSG00000057521; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 123

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SQ SEQUENCE 123 AA; 13806 MW; CC0037A806B9911E CRC64;

Query Match 53.8%; Score 50; DB 2; Length 123;
Best Local Similarity 62.5%; Pred. No. 4.4;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOKFKD 17
DB 51 INPYGGTRYSQKFD 66

RESULT 33
Q65ZR6 MOUSE
ID Q65ZR6 MOUSE PRELIMINARY; PRT; 134 AA.
AC Q65ZR6
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Ab 126.33 heavy chain variable and joining regions (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=91237115; PubMed=1709665;
RA Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
RT "Functional diversity of H and L chains allows the coexpression of two
RT mutually exclusive idiotopes (Id1104 and Id1558).";
RL J. Immunol. 146:4024-4030(1991).
DR EMBL; M74139; AAA3776.1; -, mRNA.
DR SMR; Q65ZR6; 18-134.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 134
SQ SEQUENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;

Query Match 53.8%; Score 50; DB 2; Length 134;
Best Local Similarity 60.0%; Pred. No. 4.9;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOKFK 16
DB 68 INPNNGGTSYNOKFK 82

RESULT 34
Q5BUI2_RAT
ID Q5BUI2_RAT PRELIMINARY; PRT; 458 AA.
AC Q5BUI2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC67586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Usdin T.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Czech II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC histocompatibility complex class I molecules (By similarity).
 CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
 CC EMBL; BC091272; AAH91272.1; -; mRNA.
 DR SMR; OSB722; 21-454.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGcl; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR Immunoglobulin domain; Repeat.
 KW SEQUENCE 458 AA; 50161 MW; A0A1DCDD2CA4336 CRC64;
 SQ

Query Match 53.8%; Score 50; DB 2; Length 458;
 Best Local Similarity 57.1%; Pred. No. 18;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 IHPDSETRYNOKF 15
 |||:|||||
 DB 70 IYPGNGNTKYNOKF 83

RESULT 35
 OS05N9 MOUSE PRELIMINARY; PRT; 468 AA.
 ID OS05N9_9
 AC 0505N9-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN Name=Igh-1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Czech II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Shemen C.M., Schler G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Czech II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RG NIH MGC Project;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC094467; AAH94467.1; -; mRNA.
 DR SMR; OS05N9; 20-464.
 DR MGI; MGI:96443; Igh-1a.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003596; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 468 AA; 51672 MW; B2A42DC85C33B927 CRC64;
 SQ

Query Match 53.8%; Score 50; DB 2; Length 468;
 Best Local Similarity 56.2%; Pred. No. 19;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 IHPDSETRYNOKF 17
 |||:|||||
 DB 70 IDPDSETRYNOKF 85

RESULT 36
 OSRE17 PONY PRELIMINARY; PRT; 475 AA.
 ID OSRE17_1
 AC 05RE17-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Hypothetical protein DKFZp69C2335.
 GN Name=DKFZp69C2335;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Pongo.
 OC NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RC The German cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schnupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amlid C., Osanger A., Robo G., Han M., Wiemann S.,
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR857722; CAH89990.1; -; mRNA.
 DR SMR; OSRE17; 21-475.
 DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
 DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
 DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
 DR InterPro; IPR007110; IG-like.

DR Ensembl; ENSMUTG0000021155; Mus musculus.
 DR InterPro; IPR007110; IG-1ike.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 143 143
 SQ SEQUENCE 143 AA; 15704 MW; C99D243F2BAD8A0 CRC64;
 Query Match 52.7%; Score 49; DB 2; Length 143;
 Best Local Similarity 53.3%; Pred. No. 7.6;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 IHPDSETRYNOKFK 16
 Db 51 ITPGSGSTYNEKFK 65
 RESULT 40
 O569X1 MOUSE PRELIMINARY; PRT; 476 AA.
 AC O569X1;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Ighg protein.
 GN Name=Ighg;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RX MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 Altshul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.B.,
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/mtl model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RC NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092269; AA92269.1; -; mRNA.
 DR SMR; O569X1: 20-472.
 DR MGI; MGI:214967; Ighg.
 DR InterPro; IPR003599; Igh.
 DR InterPro; IPR007110; IG-1ike.
 DR InterPro; IPR003597; IG-CL.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.

DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
 SQ SEQUENCE 476 AA; 52149 MW; 7B1F055CDD85F13A CRC64;
 Query Match 52.7%; Score 49; DB 2; Length 476;
 Best Local Similarity 56.2%; Pred. No. 28;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 IHPDSETRYNOKFKD 17
 Db 70 IDPEDGETRYKVPKFD 85
 RESULT 41
 O925S3 MOUSE PRELIMINARY; PRT; 147 AA.
 AC O925S3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MRP3.
 GN Name=Musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RX PubMed=11819679;
 RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
 Yan X.J., Hou Y., Su C.Z.;
 "Mechanism of exogenous nucleic acids and their precursors improving
 the repair of intestinal epithelium after gamma-irradiation in mice.";
 World J. Gastroenterol. 6:709-717(2000).
 [2]
 NUCLEOTIDE SEQUENCE.
 RC STRAIN=BA/Bc;
 RC STRAIN=BA/Bc;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 "Cloning of mouse genes related to repairing of intestinal epithelium
 of the irradiated mice by treatment with the intestinal RNA of mice of
 the same strain";
 Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240166; AA43731.1; -; mRNA.
 DR HSSP; P01751; 1A6W.
 DR SMR; O925S3: 3-139.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;
 Query Match 51.6%; Score 48; DB 2; Length 147;
 Best Local Similarity 53.3%; Pred. No. 11;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 IHPDSETRYNOKFK 16
 Db 53 ITPGSGSTYNEKFK 67
 RESULT 42
 O569W9 MOUSE PRELIMINARY; PRT; 468 AA.
 AC O569W9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

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DE Hypothetical protein.
GN Name=Igh-1a; (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECB II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECB II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RG NIH MGC Project;
RX Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC092271; AAH92271.1; -, mRNA.
DR SMR, Q569W9; 20-464.
DR MGI, MGI:96443; Igh-1a.
DR GO, GO:0003823; F:antigen binding; IEA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam, PF07654; CI-sec; 3.
DR SMART, SM00409; IG; 2.
DR SMART, SM00406; IGV; 1.
DR PROSITE, PS00835; IG_LIKE; 4.
DR PROSITE, PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 468 AA; 5166 MW; 5BF6E52329F8461 CRC64;

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Query Match 51.6%; Score 48; DB 2; Length 468;
Best Local Similarity 53.3%; Pred. No. 40;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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OY 2 IHPDSETRYNOKFK 16
DB 70 IYPGNGYTRYNEKFK 84

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RESULT 43
08K024 MOUSE PRELIMINARY; PRT; 480 AA.
AC 08K024_
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE LOC238447 protein.

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GN Name=LOC238447;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. MAP-1GF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Mix FVB/N;
RC TISSUE=Mammary tumor. MAP-1GF alpha model. 7 months old;
RG NIH MGC Project;
RX Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC029188; AAH29188.1; -, mRNA.
DR HSSP, P01820; 1G7J.
DR SMR, P01820; 1G7J.
DR Ensemble, ENSMUSG00000021155; Mus musculus.
DR GO, GO:0003823; F:antigen binding; IEA.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam, PF07654; CI-sec; 2.
DR SMART, SM00406; IGV; 1.
DR PROSITE, PS00835; IG_LIKE; 4.
DR PROSITE, PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 480 AA; 51646 MW; 8690A63C669CDBED CRC64;

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Query Match 51.6%; Score 48; DB 2; Length 480;
Best Local Similarity 53.3%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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OY 2 IHPDSETRYNOKFK 16
DB 70 ISPGDSSSETRNEKFK 84

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RESULT 44
06N041 HUMAN PRELIMINARY; PRT; 498 AA.
AC 06N041_
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686016217 (Fragment).
GN Name=DKFZp686016217;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Human rectum tumor;
 RA The German Human CDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amdt C., Osanger A., Fobo G., Han M., Wiemann S.,
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBD databases.
 DR EMBL; BX640710; CAE45829.1; -, mRNA.
 DR HSSP; P01751; 1A6W.
 DR SMR; Q6N041; 268--476.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-sec; 2.
 DR SMART; SM00409; IG; 4.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;
 Query Match 51.6%; Score 48; DB 2; Length 498;
 Best Local Similarity 50.0%; Pred. No. 43;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 MHPDSETRYNQKFK 16
 Db 84 MINPRDGTGYAQRQ 99

RESULT 45
 O9UL75_MOUSE PRELIMINARY; PRT; 109 AA.
 ID O9UL75_MOUSE PRELIMINARY; PRT; 109 AA.
 AC O9UL75;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RX MEDLINE=20448942; PubMed=10992488;
 RX DOI=10.1128/JAI.68.10.5803-5808.2000;
 RA Malirel S., Liao L., Cunningham M.W., Diamond B.,
 RA "T-cell-dependent antibody response to the dominant epitope of
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 RT with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2457627;
 RA Bilt D., Webster D.M., Rees A.R.,
 RA "V region sequences of anti-DNA and anti-RNA autoantibodies from
 RT NZB/NZW F1 mice.";
 RL J. Immunol. 141:1745-1753(1988).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=9281444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
 RA Tillman D.M., Jou N.T., Hill R.J., Marion T.N.,
 RA "Both IgM and IgG anti-DNA antibodies are the products of clonally

RT selective B cell stimulation in (NZB x NZW) F1 mice.";
 RL J. Exp. Med. 176:761-779(1992).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
 RA Stark S.E., Caton A.J.,
 RA "Antibodies that are specific for a single amino acid interchange in a
 RT protein epitope use structurally distinct variable regions.";
 RL J. Exp. Med. 174:613-624(1991).
 DR EMBL; AF206031; AAF69329.1; -, mRNA.
 DR PIR; A30502; A30502.
 DR PIR; PH0989; PH0989.
 DR PIR; PH0990; PH0990.
 DR PIR; PH0991; PH0991.
 DR PIR; PH0992; PH0992.
 DR PIR; PH0993; PH0993.
 DR PIR; PH0994; PH0994.
 DR PIR; PH0995; PH0995.
 DR PIR; PH1094; PH1094.
 DR PIR; PH1096; PH1096.
 DR PIR; S26312; S26312.
 DR PIR; S26313; S26313.
 DR HSSP; P01751; 1N0B.
 DR Ensembl; ENSMUSG0000021155; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;
 Query Match 50.5%; Score 47; DB 2; Length 109;
 Best Local Similarity 53.3%; Pred. No. 12;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 IHPDSETRYNQKFK 16
 Db 42 INPYNDGTGYKNEKFK 56

RESULT 46
 HV04_MOUSE STANDARD; PRT; 117 AA.
 ID HV04_MOUSE STANDARD; PRT; 117 AA.
 AC P01748;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region 23 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
 RX Botwell A.L.M., Paeklin M., Reith M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.,
 RA "Heavy chain variable region contribution to the NpB family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -I- MISCELLANEOUS: This germline gene belongs to a set of closely
 CC related genes that could encode V regions of NpB antibodies.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 DR PIR; A02030; HVMS23.

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DR HSSP; P01751; 1A6W.
DR SMR; P01748; 20-117.
DR Ensembl; ENSMUSG0000063737; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 23.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 50.5%; Score 47; DB 1; Length 117;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IHPDSETRYNQKFK 16
Db 70 INPNGSGTNYNEKFK 84

RESULT 47
HV09_MOUSE STANDARD; PRT; 117 AA.
ID HV09_MOUSE
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: This germline gene belongs to a set of closely
CC related genes that could encode V regions of NPB antibodies.
-----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC PIR; D90809; HVMS61.
DR HSSP; P01751; 1A6W.
DR SMR; P01753; 20-117.
DR Ensembl; ENSMUSG0000063737; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 186-1.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.

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FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A086CB17F5A CRC64;

Query Match 50.5%; Score 47; DB 1; Length 117;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IHPDSETRYNQKFK 16
Db 70 IDPNSGCTNYNEKFK 84

RESULT 48
HV10_MOUSE STANDARD; PRT; 117 AA.
ID HV10_MOUSE
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 145 precursor.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: This germline gene belongs to a set of closely
CC related genes that could encode V regions of NPB antibodies.
-----
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CC use as long as its content is in no way modified and this statement is not
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CC EMBL; J00533; AAA38602.1; -; Genomic_DNA.
DR PIR; C90809; HVMS45.
DR HSSP; P01754; 20-117.
DR SMR; P01754; 20-117.
DR Ensembl; ENSMUSG0000063737; Mus musculus.
DR MGI; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 145.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DEBA3F543B996 CRC64;

Query Match 50.5%; Score 47; DB 1; Length 117;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IHPDSETRYNQKFK 16

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Db | | | | | | | | | |
70 IDPNSGCTKYNEKFK 84

RESULT 49
HVA4 MOUSE STANDARD; PRT; 117 AA.
ID HV14 MOUSE
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN Name-IgH-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81245215; PubMed=6789211;
RT Girol D., Zakut R., Effron K., Rechavi G., Ram D., Cohen J.B.;
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
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DR EMBL, J00488; AAA38519.1; -; Genomic_DNA.
DR PIR, A02041; HVMS8A.
DR HSSP, P01751; INOB.
DR SMR, P01758; 20-116.
DR MGI, MGI:96486; Igh-VJ558.
DR InterPro, IPR007110; Ig-like.
DR InterPro, IPR003596; Ig_v.
DR SMART, SM00406; IGV, 1.
DR PROSITE, PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region 108A.
FT DOMAIN 20 >117 Ig-like.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 50.5%; Score 47; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPSDETRYNOKFK 16
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Db 70 IYYPNGTGYNOKFK 84

RESULT 50
HVA9 MOUSE STANDARD; PRT; 117 AA.
ID HV49 MOUSE
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85099340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;

RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.",
RI Cell 40:271-281(1985).
CC -----

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CC removed.
CC -----
DR EMBL, M13788; AAA38506.1; -; mRNA.
DR PIR, A02035; MEMSB4.
DR HSSP, P01751; 1A6W.
DR Ensembl, ENSMUSG0000063737; Mus musculus.
DR InterPro, IPR007110; Ig-like.
DR InterPro, IPR003596; Ig_v.
DR SMART, SM00406; IGV, 1.
DR PROSITE, PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig heavy chain V region VH558 B4.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT DISULFID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 50.5%; Score 47; DB 1; Length 117;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPSDETRYNOKFK 16
| | | | | | | | | |
Db 70 IDPNSGCTKYNEKFK 84

Search completed: January 17, 2006, 12:05:14
Job time : 126.818 secs

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:50:24 ; Search time 29.3636 Seconds
(without alignments)
47.865 Million cell updates/sec

Title: US-10-665-658-11
Perfect score: 93
Sequence: 1 MIHPDSETRYNQKFKD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:
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2: /cgn2_6/prodata/1/1aa/6/COMB.pep:*
3: /cgn2_6/prodata/1/1aa/8/COMB.pep:*
4: /cgn2_6/prodata/1/1aa/ECTUS_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/RB_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	17	2	US-08-974-899-11
2	93	100.0	17	2	US-09-795-798-11
3	93	100.0	121	2	US-08-974-899-5
4	93	100.0	121	2	US-09-795-798-5
5	85	91.4	118	2	US-08-767-128-2
6	85	91.4	118	2	US-08-767-128-8
7	85	91.4	121	2	US-08-974-899-4
8	85	91.4	121	2	US-09-795-798-4
9	80	86.0	19	2	US-09-948-004-33
10	80	86.0	117	2	US-09-948-004-16
11	80	86.0	138	2	US-09-948-004-14
12	80	86.0	495	2	US-09-948-004-18
13	74	79.6	119	2	US-08-767-128-6
14	74	79.6	241	1	US-08-335-838-11
15	74	79.6	241	1	US-08-665-4738-11
16	74	79.6	637	1	US-08-235-838-16
17	74	79.6	637	1	US-08-465-4738-16
18	69	74.2	17	2	US-08-974-899-23
19	69	74.2	17	2	US-09-795-798-23
20	69	74.2	118	2	US-09-698-705-9
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23	63	67.7	119	1	US-09-091-071-7
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27	63	67.7	466	2	US-09-698-705-11

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30	62	66.7	116	2	US-09-026-985-50	Sequence 50, Appl
31	62	66.7	116	2	US-09-121-952A-50	Sequence 50, Appl
32	62	66.7	116	2	US-09-234-340A-50	Sequence 50, Appl
33	62	66.7	116	2	US-09-355-014-50	Sequence 50, Appl
34	61	65.6	119	1	US-08-553-497A-8	Sequence 8, Appl
35	61	65.6	119	1	US-08-553-497A-12	Sequence 12, Appl
36	61	65.6	230	2	US-08-952-235-2	Sequence 2, Appl
37	61	65.6	230	2	US-09-669-971-2	Sequence 2, Appl
38	59	63.4	17	1	US-08-482-228-40	Sequence 40, Appl
39	59	63.4	17	2	US-08-482-528-40	Sequence 40, Appl
40	59	63.4	98	2	US-08-881-037-59	Sequence 59, Appl
41	59	63.4	111	2	US-08-881-037-14	Sequence 14, Appl
42	59	63.4	111	2	US-08-881-037-16	Sequence 16, Appl
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72	59	63.4	152	1	US-07-634-278-101	Sequence 101, Appl
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94	58	62.4	114	2	US-09-196-522-226	Sequence 226, Appl
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112	58	62.4	116	1	US-08-487-200-5	Sequence 5, Appl1	185	58	62.4	253	2	US-09-026-985-52	Sequence 52, Appl1
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116	58	62.4	116	1	US-08-488-113B-169	Sequence 169, App	189	58	62.4	253	2	US-09-121-952A-55	Sequence 55, Appl1
117	58	62.4	116	1	US-08-477-484B-167	Sequence 167, App	190	58	62.4	253	2	US-09-234-340A-44	Sequence 44, Appl1
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123	58	62.4	116	1	US-08-477-531B-86	Sequence 86, Appl1	196	58	62.4	256	2	US-09-027-449-70	Sequence 70, Appl1
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135	58	62.4	116	2	US-08-484-537-3	Sequence 3, Appl1	208	58	62.4	452	2	US-09-026-985-71	Sequence 71, Appl1
136	58	62.4	116	2	US-08-484-537-5	Sequence 5, Appl1	209	58	62.4	452	2	US-09-121-952A-71	Sequence 71, Appl1
137	58	62.4	116	2	US-08-484-537-6	Sequence 6, Appl1	210	58	62.4	452	2	US-09-234-340A-71	Sequence 71, Appl1
138	58	62.4	116	2	US-08-484-537-14	Sequence 14, Appl1	211	58	62.4	599	2	US-09-355-014-71	Sequence 71, Appl1
139	58	62.4	116	2	US-09-610-838-167	Sequence 167, App	212	58	62.4	599	1	US-08-463-163-3	Sequence 3, Appl1
140	58	62.4	116	2	US-09-610-838-169	Sequence 169, App	213	57	61.3	17	2	US-09-269-921-7	Sequence 7, Appl1
141	58	62.4	116	2	US-09-711-485-167	Sequence 167, App	214	57	61.3	102	1	US-08-793-480-1	Sequence 1, Appl1
142	58	62.4	116	2	US-09-711-485-169	Sequence 169, App	215	57	61.3	115	1	US-08-672-345C-16	Sequence 16, Appl1
143	58	62.4	117	2	US-09-027-449-48	Sequence 48, Appl1	216	57	61.3	115	2	US-09-214-095D-16	Sequence 16, Appl1
144	58	62.4	117	2	US-09-027-449-49	Sequence 49, Appl1	217	57	61.3	115	2	US-09-940-727B-16	Sequence 16, Appl1
145	58	62.4	117	2	US-08-804-444A-48	Sequence 48, Appl1	218	57	61.3	116	1	US-08-888-366-2	Sequence 2, Appl1
146	58	62.4	117	2	US-08-804-444A-49	Sequence 49, Appl1	219	57	61.3	119	1	US-08-303-569B-11	Sequence 11, Appl1
147	58	62.4	117	2	US-09-026-985-48	Sequence 48, Appl1	220	57	61.3	119	1	US-08-303-569B-30	Sequence 30, Appl1
148	58	62.4	117	2	US-09-026-985-49	Sequence 49, Appl1	221	57	61.3	119	1	US-08-070-116A-12	Sequence 12, Appl1
149	58	62.4	117	2	US-09-121-952A-48	Sequence 48, Appl1	222	57	61.3	119	1	US-08-070-116A-13	Sequence 13, Appl1
150	58	62.4	117	2	US-09-121-952A-49	Sequence 49, Appl1	223	57	61.3	119	1	US-08-070-116A-13	Sequence 14, Appl1
151	58	62.4	117	2	US-09-234-340A-48	Sequence 48, Appl1	224	57	61.3	119	1	US-08-116-247-12	Sequence 12, Appl1
152	58	62.4	117	2	US-09-234-340A-49	Sequence 49, Appl1	225	57	61.3	119	1	US-08-116-247-19	Sequence 19, Appl1
153	58	62.4	117	2	US-09-355-014-48	Sequence 48, Appl1	226	57	61.3	119	2	US-08-116-247-19	Sequence 12, Appl1
154	58	62.4	117	2	US-09-355-014-49	Sequence 49, Appl1	227	57	61.3	119	2	US-08-557-050-10	Sequence 10, Appl1
155	58	62.4	117	2	US-07-634-278-19	Sequence 19, Appl1	228	57	61.3	119	2	US-08-557-050-12	Sequence 12, Appl1
156	58	62.4	117	2	US-08-477-728-19	Sequence 19, Appl1	229	57	61.3	119	2	US-08-557-050-13	Sequence 13, Appl1
157	58	62.4	117	2	US-08-398-613A-50	Sequence 50, Appl1	230	57	61.3	119	2	US-08-557-050-14	Sequence 14, Appl1
158	58	62.4	117	2	US-08-398-613A-50	Sequence 50, Appl1	231	57	61.3	119	2	US-09-795-515-11	Sequence 11, Appl1
159	58	62.4	117	2	US-08-398-612A-50	Sequence 50, Appl1	232	57	61.3	119	2	US-09-795-515-10	Sequence 30, Appl1
160	58	62.4	117	2	US-08-474-040-19	Sequence 19, Appl1	233	57	61.3	119	2	US-09-348-224-12	Sequence 12, Appl1
161	58	62.4	117	2	US-08-487-200-19	Sequence 19, Appl1	234	57	61.3	119	2	US-09-348-224-19	Sequence 19, Appl1
162	58	62.4	117	2	US-08-398-611A-50	Sequence 50, Appl1	235	57	61.3	121	2	US-09-948-004-26	Sequence 26, Appl1
163	58	62.4	117	2	US-08-303-569B-31	Sequence 31, Appl1	236	57	61.3	139	2	US-09-355-925-7	Sequence 7, Appl1
164	58	62.4	117	2	US-08-491-334A-50	Sequence 50, Appl1	237	57	61.3	139	2	US-09-355-925-8	Sequence 8, Appl1
165	58	62.4	117	2	US-09-027-449-37	Sequence 37, Appl1	238	57	61.3	139	2	US-09-269-921-105	Sequence 105, App
166	58	62.4	117	2	US-08-804-444A-37	Sequence 37, Appl1	239	57	61.3	139	2	US-09-269-921-108	Sequence 108, App
167	58	62.4	117	2	US-09-026-985-37	Sequence 37, Appl1	240	57	61.3	139	2	US-09-269-921-109	Sequence 109, App
168	58	62.4	117	2	US-08-484-537-19	Sequence 19, Appl1	241	57	61.3	139	2	US-09-269-921-110	Sequence 110, App
169	58	62.4	117	2	US-09-121-952A-37	Sequence 37, Appl1	242	57	61.3	139	2	US-09-269-921-111	Sequence 111, App
170	58	62.4	117	2	US-09-355-014-37	Sequence 37, Appl1	243	57	61.3	139	2	US-09-269-921-112	Sequence 112, App
171	58	62.4	117	2	US-09-069-628-30	Sequence 30, Appl1	244	57	61.3	139	2	US-09-269-921-113	Sequence 113, App
172	58	62.4	239	2	US-08-279-772A-8	Sequence 8, Appl1	245	57	61.3	139	2	US-09-269-921-114	Sequence 114, App
173	58	62.4	239	2	US-08-902-486-11	Sequence 11, Appl1	246	57	61.3	139	2	US-09-269-921-115	Sequence 115, App

247	57	61.3	139	2	US-09-269-921-116	Sequence 116, App	320	54	58.1	140	2	US-08-475-813-6	Sequence 6, Appli
248	57	61.3	139	2	US-09-269-921-117	Sequence 117, App	321	54	58.1	140	2	US-09-630-198-44	Sequence 44, Appli
249	57	61.3	139	2	US-09-269-921-118	Sequence 118, App	322	54	58.1	231	1	US-08-681-432-1	Sequence 1, Appli
250	57	61.3	139	2	US-09-269-921-119	Sequence 119, App	323	54	58.1	237	1	US-08-468-252-5	Sequence 5, Appli
251	57	61.3	139	2	US-09-269-921-120	Sequence 120, App	324	54	58.1	237	2	US-08-668-706B-5	Sequence 5, Appli
252	57	61.3	139	2	US-09-269-921-121	Sequence 121, App	325	54	58.1	237	4	PCT-US95-10740-5	Sequence 5, Appli
253	57	61.3	139	2	US-09-269-921-122	Sequence 122, App	326	54	58.1	470	2	US-09-238-741-4	Sequence 4, Appli
254	57	61.3	139	2	US-09-269-921-123	Sequence 123, App	327	53	57.0	114	2	US-09-726-219A-228	Sequence 228, App
255	57	61.3	139	2	US-09-269-921-124	Sequence 124, App	328	53	57.0	114	2	US-09-196-522-228	Sequence 228, App
256	57	61.3	139	2	US-09-269-921-125	Sequence 125, App	329	53	57.0	115	1	US-08-308-494A-17	Sequence 17, Appl
257	57	61.3	139	2	US-09-269-921-126	Sequence 126, App	330	53	57.0	115	2	US-09-726-219A-216	Sequence 216, App
258	57	61.3	139	2	US-09-269-921-127	Sequence 127, App	331	53	57.0	115	2	US-09-196-522-216	Sequence 216, App
259	57	61.3	139	2	US-09-269-921-128	Sequence 128, App	332	53	57.0	118	1	US-08-553-457A-16	Sequence 16, Appl
260	57	61.3	256	2	US-09-526-738A-2	Sequence 2, Appli	333	53	57.0	119	1	US-08-467-333-2	Sequence 17, Appl
261	57	61.3	258	2	US-09-526-738A-4	Sequence 4, Appli	334	53	57.0	137	2	US-08-444-644-17	Sequence 17, Appl
262	57	61.3	273	1	US-08-403-853-18	Sequence 18, Appl	335	53	57.0	233	2	US-08-232-246A-13	Sequence 33, Appl
263	57	61.3	468	1	US-08-303-569B-7	Sequence 7, Appli	336	53	57.0	233	2	US-08-232-246A-33	Sequence 33, Appl
264	57	61.3	468	1	US-08-116-247-7	Sequence 7, Appli	337	53	57.0	233	2	US-08-444-644-19	Sequence 19, Appl
265	57	61.3	468	1	US-09-795-515-7	Sequence 7, Appli	338	53	57.0	235	2	US-08-444-644-28	Sequence 42, Appl
266	57	61.3	468	2	US-09-348-224-7	Sequence 7, Appli	339	53	57.0	235	2	US-08-444-644-42	Sequence 19, Appl
267	56	60.2	117	1	US-08-318-970B-7	Sequence 7, Appli	340	53	57.0	235	2	US-08-232-246A-19	Sequence 28, Appl
268	56	60.2	111	2	US-08-881-037-15	Sequence 15, Appl	341	53	57.0	235	2	US-08-232-246A-28	Sequence 42, Appl
269	56	60.2	119	2	US-08-881-037-60	Sequence 60, Appl	342	53	57.0	235	2	US-08-232-246A-42	Sequence 21, Appl
270	56	60.2	124	1	US-08-657-012-16	Sequence 16, Appl	343	53	57.0	247	2	US-10-620-049-21	Sequence 113, App
271	56	60.2	124	1	US-08-657-012-17	Sequence 17, Appl	344	53	57.0	257	2	US-09-419-768-113	Sequence 14, Appl
272	56	60.2	124	1	US-08-657-012-18	Sequence 18, Appl	345	52	55.9	17	1	US-08-465-313-14	Sequence 14, Appl
273	56	60.2	124	1	US-08-657-012-19	Sequence 19, Appl	346	52	55.9	17	1	US-08-465-313-14	Sequence 14, Appl
274	56	60.2	124	1	US-08-657-012-23	Sequence 23, Appl	347	52	55.9	17	2	US-09-809-729-7	Sequence 7, Appli
275	56	60.2	124	1	US-09-013-872-16	Sequence 16, Appl	348	52	55.9	17	2	US-09-378-967-14	Sequence 14, Appl
276	56	60.2	124	2	US-09-013-872-17	Sequence 17, Appl	349	52	55.9	115	2	US-08-838-662-8	Sequence 8, Appli
277	56	60.2	124	2	US-09-013-872-18	Sequence 18, Appl	350	52	55.9	115	2	US-08-895-914-8	Sequence 8, Appli
278	56	60.2	124	2	US-09-013-872-19	Sequence 19, Appl	351	52	55.9	115	2	US-09-357-710A-8	Sequence 8, Appli
279	56	60.2	124	2	US-09-013-872-23	Sequence 23, Appl	352	52	55.9	115	2	US-09-357-707-8	Sequence 8, Appli
280	56	60.2	124	2	US-09-184-198-16	Sequence 16, Appl	353	52	55.9	115	2	US-09-357-707-8	Sequence 8, Appli
281	56	60.2	124	2	US-09-184-198-17	Sequence 17, Appl	354	52	55.9	115	2	US-09-357-708-8	Sequence 8, Appli
282	56	60.2	124	2	US-09-184-198-18	Sequence 18, Appl	355	52	55.9	116	1	US-08-488-113B-168	Sequence 168, App
283	56	60.2	124	2	US-09-184-198-19	Sequence 19, Appl	356	52	55.9	116	1	US-08-477-484B-168	Sequence 54, Appl
284	56	60.2	124	2	US-09-184-198-23	Sequence 23, Appl	357	52	55.9	116	1	US-08-107-669D-54	Sequence 54, Appl
285	56	60.2	124	2	US-09-633-653-16	Sequence 16, Appl	358	52	55.9	116	1	US-08-477-531B-54	Sequence 54, Appl
286	56	60.2	124	2	US-09-633-653-17	Sequence 17, Appl	359	52	55.9	116	1	US-08-477-531B-54	Sequence 54, Appl
287	56	60.2	124	2	US-09-633-653-18	Sequence 18, Appl	360	52	55.9	116	1	US-08-082-842A-84	Sequence 54, Appl
288	56	60.2	124	2	US-09-633-653-19	Sequence 19, Appl	361	52	55.9	116	1	US-08-833-765-168	Sequence 168, App
289	55	59.1	124	2	US-09-633-653-23	Sequence 23, Appl	362	52	55.9	116	2	US-09-136-389-168	Sequence 168, App
290	55	59.1	17	2	US-09-406-532-6	Sequence 6, Appli	363	52	55.9	116	2	US-09-610-838-168	Sequence 168, App
291	55	59.1	114	2	US-09-726-219A-234	Sequence 234, App	364	52	55.9	116	2	US-09-711-485-168	Sequence 168, App
292	55	59.1	114	2	US-09-196-522-234	Sequence 217, App	365	52	55.9	119	2	US-10-194-975-121	Sequence 121, App
293	55	59.1	116	2	US-09-726-219A-217	Sequence 217, App	366	52	55.9	119	2	US-08-838-662-4	Sequence 4, Appli
294	55	59.1	116	2	US-09-196-522-217	Sequence 48, Appl	367	52	55.9	130	2	US-08-895-914-4	Sequence 4, Appli
295	55	59.1	118	2	US-08-766-350B-48	Sequence 2, Appli	368	52	55.9	130	2	US-09-357-710A-4	Sequence 4, Appli
296	55	59.1	119	2	US-09-406-532-2	Sequence 18, Appl	369	52	55.9	130	2	US-09-357-707-4	Sequence 4, Appli
297	55	59.1	249	1	US-08-797-689-18	Sequence 18, Appl	370	52	55.9	130	2	US-09-357-707-4	Sequence 4, Appli
298	55	59.1	249	2	US-09-984-186-18	Sequence 8, Appli	371	52	55.9	130	2	US-08-182-067-10	Sequence 10, Appl
299	54	58.1	17	2	US-08-479-089A-8	Sequence 8, Appli	372	52	55.9	139	1	US-08-465-313-10	Sequence 10, Appl
300	54	58.1	17	2	US-07-669-545B-8	Sequence 8, Appli	373	52	55.9	139	2	US-09-809-739-5	Sequence 9, Appli
301	54	58.1	96	2	US-09-905-243-12	Sequence 12, Appl	374	52	55.9	139	2	US-09-809-739-5	Sequence 9, Appli
302	54	58.1	96	2	US-09-905-243-13	Sequence 13, Appl	375	52	55.9	139	2	US-09-378-967-10	Sequence 10, Appl
303	54	58.1	117	2	US-08-479-089A-2	Sequence 2, Appli	376	52	55.9	20	2	US-08-913-994B-7	Sequence 7, Appli
304	54	58.1	117	2	US-08-479-089A-3	Sequence 3, Appli	377	51	54.8	98	1	US-08-428-197-17	Sequence 17, Appl
305	54	58.1	117	2	US-07-669-545B-2	Sequence 3, Appli	378	51	54.8	98	4	PCT-US93-10555-17	Sequence 17, Appl
306	54	58.1	117	2	US-07-669-545B-3	Sequence 3, Appli	379	51	54.8	122	1	US-08-236-520-9	Sequence 9, Appli
307	54	58.1	121	1	US-07-634-278-52	Sequence 52, Appl	380	51	54.8	122	4	PCT-US95-05262-9	Sequence 9, Appli
308	54	58.1	121	1	US-07-634-278-53	Sequence 53, Appl	381	51	54.8	122	4	US-08-513-966-44	Sequence 44, Appl
309	54	58.1	121	1	US-08-477-728-52	Sequence 52, Appl	382	51	54.8	138	2	US-08-513-966-44	Sequence 44, Appl
310	54	58.1	121	1	US-08-477-728-53	Sequence 53, Appl	383	51	54.8	143	1	PCT-US95-05262-7	Sequence 7, Appli
311	54	58.1	121	1	US-08-474-040-52	Sequence 52, Appl	384	51	54.8	269	4	US-09-358-321C-32	Sequence 32, Appl
312	54	58.1	121	1	US-08-474-040-53	Sequence 53, Appl	385	50	53.8	17	1	US-08-116-778B-7	Sequence 7, Appli
313	54	58.1	121	1	US-08-487-200-52	Sequence 52, Appl	386	50	53.8	17	1	US-08-438-562-7	Sequence 7, Appli
314	54	58.1	121	1	US-08-487-200-53	Sequence 53, Appl	387	50	53.8	17	1	US-08-483-528B-95	Sequence 95, Appl
315	54	58.1	121	2	US-08-484-537-52	Sequence 52, Appl	388	50	53.8	17	1	US-09-393-385B-106	Sequence 106, App
316	54	58.1	121	2	US-08-484-537-53	Sequence 53, Appl	389	50	53.8	17	2	US-10-195-752-106	Sequence 106, App
317	54	58.1	140	1	US-08-476-275-6	Sequence 6, Appli	390	50	53.8	45	2	US-09-627-218B-5	Sequence 5, Appli
318	54	58.1	140	2	US-08-475-815B-11	Sequence 11, Appl	391	50	53.8	88	2	US-09-726-219A-172	Sequence 172, App
319	54	58.1	140	2	US-09-724-138-44	Sequence 44, Appl	392	50	53.8	88	2		

393	50	53.8	88	2	US-09-196-522-172	Sequence 172, App
394	50	53.8	96	2	US-09-905-243-15	Sequence 18, Appl
395	50	53.8	98	1	US-08-478-039-81	Sequence 20, Appl
396	50	53.8	98	1	US-08-476-349A-81	Sequence 21, Appl
397	50	53.8	98	1	US-08-665-202-33	Sequence 22, Appl
398	50	53.8	98	1	US-09-315-574-33	Sequence 23, Appl
399	50	53.8	98	2	US-10-194-975-45	Sequence 24, Appl
400	50	53.8	98	2	US-09-905-243-47	Sequence 25, Appl
401	50	53.8	111	2	US-09-726-219A-171	Sequence 26, Appl
402	50	53.8	111	2	US-09-196-522-171	Sequence 27, Appl
403	50	53.8	114	2	US-09-726-219A-221	Sequence 28, Appl
404	50	53.8	114	2	US-09-196-522-221	Sequence 29, Appl
405	50	53.8	115	2	US-09-513-999C-4117	Sequence 30, Appl
406	50	53.8	116	1	US-08-690-102A-4	Sequence 31, Appl
407	50	53.8	116	1	US-08-690-102A-8	Sequence 32, Appl
408	50	53.8	116	1	US-08-690-102A-9	Sequence 33, Appl
409	50	53.8	116	2	US-09-127-902-4	Sequence 34, Appl
410	50	53.8	116	2	US-09-127-902-8	Sequence 35, Appl
411	50	53.8	116	2	US-09-127-902-9	Sequence 36, Appl
412	50	53.8	116	2	US-09-155-107-4	Sequence 37, Appl
413	50	53.8	116	2	US-09-155-107-8	Sequence 38, Appl
414	50	53.8	116	2	US-09-155-107-21	Sequence 39, Appl
415	50	53.8	116	4	PCT-US95-09641-4	Sequence 40, Appl
416	50	53.8	116	4	PCT-US95-09641-8	Sequence 41, Appl
417	50	53.8	116	4	PCT-US95-09641-9	Sequence 42, Appl
418	50	53.8	117	2	US-08-545-809A-133	Sequence 43, Appl
419	50	53.8	117	2	US-09-515-697-133	Sequence 44, Appl
420	50	53.8	118	2	US-09-802-083-5	Sequence 45, Appl
421	50	53.8	119	1	US-08-303-569B-12	Sequence 46, Appl
422	50	53.8	119	1	US-08-303-569B-13	Sequence 47, Appl
423	50	53.8	119	1	US-08-303-569B-14	Sequence 48, Appl
424	50	53.8	119	1	US-08-303-569B-15	Sequence 49, Appl
425	50	53.8	119	1	US-08-303-569B-16	Sequence 50, Appl
426	50	53.8	119	1	US-08-303-569B-17	Sequence 51, Appl
427	50	53.8	119	1	US-08-303-569B-18	Sequence 52, Appl
428	50	53.8	119	1	US-08-303-569B-19	Sequence 53, Appl
429	50	53.8	119	1	US-08-303-569B-20	Sequence 54, Appl
430	50	53.8	119	1	US-08-303-569B-21	Sequence 55, Appl
431	50	53.8	119	1	US-08-303-569B-22	Sequence 56, Appl
432	50	53.8	119	1	US-08-303-569B-23	Sequence 57, Appl
433	50	53.8	119	1	US-08-303-569B-24	Sequence 58, Appl
434	50	53.8	119	1	US-08-116-247-13	Sequence 59, Appl
435	50	53.8	119	1	US-08-116-247-14	Sequence 60, Appl
436	50	53.8	119	1	US-08-116-247-15	Sequence 61, Appl
437	50	53.8	119	1	US-08-116-247-16	Sequence 62, Appl
438	50	53.8	119	1	US-08-116-247-17	Sequence 63, Appl
439	50	53.8	119	1	US-08-116-247-18	Sequence 64, Appl
440	50	53.8	119	1	US-08-116-247-20	Sequence 65, Appl
441	50	53.8	119	1	US-08-116-247-21	Sequence 66, Appl
442	50	53.8	119	1	US-08-116-247-22	Sequence 67, Appl
443	50	53.8	119	1	US-08-116-247-23	Sequence 68, Appl
444	50	53.8	119	1	US-08-116-247-24	Sequence 69, Appl
445	50	53.8	119	1	US-08-116-247-25	Sequence 70, Appl
446	50	53.8	119	2	US-09-025-769B-26	Sequence 71, Appl
447	50	53.8	119	2	US-09-795-515-12	Sequence 72, Appl
448	50	53.8	119	2	US-09-795-515-13	Sequence 73, Appl
449	50	53.8	119	2	US-09-795-515-14	Sequence 74, Appl
450	50	53.8	119	2	US-09-795-515-15	Sequence 75, Appl
451	50	53.8	119	2	US-09-795-515-16	Sequence 76, Appl
452	50	53.8	119	2	US-09-795-515-17	Sequence 77, Appl
453	50	53.8	119	2	US-09-795-515-18	Sequence 78, Appl
454	50	53.8	119	2	US-09-795-515-19	Sequence 79, Appl
455	50	53.8	119	2	US-09-795-515-20	Sequence 80, Appl
456	50	53.8	119	2	US-09-795-515-21	Sequence 81, Appl
457	50	53.8	119	2	US-09-795-515-22	Sequence 82, Appl
458	50	53.8	119	2	US-09-795-515-23	Sequence 83, Appl
459	50	53.8	119	2	US-09-795-515-24	Sequence 84, Appl
460	50	53.8	119	2	US-09-490-070A-26	Sequence 85, Appl
461	50	53.8	119	2	US-09-490-153-26	Sequence 86, Appl
462	50	53.8	119	2	US-09-348-224-13	Sequence 87, Appl
463	50	53.8	119	2	US-09-348-224-14	Sequence 88, Appl
464	50	53.8	119	2	US-09-348-224-15	Sequence 89, Appl
465	50	53.8	119	2	US-09-348-224-16	Sequence 90, Appl

539	49	52.7	119	1	US-08-487-200-89	Sequence 89, Appl	612	48	51.6	125	1	US-08-665-202-44	Sequence 44, Appl
540	49	52.7	119	1	US-08-737-560A-10	Sequence 10, Appl	613	48	51.6	125	1	US-08-665-202-45	Sequence 45, Appl
541	49	52.7	119	2	US-08-484-537-64	Sequence 64, Appl	614	48	51.6	125	1	US-08-665-202-46	Sequence 46, Appl
542	49	52.7	119	2	US-08-484-537-65	Sequence 65, Appl	615	48	51.6	125	1	US-08-665-202-47	Sequence 47, Appl
543	49	52.7	119	2	US-08-484-537-89	Sequence 89, Appl	616	48	51.6	125	1	US-08-665-202-48	Sequence 48, Appl
544	49	52.7	119	2	US-09-438-954-2	Sequence 2, Appl	617	48	51.6	125	1	US-08-665-202-49	Sequence 49, Appl
545	49	52.7	121	2	US-09-438-954-39	Sequence 39, Appl	618	48	51.6	125	1	US-08-665-202-50	Sequence 50, Appl
546	49	52.7	121	2	US-09-254-180C-7	Sequence 7, Appl	619	48	51.6	125	1	US-08-665-202-51	Sequence 51, Appl
547	49	52.7	122	1	US-07-934-373C-20	Sequence 19, Appl	620	48	51.6	125	1	US-08-665-202-52	Sequence 52, Appl
548	49	52.7	122	1	US-07-934-373C-20	Sequence 20, Appl	621	48	51.6	125	1	US-08-665-202-53	Sequence 53, Appl
549	49	52.7	122	1	US-08-437-642B-19	Sequence 19, Appl	622	48	51.6	125	1	US-08-665-202-54	Sequence 54, Appl
550	49	52.7	122	2	US-08-437-642B-20	Sequence 20, Appl	623	48	51.6	125	1	US-08-665-202-55	Sequence 55, Appl
551	49	52.7	122	2	US-08-983-607-30	Sequence 30, Appl	624	48	51.6	125	1	US-08-665-202-57	Sequence 57, Appl
552	49	52.7	122	2	US-08-146-206C-19	Sequence 19, Appl	625	48	51.6	125	1	US-08-665-202-58	Sequence 58, Appl
553	49	52.7	122	2	US-08-146-206C-19	Sequence 20, Appl	626	48	51.6	125	2	US-09-315-574-44	Sequence 44, Appl
554	49	52.7	122	2	US-09-705-686-19	Sequence 19, Appl	627	48	51.6	125	2	US-09-315-574-45	Sequence 45, Appl
555	49	52.7	122	2	US-09-705-686-20	Sequence 20, Appl	628	48	51.6	125	2	US-09-315-574-46	Sequence 46, Appl
556	49	52.7	122	2	US-09-705-686-20	Sequence 20, Appl	629	48	51.6	125	2	US-09-315-574-47	Sequence 47, Appl
557	49	52.7	122	2	US-09-705-392A-19	Sequence 19, Appl	630	48	51.6	125	2	US-09-315-574-48	Sequence 48, Appl
558	49	52.7	122	2	US-09-705-392A-20	Sequence 20, Appl	631	48	51.6	125	2	US-09-315-574-49	Sequence 49, Appl
559	49	52.7	122	2	US-09-705-398-19	Sequence 19, Appl	632	48	51.6	125	2	US-09-315-574-50	Sequence 50, Appl
560	49	52.7	122	2	US-09-705-398-20	Sequence 20, Appl	633	48	51.6	125	2	US-09-315-574-51	Sequence 51, Appl
561	49	52.7	122	4	PCT-US93-07832-20	Sequence 20, Appl	634	48	51.6	125	2	US-09-315-574-52	Sequence 52, Appl
562	49	52.7	125	2	US-09-357-710A-20	Sequence 20, Appl	635	48	51.6	125	2	US-09-315-574-53	Sequence 53, Appl
563	49	52.7	125	2	US-09-357-707-20	Sequence 20, Appl	636	48	51.6	125	2	US-09-315-574-54	Sequence 54, Appl
564	49	52.7	126	2	US-09-914-695-10	Sequence 20, Appl	637	48	51.6	125	2	US-09-315-574-55	Sequence 55, Appl
565	49	52.7	128	1	US-08-202-047-21	Sequence 21, Appl	638	48	51.6	125	2	US-09-315-574-57	Sequence 57, Appl
566	49	52.7	128	2	US-08-964-690-21	Sequence 21, Appl	639	48	51.6	125	2	US-08-665-202-32	Sequence 32, Appl
567	49	52.7	129	4	PCT-US93-07832-19	Sequence 19, Appl	640	48	51.6	129	2	US-09-315-574-32	Sequence 32, Appl
568	49	52.7	136	2	US-08-525-539A-47	Sequence 47, Appl	641	48	51.6	135	1	US-08-860-114A-4	Sequence 4
569	49	52.7	136	2	US-08-525-539A-63	Sequence 63, Appl	642	48	51.6	137	2	US-08-513-968-38	Sequence 38, Appl
570	49	52.7	138	1	US-07-634-278-85	Sequence 85, Appl	643	48	51.6	138	1	US-08-482-882-78	Sequence 78, Appl
571	49	52.7	138	1	US-08-477-728-85	Sequence 85, Appl	644	48	51.6	138	1	US-08-458-516-7	Sequence 7, Appl
572	49	52.7	138	1	US-08-474-040-85	Sequence 85, Appl	645	48	51.6	138	1	US-08-483-389-78	Sequence 78, Appl
573	49	52.7	138	1	US-08-487-200-85	Sequence 85, Appl	646	48	51.6	138	1	US-08-473-503-78	Sequence 78, Appl
574	49	52.7	140	1	US-08-484-537-85	Sequence 85, Appl	647	48	51.6	138	1	US-08-483-932-78	Sequence 78, Appl
575	49	52.7	140	1	US-07-946-421-24	Sequence 24, Appl	648	48	51.6	138	1	US-08-483-932-78	Sequence 78, Appl
576	49	52.7	140	1	US-07-946-421-28	Sequence 28, Appl	649	48	51.6	138	1	US-08-720-430A-78	Sequence 78, Appl
577	49	52.7	212	1	US-08-737-129A-2	Sequence 2, Appl	650	48	51.6	138	1	US-08-603-024-2	Sequence 2, Appl
578	49	52.7	242	1	US-08-553-497A-28	Sequence 28, Appl	651	48	51.6	138	2	US-08-714-017-78	Sequence 78, Appl
579	49	52.7	243	1	US-08-230-843-4	Sequence 4, Appl	652	48	51.6	138	2	US-08-475-660-78	Sequence 78, Appl
580	49	52.7	244	1	US-08-636-936-4	Sequence 4, Appl	653	48	51.6	139	1	US-08-253-877C-19	Sequence 19, Appl
581	49	52.7	244	1	US-08-553-497A-20	Sequence 20, Appl	654	48	51.6	139	1	US-08-253-877C-19	Sequence 19, Appl
582	49	52.7	245	1	US-08-553-497A-24	Sequence 24, Appl	655	48	51.6	139	1	US-08-656-586-8	Sequence 8, Appl
583	48	51.6	17	1	US-08-318-970B-4	Sequence 4, Appl	656	48	51.6	139	1	US-08-656-586-8	Sequence 8, Appl
584	48	51.6	17	2	US-09-508-413A-4	Sequence 4, Appl	657	48	51.6	139	1	US-08-894-922A-5	Sequence 5, Appl
585	48	51.6	22	2	US-08-918-148-4	Sequence 4, Appl	658	48	51.6	139	1	US-08-452-164A-8	Sequence 8, Appl
586	48	51.6	22	2	US-09-138-091A-4	Sequence 4, Appl	659	48	51.6	139	1	US-08-452-164A-8	Sequence 8, Appl
587	48	51.6	111	2	US-09-823-746-10	Sequence 10, Appl	660	48	51.6	139	2	US-08-603-024-18	Sequence 18, Appl
588	48	51.6	111	2	US-09-823-746-14	Sequence 14, Appl	661	48	51.6	139	2	US-08-450-809-14	Sequence 14, Appl
589	48	51.6	113	2	US-08-211-202-115	Sequence 115, Appl	662	48	51.6	140	2	US-08-579-378A-4	Sequence 4, Appl
590	48	51.6	113	2	US-09-508-413A-14	Sequence 14, Appl	663	48	51.6	140	2	US-08-579-378A-4	Sequence 4, Appl
591	48	51.6	118	1	US-08-491-845-6	Sequence 6, Appl	664	48	51.6	140	2	PCT-US93-11612-4	Sequence 4, Appl
592	48	51.6	118	1	US-08-491-845-14	Sequence 14, Appl	665	48	51.6	140	4	PCT-US93-11612-4	Sequence 4, Appl
593	48	51.6	118	1	US-08-116-247-10	Sequence 10, Appl	666	48	51.6	141	4	US-08-461-284-4	Sequence 4, Appl
594	48	51.6	118	2	US-09-348-224-10	Sequence 10, Appl	667	48	51.6	141	1	US-08-462-939-4	Sequence 4, Appl
595	48	51.6	119	1	US-08-458-516-10	Sequence 10, Appl	668	48	51.6	141	1	US-08-462-939-4	Sequence 4, Appl
596	48	51.6	119	1	US-08-458-516-11	Sequence 11, Appl	669	48	51.6	141	1	US-08-253-877C-4	Sequence 4, Appl
597	48	51.6	119	2	US-09-556-605-1	Sequence 1, Appl	670	48	51.6	141	1	US-08-452-164A-4	Sequence 4, Appl
598	48	51.6	120	1	US-08-211-202-1	Sequence 1, Appl	671	48	51.6	163	2	US-09-318-786-27	Sequence 27, Appl
599	48	51.6	120	1	US-07-934-373C-6	Sequence 6, Appl	672	48	51.6	222	1	US-08-458-516-22	Sequence 22, Appl
600	48	51.6	120	2	US-08-437-642B-6	Sequence 6, Appl	673	48	51.6	235	1	US-08-458-516-23	Sequence 23, Appl
601	48	51.6	120	2	US-08-397-411-11	Sequence 10, Appl	674	48	51.6	246	1	US-08-460-486-57	Sequence 57, Appl
602	48	51.6	120	2	US-08-397-411-11	Sequence 11, Appl	675	48	51.6	246	1	US-08-460-486-57	Sequence 57, Appl
603	48	51.6	120	2	US-08-146-206C-6	Sequence 6, Appl	676	48	51.6	249	2	US-08-918-148-74	Sequence 74, Appl
604	48	51.6	120	2	US-09-705-686-6	Sequence 6, Appl	677	48	51.6	249	2	US-09-138-091A-12	Sequence 12, Appl
605	48	51.6	120	2	US-09-705-392A-6	Sequence 6, Appl	678	48	51.6	252	1	US-08-894-922A-14	Sequence 14, Appl
606	48	51.6	120	2	US-09-705-392A-6	Sequence 6, Appl	679	48	51.6	258	1	US-08-665-202-5	Sequence 5, Appl
607	48	51.6	120	4	PCT-US93-07832-6	Sequence 6, Appl	680	48	51.6	258	2	US-09-315-574-5	Sequence 5, Appl
608	48	51.6	121	2	US-08-579-378A-7	Sequence 7, Appl	681	48	51.6	262	2	US-09-069-821-4	Sequence 4, Appl
609	48	51.6	121	2	US-08-579-378A-8	Sequence 8, Appl	682	48	51.6	262	2	US-09-956-086-4	Sequence 4, Appl
610	48	51.6	121	4	PCT-US93-11612-7	Sequence 7, Appl	683	48	51.6	262	2	US-09-956-086-4	Sequence 4, Appl
611	48	51.6	121	4	PCT-US93-11612-8	Sequence 8, Appl	684	48	51.6	271	1	US-08-894-922A-10	Sequence 10, Appl

685	48	51.6	274	1	US-08-860-174A-12	Sequence 12, Appl	758	46	49.5	118	2	US-07-987-264-60	Sequence 60, Appl
686	48	51.6	279	2	US-08-397-411-13	Sequence 13, Appl	759	46	49.5	121	2	US-08-881-037-55	Sequence 65, Appl
687	48	51.6	282	2	US-09-420-592A-7	Sequence 7, Appl	760	46	49.5	121	2	US-09-698-705-8	Sequence 8, Appl
688	48	51.6	282	2	US-09-985-442-7	Sequence 7, Appl	761	46	49.5	135	1	US-08-621-751A-12	Sequence 12, Appl
689	48	51.6	282	2	US-09-983-580-7	Sequence 7, Appl	762	46	49.5	135	1	US-08-621-751A-16	Sequence 16, Appl
690	48	51.6	287	2	US-09-318-786-37	Sequence 37, Appl	763	46	49.5	140	2	US-09-068-628-28	Sequence 28, Appl
691	48	51.6	449	1	US-08-458-516-13	Sequence 13, Appl	764	46	49.5	141	1	US-08-659-567-4	Sequence 4, Appl
692	47	50.5	16	2	US-09-269-332-63	Sequence 63, Appl	765	46	49.5	222	2	US-09-698-705-13	Sequence 13, Appl
693	47	50.5	17	2	US-10-146-305-13	Sequence 13, Appl	766	46	49.5	242	1	US-08-553-497A-26	Sequence 26, Appl
694	47	50.5	98	2	US-08-881-037-64	Sequence 64, Appl	767	46	49.5	274	2	US-08-813-659-30	Sequence 30, Appl
695	47	50.5	105	1	US-08-793-490-10	Sequence 10, Appl	768	46	49.5	274	2	US-09-549-067A-30	Sequence 30, Appl
696	47	50.5	108	1	US-08-273-146-57	Sequence 57, Appl	769	46	49.5	302	1	US-08-121-054C-30	Sequence 30, Appl
697	47	50.5	108	2	US-09-486-814A-4	Sequence 4, Appl	770	46	49.5	302	2	US-08-539-436-30	Sequence 30, Appl
698	47	50.5	116	1	US-07-634-278-57	Sequence 56, Appl	771	46	49.5	302	2	US-09-813-659-32	Sequence 32, Appl
699	47	50.5	116	1	US-07-634-278-57	Sequence 57, Appl	772	46	49.5	302	2	US-09-549-067A-32	Sequence 32, Appl
700	47	50.5	116	1	US-07-634-278-73	Sequence 73, Appl	773	45	48.4	17	1	US-08-353-400-28	Sequence 28, Appl
701	47	50.5	116	1	US-08-477-728-56	Sequence 56, Appl	774	45	48.4	17	1	US-08-137-117D-144	Sequence 144, App
702	47	50.5	116	1	US-08-477-728-57	Sequence 57, Appl	775	45	48.4	17	1	US-08-436-717-144	Sequence 144, App
703	47	50.5	116	1	US-08-477-728-73	Sequence 73, Appl	776	45	48.4	17	2	US-09-914-695-46	Sequence 46, Appl
704	47	50.5	116	1	US-08-474-040-56	Sequence 56, Appl	777	45	48.4	17	2	US-09-724-409-9	Sequence 9, Appl
705	47	50.5	116	1	US-08-474-040-57	Sequence 57, Appl	778	45	48.4	17	2	US-09-724-530-9	Sequence 9, Appl
706	47	50.5	116	1	US-08-474-040-73	Sequence 73, Appl	779	45	48.4	17	2	US-09-328-286-9	Sequence 9, Appl
707	47	50.5	116	1	US-08-487-200-56	Sequence 56, Appl	780	45	48.4	20	2	US-09-556-605-9	Sequence 9, Appl
708	47	50.5	116	1	US-08-487-200-57	Sequence 57, Appl	781	45	48.4	111	2	US-08-881-037-20	Sequence 20, Appl
709	47	50.5	116	1	US-08-487-200-73	Sequence 73, Appl	782	45	48.4	114	2	US-09-344-587-10	Sequence 10, Appl
710	47	50.5	116	2	US-08-881-037-19	Sequence 19, Appl	783	45	48.4	114	2	US-09-724-409-7	Sequence 7, Appl
711	47	50.5	116	2	US-08-484-537-56	Sequence 56, Appl	784	45	48.4	114	2	US-09-724-530-7	Sequence 7, Appl
712	47	50.5	116	2	US-08-484-537-57	Sequence 57, Appl	785	45	48.4	114	2	US-09-328-286-7	Sequence 7, Appl
713	47	50.5	116	2	US-08-484-537-73	Sequence 73, Appl	786	45	48.4	115	2	US-09-223-280-33	Sequence 33, Appl
714	47	50.5	117	4	PCT-US93-11611-6	Sequence 6, Appl	787	45	48.4	116	1	US-08-561-521-81	Sequence 41, Appl
715	47	50.5	117	4	PCT-US93-11611-7	Sequence 7, Appl	788	45	48.4	116	4	US-08-561-521-41	Sequence 41, Appl
716	47	50.5	119	4	US-08-767-128-10	Sequence 10, Appl	789	45	48.4	117	1	US-08-822-028-2	Sequence 2, Appl
717	47	50.5	120	1	US-08-111-080-25	Sequence 25, Appl	790	45	48.4	117	2	US-08-479-285-2	Sequence 2, Appl
718	47	50.5	120	1	US-08-211-980-25	Sequence 25, Appl	791	45	48.4	117	2	US-08-961-309-45	Sequence 45, Appl
719	47	50.5	120	4	PCT-US93-07967-25	Sequence 25, Appl	792	45	48.4	117	2	US-09-503-653A-2	Sequence 2, Appl
720	47	50.5	122	2	US-08-767-128-4	Sequence 4, Appl	793	45	48.4	119	1	US-08-800-198-2	Sequence 2, Appl
721	47	50.5	122	2	US-10-092-246-10	Sequence 10, Appl	794	45	48.4	119	2	US-09-296-595-2	Sequence 2, Appl
722	47	50.5	122	2	US-10-092-246-11	Sequence 11, Appl	795	45	48.4	120	2	US-10-096-246A-9	Sequence 9, Appl
723	47	50.5	122	2	US-10-096-246A-10	Sequence 10, Appl	796	45	48.4	121	2	US-08-487-761-11	Sequence 11, Appl
724	47	50.5	122	2	US-10-096-246A-11	Sequence 11, Appl	797	45	48.4	122	2	US-09-914-695-42	Sequence 42, Appl
725	47	50.5	127	2	US-09-561-500-7	Sequence 7, Appl	798	45	48.4	123	1	US-08-478-039-82	Sequence 82, Appl
726	47	50.5	127	2	US-09-561-108-7	Sequence 7, Appl	799	45	48.4	123	1	US-08-476-349A-82	Sequence 82, Appl
727	47	50.5	127	2	US-09-561-526-7	Sequence 7, Appl	800	45	48.4	124	2	US-09-257-069-2	Sequence 2, Appl
728	47	50.5	127	2	US-09-561-499-7	Sequence 7, Appl	801	45	48.4	124	2	US-10-007-790-2	Sequence 2, Appl
729	47	50.5	127	2	US-09-998-831-7	Sequence 7, Appl	802	45	48.4	130	2	US-09-556-605-3	Sequence 3, Appl
730	47	50.5	127	2	US-09-561-005-7	Sequence 7, Appl	803	45	48.4	130	1	US-08-822-028-6	Sequence 6, Appl
731	47	50.5	127	2	US-09-562-245-7	Sequence 7, Appl	804	45	48.4	133	1	US-08-822-028-10	Sequence 30, Appl
732	47	50.5	135	1	US-07-634-278-69	Sequence 69, Appl	805	45	48.4	133	2	US-08-718-333A-6	Sequence 6, Appl
733	47	50.5	135	1	US-08-477-728-69	Sequence 69, Appl	806	45	48.4	133	2	US-08-718-333A-8	Sequence 8, Appl
734	47	50.5	135	1	US-08-474-040-69	Sequence 69, Appl	807	45	48.4	133	2	US-08-479-285-6	Sequence 6, Appl
735	47	50.5	135	1	US-08-487-200-69	Sequence 69, Appl	808	45	48.4	133	2	US-08-479-285-10	Sequence 30, Appl
736	47	50.5	135	2	US-08-484-537-69	Sequence 69, Appl	809	45	48.4	133	2	US-09-587-526-6	Sequence 6, Appl
737	47	50.5	136	4	PCT-US93-11611-4	Sequence 4, Appl	810	45	48.4	133	2	US-09-587-526-8	Sequence 8, Appl
738	47	50.5	136	4	PCT-US93-11611-11	Sequence 11, Appl	811	45	48.4	133	2	US-08-961-309-48	Sequence 48, Appl
739	47	50.5	138	2	US-10-146-305-8	Sequence 8, Appl	812	45	48.4	133	2	US-09-503-653A-6	Sequence 6, Appl
740	47	50.5	139	2	US-08-454-899G-15	Sequence 15, Appl	813	45	48.4	133	2	US-09-503-653A-30	Sequence 30, Appl
741	47	50.5	269	1	US-08-428-257A-72	Sequence 72, Appl	814	45	48.4	133	6	US-09-996-17	Parent No. 5219996
742	47	50.5	269	1	US-08-491-988-3	Sequence 3, Appl	815	45	48.4	134	1	US-08-822-028-10	Sequence 10, Appl
743	47	50.5	297	2	US-09-486-814A-2	Sequence 2, Appl	816	45	48.4	134	2	US-08-479-285-10	Sequence 10, Appl
744	47	50.5	355	2	US-08-875-811-57	Sequence 57, Appl	817	45	48.4	134	2	US-08-961-309-49	Sequence 49, Appl
745	47	50.5	402	1	US-08-491-988-9	Sequence 9, Appl	818	45	48.4	134	2	US-09-503-653A-10	Sequence 10, Appl
746	47	50.5	435	1	US-08-491-988-7	Sequence 7, Appl	819	45	48.4	135	1	US-08-137-117D-27	Sequence 27, Appl
747	47	50.5	435	1	US-08-491-988-5	Sequence 5, Appl	820	45	48.4	135	1	US-08-137-117D-100	Sequence 100, App
748	46	49.5	17	2	US-07-987-264-2	Sequence 2, Appl	821	45	48.4	135	1	US-08-137-117D-102	Sequence 102, App
749	46	49.5	84	2	US-08-928-383B-16	Sequence 16, Appl	822	45	48.4	135	1	US-08-137-117D-112	Sequence 112, App
750	46	49.5	113	2	US-08-881-037-18	Sequence 18, Appl	823	45	48.4	135	1	US-08-436-717-27	Sequence 27, Appl
751	46	49.5	116	2	US-09-065-059-9	Sequence 9, Appl	824	45	48.4	135	1	US-08-436-717-102	Sequence 102, App
752	46	49.5	116	2	US-08-913-555-9	Sequence 9, Appl	825	45	48.4	135	1	US-08-436-717-102	Sequence 102, App
753	46	49.5	117	2	US-09-157-370-2	Sequence 2, Appl	826	45	48.4	135	1	US-08-436-717-112	Sequence 112, App
754	46	49.5	117	2	US-08-913-555-27	Sequence 27, Appl	827	45	48.4	139	1	US-08-202-047-3	Sequence 3, Appl
755	46	49.5	118	1	US-08-428-257A-74	Sequence 74, Appl	828	45	48.4	139	1	US-08-202-047-7	Sequence 7, Appl
756	46	49.5	118	1	US-08-428-257A-78	Sequence 78, Appl	829	45	48.4	139	1	US-08-202-047-9	Sequence 9, Appl
757	46	49.5	118	2	US-07-987-264-14	Sequence 14, Appl	830	45	48.4	139	1	US-08-202-047-11	Sequence 11, Appl

831	45	48.4	139	1	US-08-039-198B-10	Sequence 10, Appl	904	43	46.2	118	2	US-09-647-468-144	Sequence 144, App
832	45	48.4	139	2	US-08-964-690-3	Sequence 3, Appl	905	43	46.2	118	2	US-09-232-290-03	Sequence 73, Appl
833	45	48.4	139	2	US-08-964-690-7	Sequence 7, Appl	906	43	46.2	118	2	US-09-905-243-74	Sequence 4, Appl
834	45	48.4	139	2	US-08-964-690-9	Sequence 9, Appl	907	43	46.2	119	2	US-09-438-954-4	Sequence 1, Appl
835	45	48.4	139	2	US-08-964-690-11	Sequence 11, Appl	908	43	46.2	120	2	US-08-913-555-1	Sequence 1, Appl
836	45	48.4	150	1	US-08-400-115-2	Sequence 2, Appl	909	43	46.2	120	2	US-08-913-555-1	Sequence 1, Appl
837	45	48.4	240	1	US-08-800-198-8	Sequence 8, Appl	910	43	46.2	121	2	US-08-913-555-19	Sequence 19, Appl
838	45	48.4	240	1	US-09-296-595-8	Sequence 8, Appl	911	43	46.2	125	2	US-08-665-202-59	Sequence 59, Appl
839	45	48.4	247	2	US-10-620-048-23	Sequence 23, Appl	912	43	46.2	125	2	US-09-315-574-59	Sequence 59, Appl
840	45	48.4	247	2	US-10-620-048-25	Sequence 25, Appl	913	43	46.2	128	2	US-09-199-149-12	Sequence 12, Appl
841	45	48.4	267	2	US-09-419-788-30	Sequence 30, Appl	914	43	46.2	134	2	US-09-270-767-37541	Sequence 37541, A
842	45	48.4	271	1	US-08-400-115-4	Sequence 30, Appl	915	43	46.2	134	2	US-08-646-265A-29	Sequence 29, Appl
843	45	48.4	288	1	US-09-423-439-38	Sequence 38, Appl	916	43	46.2	136	2	US-08-646-265A-99	Sequence 99, Appl
844	45	48.4	302	1	US-08-121-054C-18	Sequence 18, Appl	917	43	46.2	137	2	US-08-647-468-153	Sequence 153, App
845	45	48.4	302	2	US-08-539-435-18	Sequence 18, Appl	918	43	46.2	137	2	US-09-647-468-154	Sequence 154, App
846	45	48.4	302	2	US-09-813-659-18	Sequence 18, Appl	919	43	46.2	137	2	US-09-647-468-157	Sequence 157, App
847	45	48.4	302	2	US-09-549-067A-18	Sequence 18, Appl	920	43	46.2	137	2	US-09-647-468-158	Sequence 158, App
848	45	48.4	445	1	US-08-353-400-33	Sequence 33, Appl	921	43	46.2	139	1	US-08-137-117D-35	Sequence 35, Appl
849	45	48.4	464	1	US-08-353-400-36	Sequence 36, Appl	922	43	46.2	139	1	US-08-436-717-35	Sequence 35, Appl
850	45	48.4	673	2	US-09-423-439-32	Sequence 32, Appl	923	43	46.2	147	1	US-08-579-940-4	Sequence 4, Appl
851	44	47.3	17	2	US-08-836-561-41	Sequence 41, Appl	924	43	46.2	147	1	US-08-838-692-6	Sequence 6, Appl
852	44	47.3	17	2	US-09-434-122-41	Sequence 41, Appl	925	43	46.2	147	1	US-08-553-497A-22	Sequence 22, Appl
853	44	47.3	45	2	US-09-627-218B-4	Sequence 4, Appl	926	43	46.2	244	1	US-08-257-341-7	Sequence 7, Appl
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855	44	47.3	119	2	US-08-767-128-20	Sequence 20, Appl	928	43	46.2	252	1	US-08-461-838-4	Sequence 4, Appl
856	44	47.3	120	2	US-09-513-998C-7802	Sequence 802, Ap	929	43	46.2	252	1	US-08-461-838-4	Sequence 4, Appl
857	44	47.3	124	2	US-09-301-593-8	Sequence 8, Appl	930	43	46.2	260	1	US-08-447-402-1	Sequence 1, Appl
858	44	47.3	124	2	US-09-301-593-10	Sequence 10, Appl	931	43	46.2	269	2	US-09-070-408-132	Sequence 132, App
859	44	47.3	124	2	US-09-301-593-12	Sequence 12, Appl	932	43	46.2	269	2	US-08-646-265A-109	Sequence 109, App
860	44	47.3	124	2	US-09-301-593-14	Sequence 14, Appl	933	43	46.2	269	2	US-08-646-265A-109	Sequence 109, App
861	44	47.3	124	2	US-09-301-593-16	Sequence 16, Appl	934	43	46.2	313	7	US-08-257-341-5	Sequence 5, Appl
862	44	47.3	124	2	US-09-301-593-38	Sequence 38, Appl	935	43	46.2	513	3	US-09-543-681A-4981	Sequence 4981, Ap
863	44	47.3	124	2	US-09-301-593-39	Sequence 39, Appl	936	42	45.2	17	1	US-08-476-176B-51	Sequence 51, Appl
864	44	47.3	124	2	US-09-301-593-41	Sequence 41, Appl	937	42	45.2	17	2	US-08-127-721A-51	Sequence 51, Appl
865	44	47.3	124	2	US-09-301-593-40	Sequence 40, Appl	938	42	45.2	17	2	US-08-485-246A-51	Sequence 51, Appl
866	44	47.3	124	2	US-09-301-593-41	Sequence 41, Appl	939	42	45.2	17	2	US-09-424-840B-73	Sequence 73, Appl
867	44	47.3	137	1	US-09-301-593-108	Sequence 108, App	940	42	45.2	17	2	US-09-424-840B-98	Sequence 98, Appl
868	44	47.3	138	2	US-08-589-939-1	Sequence 18, Appl	941	42	45.2	17	2	US-09-244-592-6	Sequence 6, Appl
869	44	47.3	140	2	US-08-836-561-27	Sequence 27, Appl	942	42	45.2	42	2	US-09-244-592-3	Sequence 3, Appl
870	44	47.3	140	2	US-08-836-561-63	Sequence 63, Appl	943	42	45.2	46	2	US-09-244-592-4	Sequence 4, Appl
871	44	47.3	140	2	US-08-836-561-74	Sequence 74, Appl	944	42	45.2	75	2	US-09-244-592-5	Sequence 5, Appl
872	44	47.3	140	2	US-08-836-561-78	Sequence 78, Appl	945	42	45.2	75	2	US-09-244-592-5	Sequence 5, Appl
873	44	47.3	140	2	US-08-836-561-83	Sequence 83, Appl	946	42	45.2	90	1	US-09-244-592-2	Sequence 2, Appl
874	44	47.3	140	2	US-09-434-122-27	Sequence 27, Appl	947	42	45.2	91	1	US-08-713-939A-71	Sequence 71, Appl
875	44	47.3	140	2	US-09-434-122-63	Sequence 63, Appl	948	42	45.2	91	1	US-08-713-939A-78	Sequence 78, Appl
876	44	47.3	140	2	US-09-434-122-74	Sequence 74, Appl	949	42	45.2	91	1	US-08-713-939A-81	Sequence 81, Appl
877	44	47.3	140	2	US-09-434-122-78	Sequence 78, Appl	950	42	45.2	91	2	US-09-036-579-70	Sequence 70, Appl
878	44	47.3	140	2	US-09-434-122-83	Sequence 83, Appl	951	42	45.2	91	2	US-09-036-579-71	Sequence 71, Appl
879	44	47.3	143	2	US-09-301-593-26	Sequence 26, Appl	952	42	45.2	91	2	US-09-036-579-78	Sequence 78, Appl
880	44	47.3	244	1	US-08-330-843-2	Sequence 2, Appl	953	42	45.2	91	2	US-09-036-579-81	Sequence 81, Appl
881	44	47.3	244	1	US-08-636-936-2	Sequence 2, Appl	954	42	45.2	91	2	US-09-550-374-70	Sequence 70, Appl
882	44	47.3	259	1	US-09-419-788-29	Sequence 29, Appl	955	42	45.2	91	2	US-09-550-374-71	Sequence 71, Appl
883	44	47.3	453	2	US-09-301-593-18	Sequence 18, Appl	956	42	45.2	91	2	US-09-550-374-78	Sequence 78, Appl
884	44	47.3	472	2	US-09-301-593-30	Sequence 30, Appl	957	42	45.2	91	2	US-09-550-374-81	Sequence 81, Appl
885	44	47.3	472	2	US-09-301-593-43	Sequence 43, Appl	958	42	45.2	91	2	US-09-550-374-85	Sequence 85, Appl
886	44	47.3	1060	2	US-09-419-788-19	Sequence 19, Appl	959	42	45.2	91	2	US-09-943-906-70	Sequence 70, Appl
887	44	47.3	1060	2	US-08-672-345C-59	Sequence 59, Appl	960	42	45.2	91	2	US-09-943-906-71	Sequence 71, Appl
888	43	46.2	17	2	US-08-646-265A-116	Sequence 116, App	961	42	45.2	91	2	US-09-943-906-78	Sequence 78, Appl
889	43	46.2	17	2	US-09-214-095D-59	Sequence 59, Appl	962	42	45.2	91	2	US-09-943-906-81	Sequence 81, Appl
890	43	46.2	17	2	US-09-440-727B-59	Sequence 59, Appl	963	42	45.2	91	2	US-10-435-602-70	Sequence 70, Appl
891	43	46.2	98	2	US-10-194-975-11	Sequence 11, Appl	964	42	45.2	91	2	US-10-435-602-71	Sequence 71, Appl
892	43	46.2	110	1	US-08-672-345C-104	Sequence 104, App	965	42	45.2	91	2	US-10-435-602-78	Sequence 78, Appl
893	43	46.2	110	2	US-09-214-095D-94	Sequence 94, Appl	966	42	45.2	91	2	US-10-435-602-81	Sequence 81, Appl
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896	43	46.2	116	1	US-09-214-095D-14	Sequence 14, Appl	969	42	45.2	92	2	US-09-036-579-85	Sequence 85, Appl
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898	43	46.2	117	2	US-08-646-265A-112	Sequence 132, App	971	42	45.2	92	2	US-09-550-374-85	Sequence 85, Appl
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900	43	46.2	118	2	US-09-199-149-5	Sequence 5, Appl	973	42	45.2	92	2	US-09-943-906-85	Sequence 85, Appl
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902	43	46.2	118	2	US-09-647-468-140	Sequence 140, App	975	42	45.2	92	2	US-10-435-602-79	Sequence 79, Appl
903	43	46.2	118	2	US-09-647-468-143	Sequence 143, App	976	42	45.2	92	2	US-10-435-602-85	Sequence 85, Appl

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982 42 45.2 97 1 US-08-290-592E-16 Sequence 16, Appl
983 42 45.2 97 4 PCR-US95-10053-13 Sequence 13, Appl
984 42 45.2 97 4 PCR-US96-09448-16 Sequence 16, Appl
985 42 45.2 98 2 US-10-194-975-5 Sequence 5, Appl
986 42 45.2 98 2 US-10-194-975-7 Sequence 7, Appl
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992 42 45.2 101 1 US-08-713-939A-82 Sequence 82, Appl
993 42 45.2 101 2 US-09-036-579-82 Sequence 82, Appl
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995 42 45.2 101 2 US-09-943-906-82 Sequence 82, Appl
996 42 45.2 101 2 US-10-435-602-82 Sequence 82, Appl
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999 42 45.2 103 2 US-09-550-374-84 Sequence 84, Appl
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ALIGNMENTS

RESULT 1
US-08-974-899-11
; Sequence 11, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-11
Query Match 100.0%; Score 93; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6,1e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MIHPSDSETRYNOFKD 17

RESULT 2
US-09-795-798-11
; Sequence 11, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-795-798-11
Query Match 100.0%; Score 93; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6,1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIHPSDSETRYNOFKD 17
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Db 1 MIHPSDSETRYNOFKD 17
RESULT 3
US-08-974-899-5
; Sequence 5, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-5

Query Match 100.0%; Score 93; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNQKFXD 17
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DB 50 MHPSDSETRYNQKFXD 66

RESULT 4
US-09-795-798-5
Sequence 5, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Prestia, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-795-798-5

Query Match 100.0%; Score 93; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNQKFXD 17
|||||
DB 50 MHPSDSETRYNQKFXD 66

RESULT 5
US-08-767-128-2
Sequence 2, Application US/08767128
Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 611079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-2

Query Match 91.4%; Score 85; DB 2; Length 118;
Best Local Similarity 94.1%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKFKD 17
Db 50 MIHPDSETRYNOKFKD 66

RESULT 6
US-08-767-128-8

Sequence 8, Application US/08767128
Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYLLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: COBBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 611079 West Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

ORIGINAL SOURCE:
US-08-767-128-8

Query Match 91.4%; Score 85; DB 2; Length 118;
Best Local Similarity 94.1%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKFKD 17
Db 50 MIHPDSETRYNOKFKD 66

RESULT 7

US-08-974-899-4
Sequence 4, Application US/08974899
Patent No. 6037454

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpactin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-4

Query Match 91.4%; Score 85; DB 2; Length 121;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKFKD 17
Db 50 MIHPDSETRYNOKFKD 66

RESULT 8
US-09-795-798-4
Sequence 4, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

```

; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 4:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-795-798-4
;
Query Match          91.4%; Score 85; DB 2; Length 121;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOKEFD 17
DB 50 MHPSDSETRYNOKEFD 66

RESULT 9
US-09-948-004-33
; Sequence 33, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Mathias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-948-004-33

Query Match          86.0%; Score 80; DB 2; Length 19;
Best Local Similarity 88.2%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOKEFD 17
DB 2 MHPSDSETRYNOKEFD 18

RESULT 10
```

```

US-09-948-004-16
; Sequence 16, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Mathias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-16

Query Match          86.0%; Score 80; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 7.6e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOKEFD 17
DB 60 MHPSDSETRYNOKEFD 76

RESULT 11
US-09-948-004-14
; Sequence 14, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Mathias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-14

Query Match          86.0%; Score 80; DB 2; Length 138;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOKEFD 17
DB 69 MHPSDSETRYNOKEFD 85

RESULT 12
US-09-948-004-18
; Sequence 18, Application US/09948004
; Patent No. 6723538
; GENERAL INFORMATION:
; APPLICANT: MACK, Mathias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-18
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Query Match 86.0%; Score 80; DB 2; Length 495;
Best Local Similarity 88.2%; Pred. 3.8e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIHPSDSETRYNOXKFD 17
|||||
Db 172 MIHPSDSETRYNOXKFD 188

RESULT 13
US-08-767-128-6
; Sequence 6, Application US/08767128
; Patent No. 6111079

GENERAL INFORMATION:

APPLICANT: WILIE, DWANE E.

APPLICANT: LOPEZ, OSVALDO

APPLICANT: MURRAY, PETER JOSEPH

APPLICANT: GOEBEL, PETER

TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND

TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt

STREET: 3100 No. 6111079west Center, 90 South Seventh St

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Pasteo Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/767.128

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 424

FILING DATE: 04-DEC-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/09258

FILING DATE: 05-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/541.373

FILING DATE: 10-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/462.798

FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Carter, Charles G.

REGISTRATION NUMBER: 35,093

REFERENCE/DOCKET NUMBER: 8648.49USP1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/371-5278

TELEFAX: 612/332-9081

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

US-08-767-128-6

Query Match 79.6%; Score 74; DB 2; Length 119;

Best Local Similarity 87.5%; Pred. No. 7.7e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOXKFD 17
|||||
Db 51 IHPSDSETRYNOXKFD 66

RESULT 14
US-08-235-838-11
; Sequence 11, Application US/08235838
; Patent No. 5571894

GENERAL INFORMATION:

APPLICANT: Wels, Winfried S.

APPLICANT: Hynes, Nancy B.

APPLICANT: Harwerth, Ina-Maria

APPLICANT: Groner, Bernd

APPLICANT: Hardman, No. 5571894man

APPLICANT: Zwickl, Markus

TITLE OF INVENTION: Recombinant Antibodies Specific for a

TITLE OF INVENTION: Growth Factor Receptor

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/235.838

FILING DATE: TBA

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/828, 832

FILING DATE: 31-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 91-810079.3

FILING DATE: 05-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: Rlmet, James Scott

REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8614

TELEFAX: (919)541-8689

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-235-838-11

Query Match 79.6%; Score 74; DB 1; Length 241;
Best Local Similarity 82.4%; Pred. No. 0.00017;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIHPSDSETRYNOXKFD 17
|||||
Db 51 MIHPSDSETRYNOXKFD 67

RESULT 15
US-08-465-473B-11
; Sequence 11, Application US/08465473B
; Patent No. 5939531

GENERAL INFORMATION:

APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Heena J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-473B-11

Query Match 79.6%; Score 74; DB 1; Length 241;
Best Local Similarity 82.4%; Pred. No. 0.00017;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHPDSETRYNQKFPD 17
DB 51 MIDPDSERYNQMFDP 67

RESULT 16
US-08-235-838-16
Sequence 16, Application US/08235838
Patent No. 5571894
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5571894man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne

STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,838
FILING DATE: TBA
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-235-838-16

Query Match 79.6%; Score 74; DB 1; Length 637;
Best Local Similarity 82.4%; Pred. No. 0.0005;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHPDSETRYNQKFPD 17
DB 82 MIDPDSERYNQMFDP 98

RESULT 17
US-08-465-473B-16
Sequence 16, Application US/08465473B
Patent No. 5939531
GENERAL INFORMATION:
APPLICANT: Wels, Winfried S.
APPLICANT: Hynes, Nancy E.
APPLICANT: Harwerth, Ina-Maria
APPLICANT: Groner, Bernd
APPLICANT: Hardman, No. 5939531man
APPLICANT: Zwickl, Markus
TITLE OF INVENTION: Recombinant Antibodies Specific for a
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: NOVARTIS Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901-6940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,473B
FILING DATE: 5 June 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/828,832
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 91-810079.3
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pfeiffer, Hessa J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)522 6940
TELEFAX: (908)522 6955
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-473B-16

Query Match 79.6%; Score 74; DB 1; Length 637;
Best Local Similarity 82.4%; Pred. No. 0.0005; 2; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKEKD 17
Db 82 MIDPDSETRYNOKEKD 98

RESULT 18
US-08-974-899-23
Sequence 23, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-23

Query Match 74.2%; Score 69; DB 2; Length 17;
Best Local Similarity 76.5%; Pred. No. 6e-05; 3; Indels 0; Gaps 0;

Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKEKD 17
Db 1 MIAPASSTRYNOKEKD 17

RESULT 19
US-09-795-798-23
Sequence 23, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-795-798-23

Query Match 74.2%; Score 69; DB 2; Length 17;
Best Local Similarity 76.5%; Pred. No. 6e-05; 3; Indels 0; Gaps 0;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKEKD 17
Db 1 MIAPASSTRYNOKEKD 17

RESULT 20
US-09-698-705-9
Sequence 9, Application US/09698705
Patent No. 6824780
GENERAL INFORMATION:
APPLICANT: Devaux, B.
APPLICANT: Keller, G.
APPLICANT: Koepfen, H.
APPLICANT: Laesky, L.
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
FILE REFERENCE: P1777R1
CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/162,558

PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/182,872
PRIOR FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 25
SEQ ID NO: 9
LENGTH: 118
TYPE: PRT
ORGANISM: Mus musculus
US-09-698-705-9

Query Match 74.2%; Score 69; DB 2; Length 118;
Best Local Similarity 81.2%; Pred. No. 0.00052;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 MHPSDESTRYNOKFXD 17
DB 45 IDPSDESTRYNOKFXD 60

RESULT 21
US-08-974-899-24
Sequence 24, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-24

Query Match 74.2%; Score 69; DB 2; Length 121;
Best Local Similarity 76.5%; Pred. No. 0.00054;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHPSDESTRYNOKFXD 17
DB 50 MIPASSSTRYNOKFXD 66

RESULT 22
US-09-795-798-24
Sequence 24, Application US/09795798

Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-795-798-24

Query Match 74.2%; Score 69; DB 2; Length 121;
Best Local Similarity 76.5%; Pred. No. 0.00054;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHPSDESTRYNOKFXD 17
DB 50 MIPASSSTRYNOKFXD 66

RESULT 23
US-09-091-071-7
Sequence 7, Application US/09091071
Patent No. 6610500
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: DESIGN OF HORMONE-LIKE ANTIBODIES WITH
TITLE OF INVENTION: AGONISTIC AND ANTAGONISTIC FUNCTIONS
NUMBER OF SEQUENCES: 9
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,071
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA96/00815
FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525180.7
FILING DATE: 08-DEC-1995
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-071-7

Query Match 67.7%; Score 63; DB 2; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0006;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IHPDSETRYNQKFK 16
Db 2 IYPGSDSTSYNQKFK 16

RESULT 24
US-08-553-497A-4
Sequence 4, Application US/08553497A

Patent No. 5844093
GENERAL INFORMATION:

APPLICANT: KETTERBOROUGH, C. A.

APPLICANT: BENDIG, MARY M.

APPLICANT: ANSELL, KEITH H.

APPLICANT: GUSSEW, DETLEF

APPLICANT: ADAM, JAUME

APPLICANT: MTTJANS, FRANCES

APPLICANT: ROSELL, ELISABET

APPLICANT: BLASCO, FRANCESC

APPLICANT: PUJANTS, JAUME

APPLICANT: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR

TITLE OF INVENTION: ANTIBODIES

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P.C.

STREET: 2200 CLARENDON BLVD. SUITE 1400

CITY: ARLINGTON

STATE: VA

COUNTRY: US

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,497A

FILING DATE: 17-NOV-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP95/00978

FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94104160.0

FILING DATE: 17-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94118970.6

FILING DATE: 02-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1726

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-553-497A-4

Query Match 67.7%; Score 63; DB 1; Length 119;
Best Local Similarity 70.6%; Pred. No. 0.0052;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHPDSETRYNQKFKD 17
Db 50 MIDPSNSETRLNQNFRD 66

RESULT 25
US-09-091-071-2
Sequence 2, Application US/09091071

Patent No. 6610500
GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: DESIGN OF HORMONE-LIKE ANTIBODIES WITH

NUMBER OF SEQUENCES: 9

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,071

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/CA96/00815

FILING DATE: 06-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9525180.7

FILING DATE: 08-DEC-1995

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-091-071-2

Query Match 67.7%; Score 63; DB 2; Length 120;
Best Local Similarity 73.3%; Pred. No. 0.0053;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IHPDSETRYNQKFK 16
Db 50 IYPGSDSTSYNQKFK 64

RESULT 26
US-09-698-705-6
Sequence 6, Application US/09698705

Patent No. 6824780
GENERAL INFORMATION:

APPLICANT: Devaux, B.

APPLICANT: Keller, G.

APPLICANT: Koepfen, H.

APPLICANT: Laskey, L.

TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use

FILE REFERENCE: P1777R1

CURRENT APPLICATION NUMBER: US/09/698,705

CURRENT FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/162,558

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60/182,872

PRIOR FILING DATE: 2000-02-16

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 6

LENGTH: 124

TYPE: PRT

ORGANISM: Mus musculus

US-09-698-705-6

Query Match 67.7%; Score 63; DB 2; Length 124;
Best Local Similarity 75.0%; Pred. No. 0.0055;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IHPSDETRYNQKFKD 17
| | | | | : | | | | |
Db 51 IDPSDSEIHVDQKFKD 66

RESULT 27

US-09-698-705-11
Sequence 11, Application US/09698705
Patent No. 6824780

GENERAL INFORMATION:
APPLICANT: Devaux, B.
APPLICANT: Keller, G.
APPLICANT: Koepfen, H.

APPLICANT: Lasky, L.
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
FILE REFERENCE: P1777R1
CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/162,558
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/182,872
PRIOR FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 11

LENGTH: 466

TYPE: PRT

ORGANISM: Artificial sequence
FEATURE:

OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-11

Query Match 67.7%; Score 63; DB 2; Length 466;
Best Local Similarity 75.0%; Pred. No. 0.024;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 IHPSDETRYNQKFKD 17
| | | | | : | | | | |
Db 70 IDPSDSEIHVDQKFKD 85

RESULT 28

US-09-027-449-50
Sequence 50, Application US/09027449
Patent No. 6025158

GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

Query Match 66.7%; Score 62; DB 2; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.0075;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 MIHPSDSETRYNQKFK 16
| | | | | : | | | | |
Db 50 MIHPSDSETRYNQKFK 65

RESULT 29

US-08-804-444A-50
Sequence 50, Application US/0880444A
Patent No. 6117980

GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.

TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

Query Match 66.7%; Score 62; DB 2; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.0075;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOQKFK 16
| | | | | | | | | |
Db 50 MIHPDSETRYADSVK 65

RESULT 30
US-09-026-985-50
; Sequence 50, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-50

Query Match 66.7%; Score 62; DB 2; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.0075;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOQKFK 16
| | | | | | | | | |
Db 50 MIHPDSETRYADSVK 65

RESULT 31
US-09-121-952A-50
; Sequence 50, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., HseI, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 60/074330
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-50

Query Match 66.7%; Score 62; DB 2; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.0075;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOQKFK 16
| | | | | | | | | |
Db 50 MIHPDSETRYADSVK 65

RESULT 32
US-09-234-340A-50
; Sequence 50, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., HseI, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952

FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-50

Query Match 66.7%; Score 62; DB 2; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.0075;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOXFK 16
| | | | | | | | | | | | | | | | | | | | | |
DB 50 MHPSDSETRYADSVK 65

RESULT 33
US-09-355-014-50
Sequence 50, Application US/09355014
Patent No. 6870033
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
Koumenis, Iphigenia
Leong, Steven R.
Presta, Leonard G.
Shatrokh, Zahra
Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
FILING DATE: 21-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-355-014-50

Query Match 66.7%; Score 62; DB 2; Length 116;
Best Local Similarity 75.0%; Pred. No. 0.0075;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOXFK 16
| | | | | | | | | | | | | | | | | | | | | |
DB 50 MHPSDSETRYADSVK 65

RESULT 34
US-08-553-497A-8
Sequence 8, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSLOW, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESSE
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANTIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-553-497A-8

Query Match 65.6%; Score 61; DB 1; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 MHPSDSETRYNOXFK 16
| | | | | | | | | | | | | | | | | | | | | |

Db 51 IDPSDSTYNNOKFK 65

RESULT 35
US-08-553-497A-12

; Sequence 12, Application US/08553497A
; Patent No. 5844093

; GENERAL INFORMATION:

; APPLICANT: KETTLEBOROUGH, C. A.

; APPLICANT: BENDIG, MARY M.

; APPLICANT: ANSELL, KEITH H.

; APPLICANT: GUSOW, DETLEF

; APPLICANT: ADAN, JAUME

; APPLICANT: MTTJANS, FRANSISC

; APPLICANT: ROSELL, ELISABET

; APPLICANT: BLASCO, FRANCESC

; APPLICANT: PIJUNTS, JAUME

; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR

; TITLE OF INVENTION: ANTIBODIES

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.

; STREET: 2200 CLARENDON BLVD. SUITE 1400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: US

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 17-NOV-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/EP95/00978

; FILING DATE: 16-MAR-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 94104160.0

; FILING DATE: 17-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 94118970.6

; FILING DATE: 02-DEC-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: HAMLET-KING, DIANA

; REGISTRATION NUMBER: 33,302

; REFERENCE/DOCKET NUMBER: MERCK 1726

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-243-6333

; TELEFAX: 703-243-6410

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 119 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-553-497A-12

Query Match 65.6%; Score 61; DB 1; Length 119;

Best Local Similarity 80.0%; Pred. No. 0.011;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IHPSDSETRYNNOKFK 16

Db 51 IDPSDSTYNNOKFK 65

RESULT 36

; Sequence 2, Application US/08952235

; Patent No. 6207152

; GENERAL INFORMATION:

; APPLICANT: Schwall, Ralph H.

; APPLICANT: Tabot, Kelly H.

; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor

; TITLE OF INVENTION: Antagonists and Uses Thereof

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/952,235

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/460368

; FILING DATE: 02-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Marschang, Diane L.

; REGISTRATION NUMBER: 35,600

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5416

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 230 amino acids

; TYPE: Amino Acid

; TOPOLOGY: linear

; US-08-952-235-2

Query Match 65.6%; Score 61; DB 2; Length 230;

Best Local Similarity 64.7%; Pred. No. 0.023; Mismatches 3; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHPSDSETRYNNOKFKD 17

Db 50 MIDPSNDTRFNPXKD 66

RESULT 37
US-09-669-971-2

; Sequence 2, Application US/09669971
; Patent No. 6468529

; GENERAL INFORMATION:

; APPLICANT: Schwall, Ralph H.

; APPLICANT: Tabot, Kelly H.

; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor

; TITLE OF INVENTION: Antagonists and Uses Thereof

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/669,971

; FILING DATE: 05-Jul-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/460368
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-669-971-2

Query Match 65.6%; Score 61; DB 2; Length 230;
Best Local Similarity 64.7%; Pred. No. 0.023;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IHPDSETRYNOKPKD 17
Db 50 MIDPSNSTRFNPNEFD 66

RESULT 38
US-08-482-228-40
Sequence 40, Application US/08482228
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy L.
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESS: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-482-228-40

Query Match 63.4%; Score 59; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 0.0028;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IHPDSETRYNOKPK 16
Db 2 IYFGDGTTRYOKFK 16

RESULT 39
US-08-482-528-40
Sequence 40, Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy L.
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESS: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,528
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-482-528-40

Query Match 63.4%; Score 59; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 0.0028;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IHPDSETRYNOKPK 16
Db 2 IYFGDGTTRYOKFK 16

RESULT 40
US-08-881-037-59
Sequence 59, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Gluck, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Koneki, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-59

Query Match 63.4%; Score 59; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 0.019;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IHPSDSTRYNOXKF 16
Db 51 IDPSDSTYTYNOXKF 65

RESULT 41
US-08-881-037-14
Sequence 14, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Gluck, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540

FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Koneki, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-14

Query Match 63.4%; Score 59; DB 2; Length 111;
Best Local Similarity 80.0%; Pred. No. 0.022;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IHPSDSTRYNOXKF 16
Db 43 IDPSDSTYTYNOXKF 57

RESULT 42
US-08-881-037-16
Sequence 16, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Gluck, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Koneki, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-16

Query Match 63.4%; Score 59; DB 2; Length 111;

Best Local Similarity 80.0%; Pred. No. 0.022;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOKFK 16
| | | | | | | | | | | | | | | | | |
Db 43 IDPSDSYTYNOKFK 57

RESULT 43

US-08-881-037-17
; Sequence 17, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Gluck, Gary D.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konaki, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; INDEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-17

Query Match 63.4%; Score 59; DB 2; Length 111;
Best Local Similarity 80.0%; Pred. No. 0.022;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOKFK 16
| | | | | | | | | | | | | | | | | |
Db 43 IDPSDSYTYNOKFK 57

RESULT 44

US-09-450-520A-9
; Sequence 9, Application US/09450520A
; Patent No. 6329511
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Queen, Cary L.
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon

; FILE REFERENCE: 011823-008110US
; CURRENT APPLICATION NUMBER: US/09/450,520A
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 60/110,523
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
; US-09-450-520A-9

Query Match 63.4%; Score 59; DB 2; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOKFKD 17
| | | | | | | | | | | | | | | | | |
Db 51 IDPSDGEVHYNODFKD 66

RESULT 45

US-09-450-520A-10
; Sequence 10, Application US/09450520A
; Patent No. 6329511
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Queen, Cary L.
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
; FILE REFERENCE: 011823-008110US
; CURRENT APPLICATION NUMBER: US/09/450,520A
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 60/110,523
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:humanized
; US-09-450-520A-10

Query Match 63.4%; Score 59; DB 2; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IHPSDSETRYNOKFKD 17
| | | | | | | | | | | | | | | | | |
Db 51 IDPSDGEVHYNODFKD 66

RESULT 46

US-09-450-520A-11
; Sequence 11, Application US/09450520A
; Patent No. 6329511
; GENERAL INFORMATION:
; APPLICANT: Vasquez, Maximiliano
; APPLICANT: Landolfi, Nicholas F.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Queen, Cary L.
; APPLICANT: Protein Design Labs, Inc.
; TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
; FILE REFERENCE: 011823-008110US

```
/ CURRENT APPLICATION NUMBER: US/09/450,520A
/ CURRENT FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: 60/110,523
/ PRIOR FILING DATE: 1998-12-01
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:humanized
/ OTHER INFORMATION: Immunoglobulin haf25
US-09-450-520A-11

Query Match          63.4%; Score 59; DB 2; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      2 IHPSDETRYNQKFKD 17
        |||||
Db      51 IDPSSGTYNNQKFKD 66

RESULT 47
US-09-726-219A-214
/ Sequence 214, Application US/09726219A
/ Patent No. 6806079
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 213839-00013
/ CURRENT APPLICATION NUMBER: US/09/726,219A
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patentln version 3.1
/ SEQ ID NO 214
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
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/ OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-214

Query Match          63.4%; Score 59; DB 2; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.023;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy      2 IHPSDETRYNQKFKD 17
        |||||
Db      51 INPSSGTYNNQKFKD 66

RESULT 48
US-09-726-219A-223
/ Sequence 223, Application US/09726219A
/ Patent No. 6806079
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 213839-00013
/ CURRENT APPLICATION NUMBER: US/09/726,219A
/ CURRENT FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patentln version 3.1
/ SEQ ID NO 223
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-223

Query Match          63.4%; Score 59; DB 2; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.023;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy      2 IHPSDETRYNQKFKD 17
        |||||
Db      51 INPSSGTYNNQKFKD 66
```

```
RESULT 49
US-09-726-219A-227
; Sequence 227, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-227

Query Match      63.4%; Score 59; DB 2; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.023;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPSDETRYNOFKD 17
       1:| | | | | | | |
       51 INPSSGYTYNOFKD 66

RESULT 50
US-09-726-219A-231
; Sequence 231, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
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; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
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; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 231
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-231

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	93	100.0	121	3	US-09-795-798-5 Sequence 5, Appl
4	93	100.0	121	4	US-10-727-737-5 Sequence 5, Appl
5	93	100.0	121	5	US-10-877-532-6 Sequence 6, Appl
6	93	100.0	451	4	US-10-823-299-4 Sequence 4, Appl
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173	58	62.4	116	4	US-10-127-890-169	Sequence 169, App	246	57	61.3	113	4	US-10-307-276B-3	Sequence 3, Appl1

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248	57	61.3	113	4	US-10-307-276B-7	Sequence 7, Appl1	321	57	61.3	139	3	US-09-509-098-20	Sequence 20, Appl1
249	57	61.3	113	4	US-10-307-276B-8	Sequence 8, Appl1	322	57	61.3	139	3	US-09-509-098-22	Sequence 22, Appl1
250	57	61.3	113	4	US-10-307-276B-9	Sequence 9, Appl1	323	57	61.3	139	3	US-09-509-098-24	Sequence 24, Appl1
251	57	61.3	113	4	US-10-307-276B-10	Sequence 10, Appl1	324	57	61.3	139	3	US-09-509-098-26	Sequence 26, Appl1
252	57	61.3	113	4	US-10-307-276B-11	Sequence 11, Appl1	325	57	61.3	139	3	US-09-509-098-28	Sequence 28, Appl1
253	57	61.3	113	6	US-11-061-956-3	Sequence 3, Appl1	326	57	61.3	139	3	US-09-509-098-30	Sequence 30, Appl1
254	57	61.3	113	6	US-11-061-956-5	Sequence 5, Appl1	327	57	61.3	139	3	US-09-509-098-32	Sequence 32, Appl1
255	57	61.3	113	6	US-11-061-956-7	Sequence 7, Appl1	328	57	61.3	139	3	US-09-509-098-34	Sequence 34, Appl1
256	57	61.3	113	6	US-11-061-956-8	Sequence 8, Appl1	329	57	61.3	139	3	US-09-509-098-36	Sequence 36, Appl1
257	57	61.3	113	6	US-11-061-956-9	Sequence 9, Appl1	330	57	61.3	139	3	US-09-509-098-38	Sequence 38, Appl1
258	57	61.3	113	6	US-11-061-956-9	Sequence 10, Appl1	331	57	61.3	139	3	US-09-509-098-40	Sequence 40, Appl1
259	57	61.3	113	6	US-11-061-956-10	Sequence 11, Appl1	332	57	61.3	139	3	US-09-509-098-42	Sequence 42, Appl1
260	57	61.3	115	3	US-09-940-727B-16	Sequence 16, Appl1	333	57	61.3	139	3	US-09-509-098-44	Sequence 44, Appl1
261	57	61.3	119	3	US-09-795-515-11	Sequence 11, Appl1	334	57	61.3	139	3	US-09-509-098-46	Sequence 46, Appl1
262	57	61.3	119	3	US-09-795-515-30	Sequence 30, Appl1	335	57	61.3	139	3	US-09-509-098-48	Sequence 48, Appl1
263	57	61.3	119	4	US-10-267-286A-10	Sequence 10, Appl1	336	57	61.3	139	3	US-09-509-098-50	Sequence 50, Appl1
264	57	61.3	119	4	US-10-267-286A-12	Sequence 12, Appl1	337	57	61.3	139	3	US-09-509-098-52	Sequence 52, Appl1
265	57	61.3	119	4	US-10-267-286A-13	Sequence 13, Appl1	338	57	61.3	139	3	US-09-509-098-54	Sequence 54, Appl1
266	57	61.3	119	4	US-10-267-286A-14	Sequence 14, Appl1	339	57	61.3	139	4	US-10-315-125-8	Sequence 8, Appl1
267	57	61.3	119	4	US-10-704-352-11	Sequence 11, Appl1	340	57	61.3	139	4	US-10-218-253-105	Sequence 105, Appl1
268	57	61.3	119	4	US-10-704-352-30	Sequence 30, Appl1	341	57	61.3	139	4	US-10-218-253-108	Sequence 108, Appl1
269	57	61.3	119	4	US-10-704-071-11	Sequence 11, Appl1	342	57	61.3	139	4	US-10-218-253-109	Sequence 109, Appl1
270	57	61.3	119	4	US-10-704-071-30	Sequence 30, Appl1	343	57	61.3	139	4	US-10-218-253-110	Sequence 110, Appl1
271	57	61.3	119	4	US-10-682-845-42	Sequence 42, Appl1	344	57	61.3	139	4	US-10-218-253-111	Sequence 111, Appl1
272	57	61.3	119	4	US-10-703-963-11	Sequence 11, Appl1	345	57	61.3	139	4	US-10-218-253-112	Sequence 112, Appl1
273	57	61.3	119	4	US-10-703-963-30	Sequence 30, Appl1	346	57	61.3	139	4	US-10-218-253-113	Sequence 113, Appl1
274	57	61.3	119	5	US-10-937-971-11	Sequence 11, Appl1	347	57	61.3	139	4	US-10-218-253-114	Sequence 114, Appl1
275	57	61.3	119	5	US-10-937-971-30	Sequence 30, Appl1	348	57	61.3	139	4	US-10-218-253-115	Sequence 115, Appl1
276	57	61.3	119	5	US-10-937-949-11	Sequence 11, Appl1	349	57	61.3	139	4	US-10-218-253-116	Sequence 116, Appl1
277	57	61.3	119	5	US-10-937-949-30	Sequence 30, Appl1	350	57	61.3	139	4	US-10-218-253-117	Sequence 117, Appl1
278	57	61.3	119	5	US-10-966-406-62	Sequence 62, Appl1	351	57	61.3	139	4	US-10-218-253-118	Sequence 118, Appl1
279	57	61.3	119	5	US-10-966-406-70	Sequence 70, Appl1	352	57	61.3	139	4	US-10-218-253-119	Sequence 119, Appl1
280	57	61.3	119	5	US-10-703-344-11	Sequence 11, Appl1	353	57	61.3	139	4	US-10-218-253-120	Sequence 120, Appl1
281	57	61.3	119	5	US-10-703-344-30	Sequence 30, Appl1	354	57	61.3	139	4	US-10-218-253-121	Sequence 121, Appl1
282	57	61.3	120	3	US-09-509-098-198	Sequence 198, Appl1	355	57	61.3	139	4	US-10-218-253-122	Sequence 122, Appl1
283	57	61.3	120	3	US-09-509-098-201	Sequence 201, Appl1	356	57	61.3	139	4	US-10-218-253-123	Sequence 123, Appl1
284	57	61.3	120	3	US-09-509-098-202	Sequence 202, Appl1	357	57	61.3	139	4	US-10-218-253-124	Sequence 124, Appl1
285	57	61.3	121	3	US-09-948-004-26	Sequence 26, Appl1	358	57	61.3	139	4	US-10-218-253-125	Sequence 125, Appl1
286	57	61.3	121	4	US-10-682-845-57	Sequence 57, Appl1	359	57	61.3	139	4	US-10-218-253-126	Sequence 126, Appl1
287	57	61.3	121	5	US-10-672-932-26	Sequence 26, Appl1	360	57	61.3	139	4	US-10-218-253-127	Sequence 127, Appl1
288	57	61.3	122	5	US-10-895-135-55	Sequence 55, Appl1	361	57	61.3	139	4	US-10-218-253-128	Sequence 128, Appl1
289	57	61.3	138	2	US-08-779-784-31	Sequence 31, Appl1	362	57	61.3	139	4	US-10-428-085-7	Sequence 7, Appl1
290	57	61.3	138	4	US-10-010-729-67	Sequence 67, Appl1	363	57	61.3	139	4	US-10-428-085-8	Sequence 8, Appl1
291	57	61.3	138	4	US-10-682-845-40	Sequence 40, Appl1	364	57	61.3	139	4	US-10-474-714-6	Sequence 6, Appl1
292	57	61.3	139	3	US-09-760-723-7	Sequence 7, Appl1	365	57	61.3	139	4	US-10-966-406-2	Sequence 2, Appl1
293	57	61.3	139	3	US-09-760-723-8	Sequence 8, Appl1	366	57	61.3	243	5	US-10-966-406-41	Sequence 41, Appl1
294	57	61.3	139	3	US-09-355-925-7	Sequence 7, Appl1	367	57	61.3	243	5	US-10-966-406-43	Sequence 43, Appl1
295	57	61.3	139	3	US-09-355-925-8	Sequence 8, Appl1	368	57	61.3	243	5	US-10-966-406-45	Sequence 45, Appl1
296	57	61.3	139	3	US-09-269-921-105	Sequence 105, Appl1	369	57	61.3	243	5	US-10-247-488-2	Sequence 2, Appl1
297	57	61.3	139	3	US-09-269-921-108	Sequence 108, Appl1	370	57	61.3	256	4	US-10-247-488-4	Sequence 4, Appl1
298	57	61.3	139	3	US-09-269-921-109	Sequence 109, Appl1	371	57	61.3	258	4	US-10-743-697-1	Sequence 1, Appl1
299	57	61.3	139	3	US-09-269-921-110	Sequence 110, Appl1	372	57	61.3	378	5	US-10-362-591-2	Sequence 2, Appl1
300	57	61.3	139	3	US-09-269-921-111	Sequence 111, Appl1	373	57	61.3	409	3	US-09-795-515-7	Sequence 7, Appl1
301	57	61.3	139	3	US-09-269-921-112	Sequence 112, Appl1	374	57	61.3	468	3	US-10-704-352-7	Sequence 7, Appl1
302	57	61.3	139	3	US-09-269-921-113	Sequence 113, Appl1	375	57	61.3	468	4	US-10-704-071-7	Sequence 7, Appl1
303	57	61.3	139	3	US-09-269-921-114	Sequence 114, Appl1	376	57	61.3	468	4	US-10-682-845-38	Sequence 38, Appl1
304	57	61.3	139	3	US-09-269-921-115	Sequence 115, Appl1	377	57	61.3	468	4	US-10-703-963-7	Sequence 7, Appl1
305	57	61.3	139	3	US-09-269-921-116	Sequence 116, Appl1	378	57	61.3	468	4	US-10-682-845-61	Sequence 61, Appl1
306	57	61.3	139	3	US-09-269-921-117	Sequence 117, Appl1	379	57	61.3	468	5	US-10-682-845-63	Sequence 63, Appl1
307	57	61.3	139	3	US-09-269-921-118	Sequence 118, Appl1	380	57	61.3	468	5	US-10-937-949-7	Sequence 7, Appl1
308	57	61.3	139	3	US-09-269-921-119	Sequence 119, Appl1	381	57	61.3	468	5	US-10-937-949-7	Sequence 7, Appl1
309	57	61.3	139	3	US-09-269-921-120	Sequence 120, Appl1	382	57	61.3	468	5	US-10-703-344-7	Sequence 7, Appl1
310	57	61.3	139	3	US-09-269-921-121	Sequence 121, Appl1	383	57	61.3	492	4	US-10-682-845-59	Sequence 59, Appl1
311	57	61.3	139	3	US-09-269-921-122	Sequence 122, Appl1	384	57	61.3	492	4	US-10-682-845-61	Sequence 61, Appl1
312	57	61.3	139	3	US-09-269-921-123	Sequence 123, Appl1	385	57	61.3	492	4	US-10-682-845-65	Sequence 65, Appl1
313	57	61.3	139	3	US-09-269-921-124	Sequence 124, Appl1	386	57	61.3	492	4	US-10-682-845-67	Sequence 67, Appl1
314	57	61.3	139	3	US-09-269-921-125	Sequence 125, Appl1	387	57	61.3	492	4	US-10-682-845-69	Sequence 69, Appl1
315	57	61.3	139	3	US-09-269-921-126	Sequence 126, Appl1	388	57	61.3	492	4	US-10-682-845-71	Sequence 71, Appl1
316	57	61.3	139	3	US-09-269-921-127	Sequence 127, Appl1	389	57	61.3	492	4	US-10-682-845-73	Sequence 73, Appl1
317	57	61.3	139	3	US-09-269-921-128	Sequence 128, Appl1	390	57	61.3	492	4	US-10-682-845-75	Sequence 75, Appl1
318	57	61.3	139	3	US-09-509-098-4	Sequence 4, Appl1	391	57	61.3	492	4	US-10-682-845-77	Sequence 77, Appl1
319	57	61.3	139	3	US-09-509-098-16	Sequence 16, Appl1	392	57	61.3	492	4	US-10-682-845-77	Sequence 77, Appl1

393	57	61.3	492	4	US-10-682-845-79	Sequence 79, Appl
394	57	61.3	492	4	US-10-682-845-81	Sequence 81, Appl
395	57	61.3	492	4	US-10-682-845-83	Sequence 83, Appl
396	57	61.3	492	4	US-10-682-845-85	Sequence 85, Appl
397	57	61.3	492	4	US-10-682-845-87	Sequence 87, Appl
398	57	61.3	499	5	US-10-805-177-111	Sequence 111, App
399	57	61.3	500	4	US-10-168-809-22	Sequence 22, Appl
400	57	61.3	524	5	US-10-805-177-113	Sequence 113, App
401	56	60.2	120	5	US-10-729-441-74	Sequence 74, Appl
402	56	60.2	120	5	US-10-897-406-74	Sequence 74, Appl
403	56	60.2	246	4	US-10-251-215-53	Sequence 53, Appl
404	55	59.1	114	4	US-10-803-622-234	Sequence 234, App
405	55	59.1	114	4	US-10-803-653-234	Sequence 234, App
406	55	59.1	116	4	US-10-803-622-217	Sequence 217, App
407	55	59.1	116	4	US-10-803-653-217	Sequence 217, App
408	55	59.1	118	4	US-10-460-595-8	Sequence 8, Appl
409	55	59.1	123	5	US-10-745-890-1	Sequence 1, Appl
410	55	59.1	243	4	US-10-334-235-37	Sequence 37, Appl
411	55	59.1	249	3	US-09-984-186-18	Sequence 18, Appl
412	55	59.1	249	4	US-10-237-667-18	Sequence 18, Appl
413	55	59.1	249	4	US-10-237-708-18	Sequence 18, Appl
414	55	59.1	249	4	US-10-237-866-18	Sequence 18, Appl
415	55	59.1	249	4	US-10-237-871-18	Sequence 18, Appl
416	55	59.1	249	4	US-10-237-624-18	Sequence 18, Appl
417	55	59.1	249	4	US-10-702-536-18	Sequence 18, Appl
418	55	59.1	249	4	US-11-146-077-18	Sequence 18, Appl
419	55	59.1	249	6	US-10-702-636-18	Sequence 18, Appl
420	55	59.1	250	4	US-10-779-461-11	Sequence 11, Appl
421	55	59.1	488	5	US-10-334-235-39	Sequence 39, Appl
422	55	59.1	488	5	US-10-473-127-1954	Sequence 1954, Ap
423	55	59.1	488	5	US-10-473-127-1963	Sequence 1963, Ap
424	55	59.1	600	5	US-10-334-235-38	Sequence 38, Appl
425	55	59.1	672	3	US-09-900-766-1	Sequence 1, Appl
426	54	58.1	17	3	US-09-770-002-2	Sequence 2, Appl
427	54	58.1	17	4	US-10-366-709-9	Sequence 9, Appl
428	54	58.1	17	4	US-10-327-663-9	Sequence 9, Appl
429	54	58.1	17	4	US-10-312-316-7	Sequence 7, Appl
430	54	58.1	17	5	US-10-631-722-5	Sequence 5, Appl
431	54	58.1	17	5	US-10-473-977-16	Sequence 16, Appl
432	54	58.1	17	5	US-10-849-615-27	Sequence 27, Appl
433	54	58.1	17	5	US-10-849-615-31	Sequence 31, Appl
434	54	58.1	17	5	US-10-861-049-44	Sequence 44, Appl
435	54	58.1	17	5	US-10-996-316-171	Sequence 171, App
436	54	58.1	17	5	US-10-240-353B-2	Sequence 2, Appl
437	54	58.1	17	6	US-11-021-874-44	Sequence 44, Appl
438	54	58.1	55	3	US-09-864-408A-4416	Sequence 4416, Ap
439	54	58.1	96	3	US-09-905-243-12	Sequence 12, Appl
440	54	58.1	96	6	US-09-905-243-13	Sequence 13, Appl
441	54	58.1	96	6	US-11-099-331-12	Sequence 12, Appl
442	54	58.1	96	6	US-11-099-331-13	Sequence 13, Appl
443	54	58.1	113	5	US-10-700-633-77	Sequence 77, Appl
444	54	58.1	114	5	US-10-700-633-80	Sequence 80, Appl
445	54	58.1	117	5	US-10-631-722-31	Sequence 31, Appl
446	54	58.1	118	4	US-10-181-324-2	Sequence 2, Appl
447	54	58.1	118	5	US-10-631-722-35	Sequence 35, Appl
448	54	58.1	118	5	US-10-631-722-40	Sequence 40, Appl
449	54	58.1	119	4	US-10-372-481-9	Sequence 9, Appl
450	54	58.1	119	4	US-10-371-797-9	Sequence 9, Appl
451	54	58.1	119	5	US-10-473-977-67	Sequence 67, Appl
452	54	58.1	120	4	US-10-310-674A-38	Sequence 38, Appl
453	54	58.1	120	4	US-10-366-709-35	Sequence 35, Appl
454	54	58.1	120	4	US-10-389-679-14	Sequence 14, Appl
455	54	58.1	120	4	US-10-389-679-19	Sequence 19, Appl
456	54	58.1	121	4	US-10-366-709-39	Sequence 39, Appl
457	54	58.1	121	4	US-10-366-709-41	Sequence 41, Appl
458	54	58.1	121	4	US-10-366-709-42	Sequence 42, Appl
459	54	58.1	121	4	US-10-389-155-11	Sequence 11, Appl
460	54	58.1	121	4	US-10-389-417-11	Sequence 11, Appl
461	54	58.1	121	5	US-10-452-357-50	Sequence 50, Appl
462	54	58.1	121	5	US-10-849-615-65	Sequence 65, Appl
463	54	58.1	121	5	US-10-917-599-1	Sequence 1, Appl
464	54	58.1	121	5	US-10-917-599-2	Sequence 2, Appl
465	54	58.1	121	5	US-10-917-599-3	Sequence 3, Appl
466	54	58.1	121	5	US-10-861-049-23	Sequence 23, Appl
467	54	58.1	121	6	US-11-021-874-23	Sequence 23, Appl
468	54	58.1	122	4	US-10-818-765-2	Sequence 2, Appl
469	54	58.1	122	5	US-10-877-363-2	Sequence 2, Appl
470	54	58.1	122	5	US-10-922-661-2	Sequence 2, Appl
471	54	58.1	122	5	US-10-917-599-9	Sequence 9, Appl
472	54	58.1	122	5	US-10-917-599-10	Sequence 10, Appl
473	54	58.1	122	5	US-10-861-049-14	Sequence 14, Appl
474	54	58.1	122	5	US-10-627-556-242	Sequence 242, App
475	54	58.1	122	6	US-11-021-874-14	Sequence 14, Appl
476	54	58.1	122	6	US-11-005-677-2	Sequence 2, Appl
477	54	58.1	122	6	US-11-006-136-6	Sequence 2, Appl
478	54	58.1	123	3	US-09-892-613C-18	Sequence 18, Appl
479	54	58.1	123	5	US-10-482-759-18	Sequence 18, Appl
480	54	58.1	123	5	US-10-482-759-18	Sequence 18, Appl
481	54	58.1	126	4	US-10-312-316-44	Sequence 44, Appl
482	54	58.1	136	4	US-10-138-505-12	Sequence 12, Appl
483	54	58.1	136	4	US-10-257-864A-88	Sequence 88, Appl
484	54	58.1	136	4	US-10-221-131-93	Sequence 93, Appl
485	54	58.1	136	4	US-10-399-518-117	Sequence 117, App
486	54	58.1	136	5	US-10-399-585-117	Sequence 117, App
487	54	58.1	136	5	US-10-645-085A-88	Sequence 88, Appl
488	54	58.1	140	3	US-09-905-928-6	Sequence 6, Appl
489	54	58.1	140	4	US-10-096-964-6	Sequence 6, Appl
490	54	58.1	140	4	US-10-238-661-41	Sequence 41, Appl
491	54	58.1	140	4	US-10-366-709-50	Sequence 50, Appl
492	54	58.1	140	4	US-10-411-037-62	Sequence 62, Appl
493	54	58.1	140	4	US-10-411-037-62	Sequence 62, Appl
494	54	58.1	140	4	US-10-411-037-62	Sequence 62, Appl
495	54	58.1	140	4	US-10-410-962-62	Sequence 62, Appl
496	54	58.1	140	4	US-10-411-049-62	Sequence 62, Appl
497	54	58.1	140	4	US-10-327-663-14	Sequence 14, Appl
498	54	58.1	140	4	US-10-410-930-62	Sequence 62, Appl
499	54	58.1	140	4	US-10-410-930-62	Sequence 62, Appl
500	54	58.1	140	4	US-10-411-012-62	Sequence 62, Appl
501	54	58.1	140	4	US-10-287-994-62	Sequence 62, Appl
502	54	58.1	140	4	US-10-410-913-62	Sequence 62, Appl
503	54	58.1	140	5	US-10-723-003-36	Sequence 36, Appl
504	54	58.1	140	5	US-10-410-980-62	Sequence 62, Appl
505	54	58.1	140	5	US-10-410-897-62	Sequence 62, Appl
506	54	58.1	140	5	US-10-492-261-62	Sequence 62, Appl
507	54	58.1	140	5	US-10-941-768A-44	Sequence 44, Appl
508	54	58.1	140	5	US-10-956-039-6	Sequence 6, Appl
509	54	58.1	140	6	US-11-004-639-36	Sequence 36, Appl
510	54	58.1	245	4	US-10-138-505-40	Sequence 40, Appl
511	54	58.1	245	4	US-10-257-864A-95	Sequence 95, Appl
512	54	58.1	245	4	US-10-221-131-100	Sequence 100, App
513	54	58.1	245	4	US-10-399-518-124	Sequence 124, App
514	54	58.1	245	5	US-10-399-585-123	Sequence 123, App
515	54	58.1	245	5	US-10-645-085A-95	Sequence 95, Appl
516	54	58.1	248	6	US-11-017-030-33	Sequence 33, Appl
517	54	58.1	252	6	US-11-090-847-118	Sequence 118, App
518	54	58.1	256	4	US-10-257-864A-98	Sequence 98, Appl
519	54	58.1	256	4	US-10-257-864A-98	Sequence 98, Appl
520	54	58.1	256	4	US-10-221-131-102	Sequence 102, App
521	54	58.1	256	4	US-10-221-131-103	Sequence 103, App
522	54	58.1	256	4	US-10-399-518-126	Sequence 126, App
523	54	58.1	256	4	US-10-399-518-127	Sequence 127, App
524	54	58.1	256	5	US-10-399-585-125	Sequence 125, App
525	54	58.1	256	5	US-10-399-585-126	Sequence 126, App
526	54	58.1	256	5	US-10-645-085A-97	Sequence 97, Appl
527	54	58.1	256	5	US-10-645-085A-98	Sequence 98, Appl
528	54	58.1	266	4	US-10-207-655-11	Sequence 11, Appl
529	54	58.1	266	4	US-10-053-530-11	Sequence 11, Appl
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532	54	58.1	266	6	US-11-088-570-11	Sequence 11, Appl
533	54	58.1	266	6	US-11-088-737-11	Sequence 11, Appl
534	54	58.1	266	6	US-11-088-569-11	Sequence 11, Appl
535	54	58.1	266	6	US-11-088-693-11	Sequence 11, Appl
536	54	58.1	266	6	US-11-089-367-11	Sequence 11, Appl
537	54	58.1	266	6	US-11-089-368-11	Sequence 11, Appl
538	54	58.1	267	5	US-10-627-556-214	Sequence 214, App

539	54	58.1	268	5	US-10-627-556-212	Sequence 212, App	612	54	58.1	483	6	US-11-132-143-122	Sequence 122, App
540	54	58.1	268	5	US-10-627-556-234	Sequence 234, App	613	54	58.1	498	5	US-10-207-655-335	Sequence 23, App
541	54	58.1	268	5	US-10-627-556-236	Sequence 236, App	614	54	58.1	498	4	US-10-627-556-232	Sequence 22, App
542	54	58.1	268	5	US-10-627-556-244	Sequence 244, App	615	54	58.1	498	5	US-10-964-195-13	Sequence 13, App
543	54	58.1	271	4	US-10-138-505-34	Sequence 34, App	616	54	58.1	499	4	US-10-207-655-15	Sequence 15, App
544	54	58.1	271	4	US-10-257-864A-93	Sequence 93, App	617	54	58.1	499	4	US-10-207-655-16	Sequence 16, App
545	54	58.1	271	4	US-10-221-131-98	Sequence 98, App	618	54	58.1	499	4	US-10-207-655-17	Sequence 17, App
546	54	58.1	271	4	US-10-399-518-122	Sequence 121, App	619	54	58.1	499	4	US-10-207-655-148	Sequence 146, App
547	54	58.1	271	5	US-10-399-518-122	Sequence 121, App	620	54	58.1	499	4	US-10-053-530-15	Sequence 15, App
548	54	58.1	271	5	US-10-645-085A-93	Sequence 93, App	621	54	58.1	499	4	US-10-053-530-16	Sequence 16, App
549	54	58.1	274	4	US-10-138-505-32	Sequence 32, App	622	54	58.1	499	4	US-10-627-556-689	Sequence 689, App
550	54	58.1	274	4	US-10-257-864A-92	Sequence 92, App	623	54	58.1	499	6	US-11-089-511-15	Sequence 15, App
551	54	58.1	274	4	US-10-221-131-97	Sequence 97, App	624	54	58.1	499	6	US-11-089-511-16	Sequence 16, App
552	54	58.1	274	4	US-10-399-518-121	Sequence 121, App	625	54	58.1	499	6	US-11-089-511-17	Sequence 17, App
553	54	58.1	274	5	US-10-399-518-120	Sequence 120, App	626	54	58.1	499	6	US-11-089-190-15	Sequence 15, App
554	54	58.1	274	5	US-10-645-085A-92	Sequence 92, App	627	54	58.1	499	6	US-11-089-190-16	Sequence 16, App
555	54	58.1	368	5	US-10-880-028-47	Sequence 47, App	628	54	58.1	499	6	US-11-089-190-17	Sequence 17, App
556	54	58.1	368	5	US-10-880-320-47	Sequence 47, App	629	54	58.1	499	6	US-11-089-190-17	Sequence 17, App
557	54	58.1	412	4	US-10-013-173-6	Sequence 6, App	630	54	58.1	499	6	US-11-088-570-15	Sequence 15, App
558	54	58.1	412	4	US-10-150-762-6	Sequence 6, App	631	54	58.1	499	6	US-11-088-570-16	Sequence 16, App
559	54	58.1	412	4	US-10-244-821-6	Sequence 6, App	632	54	58.1	499	6	US-11-088-737-15	Sequence 15, App
560	54	58.1	412	4	US-10-207-655-34	Sequence 34, App	633	54	58.1	499	6	US-11-088-737-16	Sequence 16, App
561	54	58.1	422	4	US-10-207-655-152	Sequence 152, App	634	54	58.1	499	6	US-11-088-737-17	Sequence 17, App
562	54	58.1	422	4	US-10-053-530-34	Sequence 34, App	635	54	58.1	499	6	US-11-088-569-16	Sequence 16, App
563	54	58.1	422	5	US-10-627-556-693	Sequence 693, App	636	54	58.1	499	6	US-11-088-569-17	Sequence 17, App
564	54	58.1	422	5	US-11-089-511-34	Sequence 34, App	637	54	58.1	499	6	US-11-088-693-15	Sequence 15, App
565	54	58.1	422	6	US-11-089-190-34	Sequence 34, App	638	54	58.1	499	6	US-11-088-693-16	Sequence 16, App
566	54	58.1	422	6	US-11-088-570-34	Sequence 34, App	639	54	58.1	499	6	US-11-088-693-17	Sequence 17, App
567	54	58.1	422	6	US-11-088-737-34	Sequence 34, App	640	54	58.1	499	6	US-11-088-693-17	Sequence 17, App
568	54	58.1	422	6	US-11-088-569-34	Sequence 34, App	641	54	58.1	499	6	US-11-088-367-17	Sequence 17, App
569	54	58.1	422	6	US-11-088-693-34	Sequence 34, App	642	54	58.1	499	6	US-11-089-367-15	Sequence 15, App
570	54	58.1	422	6	US-11-089-367-34	Sequence 34, App	643	54	58.1	499	6	US-11-089-367-17	Sequence 17, App
571	54	58.1	422	6	US-11-089-368-34	Sequence 34, App	644	54	58.1	499	6	US-11-089-368-15	Sequence 15, App
572	54	58.1	423	4	US-10-013	Sequence 8, App	645	54	58.1	499	6	US-11-089-368-16	Sequence 16, App
573	54	58.1	423	4	US-10-150	Sequence 8, App	646	54	58.1	499	6	US-11-089-368-17	Sequence 17, App
574	54	58.1	423	4	US-10-244	Sequence 8, App	647	54	58.1	499	6	US-10-207-655-240	Sequence 240, App
575	54	58.1	451	4	US-10-679-620-118	Sequence 118, App	648	54	58.1	500	4	US-10-207-655-274	Sequence 274, App
576	54	58.1	451	5	US-10-822-231-4	Sequence 4, App	649	54	58.1	500	4	US-10-207-655-352	Sequence 352, App
577	54	58.1	451	5	US-10-822-231-5	Sequence 5, App	650	54	58.1	500	4	US-10-207-655-385	Sequence 385, App
578	54	58.1	451	6	US-11-132-143-118	Sequence 118, App	651	54	58.1	500	4	US-10-207-655-385	Sequence 385, App
579	54	58.1	452	4	US-10-818-765-4	Sequence 4, App	652	54	58.1	500	4	US-10-207-655-387	Sequence 387, App
580	54	58.1	452	5	US-10-861-049-16	Sequence 16, App	653	54	58.1	500	4	US-10-207-655-388	Sequence 388, App
581	54	58.1	452	5	US-10-861-049-17	Sequence 17, App	654	54	58.1	500	4	US-10-207-655-389	Sequence 389, App
582	54	58.1	452	5	US-10-861-049-20	Sequence 20, App	655	54	58.1	500	4	US-10-207-655-396	Sequence 396, App
583	54	58.1	452	5	US-10-861-049-22	Sequence 22, App	656	54	58.1	500	4	US-10-207-655-397	Sequence 397, App
584	54	58.1	452	6	US-11-021-874-16	Sequence 16, App	657	54	58.1	500	4	US-10-207-655-398	Sequence 398, App
585	54	58.1	452	6	US-11-021-874-17	Sequence 17, App	658	54	58.1	500	4	US-10-627-556-28	Sequence 28, App
586	54	58.1	452	6	US-11-021-874-20	Sequence 20, App	659	54	58.1	500	5	US-10-627-556-58	Sequence 58, App
587	54	58.1	452	6	US-11-021-874-22	Sequence 22, App	660	54	58.1	500	5	US-10-627-556-131	Sequence 131, App
588	54	58.1	452	6	US-11-005-677-4	Sequence 4, App	661	54	58.1	500	5	US-10-627-556-135	Sequence 135, App
589	54	58.1	452	6	US-11-006-136-4	Sequence 4, App	662	54	58.1	500	5	US-10-627-556-137	Sequence 137, App
590	54	58.1	470	5	US-10-723-003-40	Sequence 40, App	663	54	58.1	500	5	US-10-627-556-139	Sequence 139, App
591	54	58.1	470	6	US-11-019-180-4	Sequence 4, App	664	54	58.1	500	5	US-10-627-556-154	Sequence 154, App
592	54	58.1	471	5	US-11-004-639-40	Sequence 40, App	665	54	58.1	500	5	US-10-627-556-158	Sequence 158, App
593	54	58.1	471	5	US-10-877-363-4	Sequence 4, App	666	54	58.1	500	5	US-10-627-556-158	Sequence 158, App
594	54	58.1	471	5	US-10-922-651-4	Sequence 4, App	667	54	58.1	500	5	US-10-627-556-160	Sequence 160, App
595	54	58.1	471	5	US-10-861-049-4	Sequence 4, App	668	54	58.1	500	5	US-10-627-556-162	Sequence 162, App
596	54	58.1	471	5	US-10-861-049-11	Sequence 11, App	669	54	58.1	500	5	US-10-627-556-164	Sequence 164, App
597	54	58.1	471	6	US-11-021-874-4	Sequence 11, App	670	54	58.1	500	5	US-10-627-556-166	Sequence 166, App
598	54	58.1	471	6	US-11-021-874-11	Sequence 11, App	671	54	58.1	500	5	US-10-627-556-168	Sequence 168, App
599	54	58.1	482	4	US-10-207-655-33	Sequence 33, App	672	54	58.1	500	5	US-10-627-556-246	Sequence 246, App
600	54	58.1	482	4	US-10-207-655-150	Sequence 150, App	673	54	58.1	500	5	US-10-627-556-284	Sequence 284, App
601	54	58.1	482	4	US-10-053-530-33	Sequence 33, App	674	54	58.1	500	5	US-10-627-556-290	Sequence 290, App
602	54	58.1	482	5	US-10-627-556-691	Sequence 691, App	675	54	58.1	500	5	US-10-627-556-288	Sequence 288, App
603	54	58.1	482	6	US-11-089-511-33	Sequence 33, App	676	54	58.1	500	5	US-10-627-556-284	Sequence 274, App
604	54	58.1	482	6	US-11-089-190-33	Sequence 33, App	677	54	58.1	500	5	US-10-627-556-282	Sequence 276, App
605	54	58.1	482	6	US-11-088-570-33	Sequence 33, App	678	54	58.1	500	5	US-10-627-556-282	Sequence 282, App
606	54	58.1	482	6	US-11-088-737-33	Sequence 33, App	679	54	58.1	500	5	US-10-627-556-284	Sequence 284, App
607	54	58.1	482	6	US-11-088-569-33	Sequence 33, App	680	54	58.1	500	5	US-10-627-556-292	Sequence 292, App
608	54	58.1	482	6	US-11-089-367-33	Sequence 33, App	681	54	58.1	500	5	US-10-627-556-292	Sequence 292, App
609	54	58.1	482	6	US-11-089-368-33	Sequence 33, App	682	54	58.1	500	5	US-10-627-556-292	Sequence 292, App
610	54	58.1	482	6	US-11-089-368-33	Sequence 33, App	683	54	58.1	500	5	US-10-627-556-298	Sequence 298, App
611	54	58.1	483	4	US-10-679-620-122	Sequence 122, App	684	54	58.1	500	5	US-10-627-556-300	Sequence 300, App

685	54	58.1	500	5	US-10-627-556-306	Sequence 306, App	758	53	57.0	143	5	US-10-897-406-52	Sequence 52, Appl
686	54	58.1	500	5	US-10-627-556-308	Sequence 308, App	759	53	57.0	243	4	US-10-097-558-2	Sequence 2, Appl
687	54	58.1	500	5	US-10-627-556-368	Sequence 368, App	760	53	57.0	243	4	US-10-097-558-3	Sequence 3, Appl
688	54	58.1	500	5	US-10-627-556-370	Sequence 370, App	761	53	57.0	243	5	US-10-505-658-2	Sequence 2, Appl
689	54	58.1	500	5	US-10-627-556-372	Sequence 372, App	762	53	57.0	243	3	US-10-505-658-3	Sequence 3, Appl
690	54	58.1	501	5	US-10-627-556-378	Sequence 378, App	763	53	57.0	245	3	US-09-860-748-1902	Sequence 1902, Ap
691	54	58.1	501	5	US-10-627-556-228	Sequence 228, App	764	53	57.0	245	4	US-10-293-418-1902	Sequence 1902, Ap
692	54	58.1	502	5	US-10-207-655-230	Sequence 230, App	765	53	57.0	247	4	US-10-620-278-21	Sequence 21, Appl
693	54	58.1	502	5	US-10-627-655-305	Sequence 305, App	766	53	57.0	247	5	US-10-620-049-21	Sequence 21, Appl
694	54	58.1	502	4	US-10-627-556-76	Sequence 76, Appl	767	52	55.9	15	5	US-10-879-994-84	Sequence 84, Appl
695	54	58.1	503	4	US-10-207-655-237	Sequence 237, App	768	52	55.9	17	3	US-09-809-739-7	Sequence 7, Appl
696	54	58.1	503	4	US-10-627-556-26	Sequence 26, Appl	769	52	55.9	17	3	US-09-924-039-7	Sequence 7, Appl
697	54	58.1	505	4	US-10-207-655-18	Sequence 18, Appl	770	52	55.9	17	3	US-09-378-967-14	Sequence 14, Appl
698	54	58.1	505	4	US-10-207-655-284	Sequence 284, App	771	52	55.9	17	4	US-10-160-506-2	Sequence 2, Appl
699	54	58.1	505	4	US-10-053-530-18	Sequence 18, Appl	772	52	55.9	17	4	US-10-449-379-2	Sequence 2, Appl
700	54	58.1	505	4	US-10-627-556-60	Sequence 60, Appl	773	52	55.9	17	4	US-10-449-379-2	Sequence 2, Appl
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702	54	58.1	505	6	US-11-089-190-18	Sequence 18, Appl	775	52	55.9	17	5	US-10-160-505-2	Sequence 2, Appl
703	54	58.1	505	6	US-11-088-570-18	Sequence 18, Appl	776	52	55.9	17	5	US-10-849-615-33	Sequence 33, Appl
704	54	58.1	505	6	US-11-088-737-18	Sequence 18, Appl	777	52	55.9	17	5	US-10-895-135-2	Sequence 2, Appl
705	54	58.1	505	6	US-11-088-569-18	Sequence 18, Appl	778	52	55.9	113	3	US-10-662-061-7	Sequence 7, Appl
706	54	58.1	505	6	US-11-088-693-18	Sequence 18, Appl	779	52	55.9	114	4	US-09-924-039-2	Sequence 2, Appl
707	54	58.1	505	6	US-11-089-367-18	Sequence 18, Appl	780	52	55.9	114	4	US-10-308-817-188	Sequence 188, App
708	54	58.1	506	6	US-11-089-368-18	Sequence 18, Appl	781	52	55.9	114	4	US-10-308-817-194	Sequence 184, App
709	54	58.1	506	5	US-10-964-195-11	Sequence 11, Appl	782	52	55.9	114	4	US-10-453-698-188	Sequence 188, App
710	54	58.1	507	5	US-10-627-556-254	Sequence 254, App	783	52	55.9	115	3	US-10-453-698-194	Sequence 8, Appl
711	54	58.1	514	5	US-10-207-655-236	Sequence 236, App	784	52	55.9	115	3	US-09-929-665-8	Sequence 8, Appl
712	54	58.1	516	4	US-10-627-556-24	Sequence 24, Appl	785	52	55.9	115	4	US-09-929-546-8	Sequence 8, Appl
713	54	58.1	516	4	US-10-207-655-299	Sequence 299, App	786	52	55.9	115	4	US-10-160-506-19	Sequence 19, Appl
714	54	58.1	516	5	US-10-627-556-71	Sequence 71, Appl	787	52	55.9	115	4	US-10-160-506-21	Sequence 21, Appl
715	54	58.1	520	4	US-10-627-556-252	Sequence 252, App	788	52	55.9	115	4	US-10-449-379-19	Sequence 19, Appl
716	54	58.1	520	5	US-10-207-655-286	Sequence 286, App	789	52	55.9	115	4	US-10-449-379-21	Sequence 21, Appl
717	54	58.1	533	4	US-10-627-556-62	Sequence 62, App	790	52	55.9	115	4	US-10-688-015-19	Sequence 19, Appl
718	54	58.1	533	4	US-10-257-864A-96	Sequence 96, Appl	791	52	55.9	115	4	US-10-688-015-21	Sequence 21, Appl
719	54	58.1	533	4	US-10-221-131-101	Sequence 101, App	792	52	55.9	115	4	US-10-160-505-19	Sequence 19, Appl
720	54	58.1	533	4	US-10-399-518-125	Sequence 125, App	793	52	55.9	115	4	US-10-160-505-21	Sequence 21, Appl
721	54	58.1	533	5	US-10-399-585-124	Sequence 124, App	794	52	55.9	116	4	US-10-127-890-168	Sequence 168, App
722	54	58.1	551	5	US-10-645-085A-96	Sequence 96, Appl	795	52	55.9	116	4	US-10-340-189-54	Sequence 54, Appl
723	54	58.1	552	4	US-10-627-556-442	Sequence 442, App	796	52	55.9	116	4	US-10-325-656-54	Sequence 54, Appl
724	54	58.1	592	4	US-10-207-655-134	Sequence 34, App	797	52	55.9	116	6	US-10-717-243-168	Sequence 168, App
725	54	58.1	593	5	US-10-627-556-129	Sequence 129, App	798	52	55.9	119	4	US-11-133-775-14	Sequence 54, Appl
726	54	58.1	599	5	US-10-627-556-248	Sequence 248, App	799	52	55.9	119	4	US-10-194-975-121	Sequence 121, App
727	54	58.1	626	5	US-10-627-556-250	Sequence 250, App	800	52	55.9	119	4	US-10-460-595-5	Sequence 5, Appl
728	54	58.1	626	6	US-10-723-003-44	Sequence 44, Appl	801	52	55.9	120	4	US-10-632-706-70	Sequence 70, Appl
729	54	58.1	641	6	US-10-723-003-46	Sequence 46, Appl	802	52	55.9	122	5	US-10-010-729-19	Sequence 19, Appl
730	54	58.1	641	6	US-11-004-639-46	Sequence 46, Appl	803	52	55.9	122	5	US-10-729-441-73	Sequence 73, Appl
731	54	58.1	657	5	US-10-723-003-48	Sequence 48, Appl	804	52	55.9	123	5	US-10-897-406-73	Sequence 73, Appl
732	54	58.1	657	6	US-11-004-633-48	Sequence 48, Appl	805	52	55.9	123	5	US-10-729-441-88	Sequence 88, Appl
733	54	58.1	768	4	US-10-207-655-350	Sequence 350, App	806	52	55.9	123	5	US-10-729-441-92	Sequence 92, Appl
734	54	58.1	768	5	US-10-627-556-115	Sequence 115, App	807	52	55.9	123	5	US-10-897-406-88	Sequence 88, Appl
735	53	57.0	17	3	US-09-842-776A-29	Sequence 29, Appl	808	52	55.9	124	5	US-10-897-406-92	Sequence 92, Appl
736	53	57.0	17	4	US-10-297-371A-6	Sequence 6, Appl	809	52	55.9	124	5	US-10-729-441-13	Sequence 13, Appl
737	53	57.0	17	5	US-10-729-441-2	Sequence 2, Appl	810	52	55.9	130	3	US-09-929-665-4	Sequence 4, Appl
738	53	57.0	17	5	US-10-897-406-2	Sequence 2, Appl	811	52	55.9	130	3	US-09-929-546-4	Sequence 4, Appl
739	53	57.0	19	5	US-10-496-869-2	Sequence 2, Appl	812	52	55.9	134	4	US-10-160-506-6	Sequence 6, Appl
740	53	57.0	98	5	US-10-729-441-57	Sequence 57, Appl	813	52	55.9	134	4	US-10-449-379-27	Sequence 27, Appl
741	53	57.0	98	5	US-10-897-406-57	Sequence 57, Appl	814	52	55.9	134	4	US-10-688-015-27	Sequence 27, Appl
742	53	57.0	111	4	US-10-297-371A-2	Sequence 2, Appl	815	52	55.9	134	4	US-10-160-505-27	Sequence 27, Appl
743	53	57.0	114	4	US-10-803-622-228	Sequence 228, App	816	52	55.9	139	3	US-09-809-739-5	Sequence 5, Appl
744	53	57.0	114	4	US-10-803-653-228	Sequence 228, App	817	52	55.9	139	3	US-09-809-739-9	Sequence 9, Appl
745	53	57.0	115	4	US-10-803-652-216	Sequence 216, App	818	52	55.9	139	3	US-09-378-967-10	Sequence 10, Appl
746	53	57.0	115	4	US-10-803-653-216	Sequence 216, App	819	52	55.9	139	5	US-10-662-061-9	Sequence 9, Appl
747	53	57.0	119	5	US-10-496-869-28	Sequence 28, App	820	52	55.9	139	5	US-10-662-061-5	Sequence 5, Appl
748	53	57.0	121	5	US-10-938-993-42	Sequence 42, Appl	821	52	55.9	236	5	US-10-879-994-6	Sequence 6, Appl
749	53	57.0	123	3	US-09-842-776A-60	Sequence 60, Appl	822	52	55.9	236	5	US-10-610-462-6	Sequence 6, Appl
750	53	57.0	123	3	US-10-729-441-87	Sequence 87, Appl	823	52	55.9	237	3	US-09-924-039-9	Sequence 9, Appl
751	53	57.0	123	5	US-10-897-406-87	Sequence 87, Appl	824	52	55.9	242	4	US-10-259-087A-18	Sequence 18, Appl
752	53	57.0	124	5	US-10-729-441-7	Sequence 7, Appl	825	52	55.9	242	4	US-10-689-006-18	Sequence 18, Appl
753	53	57.0	124	5	US-10-729-441-70	Sequence 70, Appl	826	52	55.9	243	3	US-09-924-039-10	Sequence 10, Appl
754	53	57.0	124	5	US-10-897-406-7	Sequence 7, Appl	827	52	55.9	469	4	US-10-404-724-72	Sequence 72, Appl
755	53	57.0	124	5	US-10-897-406-70	Sequence 70, Appl	828	51	54.8	17	4	US-10-447-257-6	Sequence 6, Appl
756	53	57.0	139	4	US-10-006-773-13	Sequence 13, Appl	829	51	54.8	17	5	US-10-496-628-6	Sequence 6, Appl
757	53	57.0	143	5	US-10-729-441-52	Sequence 52, Appl	830	51	54.8	17	5	US-10-996-316-170	Sequence 170, App

831	51	54.8	20	4	US-10-468-924-2	Sequence 2, Appl1	904	50	53.8	98	4	US-10-125-667-16	Sequence 16, Appl1
832	51	54.8	20	5	US-10-620-621-7	Sequence 7, Appl1	905	50	53.8	98	4	US-10-041-860-6	Sequence 301, Appl
833	51	54.8	20	5	US-10-758-397-2	Sequence 2, Appl1	906	50	53.8	98	4	US-10-041-860-301	Sequence 301, Appl
834	51	54.8	98	5	US-10-895-135-24	Sequence 24, Appl1	907	50	53.8	98	4	US-10-041-860-302	Sequence 302, Appl
835	51	54.8	116	5	US-10-700-632-74	Sequence 74, Appl1	908	50	53.8	98	4	US-10-041-860-312	Sequence 312, Appl
836	51	54.8	117	4	US-10-447-257-2	Sequence 2, Appl1	909	50	53.8	98	4	US-10-041-860-314	Sequence 314, Appl
837	51	54.8	117	5	US-10-479-441-76	Sequence 76, Appl1	910	50	53.8	98	4	US-10-041-860-318	Sequence 318, Appl
838	51	54.8	117	5	US-10-496-628-2	Sequence 2, Appl1	911	50	53.8	98	4	US-10-041-860-320	Sequence 320, Appl
839	51	54.8	117	5	US-10-895-135-54	Sequence 54, Appl1	912	50	53.8	98	4	US-10-041-860-336	Sequence 336, Appl
840	51	54.8	117	5	US-10-897-406-76	Sequence 76, Appl1	913	50	53.8	98	4	US-10-041-860-338	Sequence 338, Appl
841	51	54.8	119	4	US-10-632-706-71	Sequence 71, Appl1	914	50	53.8	98	4	US-10-041-860-367	Sequence 367, Appl
842	51	54.8	121	4	US-10-389-155-12	Sequence 12, Appl1	915	50	53.8	98	4	US-10-032-037B-106	Sequence 106, Appl
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844	51	54.8	121	4	US-10-452-357-51	Sequence 51, Appl1	917	50	53.8	98	4	US-10-032-037B-108	Sequence 108, Appl
845	51	54.8	121	5	US-10-706-689-6	Sequence 6, Appl1	918	50	53.8	98	4	US-10-029-988B-106	Sequence 106, Appl
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847	51	54.8	122	2	US-08-779-784-28	Sequence 28, Appl1	920	50	53.8	98	4	US-10-029-988B-108	Sequence 108, Appl
848	51	54.8	128	4	US-10-800-197-108	Sequence 108, Appl	921	50	53.8	98	4	US-10-032-423A-106	Sequence 106, Appl
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853	51	54.8	128	4	US-10-800-197-118	Sequence 118, Appl	927	50	53.8	98	4	US-10-029-926B-107	Sequence 107, Appl
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859	51	54.8	251	4	US-10-800-197-4	Sequence 4, Appl1	933	50	53.8	98	6	US-11-009-721-49	Sequence 49, Appl
860	51	54.8	251	4	US-10-800-197-5	Sequence 5, Appl1	934	50	53.8	98	6	US-11-009-331-47	Sequence 47, Appl
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862	51	54.8	272	4	US-10-207-655-14	Sequence 14, Appl1	936	50	53.8	109	4	US-10-800-197-146	Sequence 146, Appl
863	51	54.8	272	4	US-10-053-530-14	Sequence 14, Appl1	937	50	53.8	109	4	US-10-800-197-147	Sequence 147, Appl
864	51	54.8	272	6	US-11-089-511-14	Sequence 14, Appl1	938	50	53.8	109	5	US-10-727-155-283	Sequence 283, Appl
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871	51	54.8	272	6	US-11-089-368-14	Sequence 14, Appl1	945	50	53.8	111	6	US-11-129-359-5	Sequence 5, Appl1
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879	50	53.8	17	4	US-10-384-060-40	Sequence 40, Appl1	953	50	53.8	116	3	US-09-894-839-8	Sequence 8, Appl1
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881	50	53.8	17	4	US-10-379-741-6	Sequence 6, Appl1	955	50	53.8	116	3	US-09-988-013A-8	Sequence 8, Appl1
882	50	53.8	17	4	US-10-128-520-369	Sequence 369, Appl	956	50	53.8	116	3	US-09-988-013A-9	Sequence 9, Appl1
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886	50	53.8	17	5	US-10-638-332-55	Sequence 55, Appl1	960	50	53.8	116	4	US-10-446-689-9	Sequence 9, Appl1
887	50	53.8	17	5	US-10-726-332-73	Sequence 73, Appl1	961	50	53.8	116	5	US-10-787-378-4	Sequence 4, Appl1
888	50	53.8	17	5	US-10-726-332-88	Sequence 88, Appl1	962	50	53.8	116	5	US-10-787-378-8	Sequence 8, Appl1
889	50	53.8	17	5	US-10-726-332-91	Sequence 91, Appl1	963	50	53.8	116	5	US-10-787-378-21	Sequence 21, Appl1
890	50	53.8	17	5	US-10-982-725-6	Sequence 6, Appl1	964	50	53.8	116	5	US-10-727-155-100	Sequence 100, Appl
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892	50	53.8	17	5	US-10-810-881A-74	Sequence 74, Appl1	966	50	53.8	116	5	US-10-974-678-8	Sequence 8, Appl1
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901	50	53.8	98	3	US-09-905-243-47	Sequence 47, Appl1	975	50	53.8	117	5	US-10-726-332-144	Sequence 144, Appl
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997 50 53.8 118 5 US-10-700-632-76 Sequence 76, Appli
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999 50 53.8 119 3 US-09-795-515-13 Sequence 13, Appli
1000 50 53.8 119 3 US-09-795-515-14 Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-795-798-11
; Sequence 11, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-795-798-11

Query Match 100.0%; Score 93; DB 3; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHPSDSETRYNOKEFD 17
Db 1 MHPSDSETRYNOKEFD 17

RESULT 2

US-10-727-737-26
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; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardieu, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-727-737-26
Query Match 100.0%; Score 93; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHPSDSETRYNOKEFD 17
Db 1 MHPSDSETRYNOKEFD 17

RESULT 3

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; Sequence 5, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.

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1 STREET: 1 DNA Way
2 CITY: South San Francisco
3 STATE: California
4 COUNTRY: USA
5 ZIP: 94080
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: WinPatIn (Genentech)
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13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/09/795,798
15 FILING DATE: 28-Feb-2001
16 CLASSIFICATION: <Unknown>
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/974,899
20 FILING DATE: <Unknown>
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Lee, Wendy M.
23 REGISTRATION NUMBER: 40,378
24 REFERENCE/DOCKET NUMBER: P1014R1
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 650/225-1994
27 TELEFAX: 650/952-9881
28
29 INFORMATION FOR SEQ ID NO: 5:
30 LENGTH: 121 amino acids
31 TYPE: Amino Acid
32 TOPOLOGY: Linear
33
34 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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36 US-09-795-798-5
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REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-727-737-5

Query Match          100.0%; Score 93; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 MIHPDSETRYNQKFKD 17
        |||
        50 MIHPDSETRYNQKFKD 66

RESULT 5
US-10-877-532-6
Sequence 6, Application US/10877532
Publication No. US20050038231A1
GENERAL INFORMATION:
APPLICANT: FAHRNER, ROBERT L.
APPLICANT: LAVERDIERE, AMY
APPLICANT: MCDONALD, PAUL, J.
APPLICANT: O'LEARY, RHONA M.
TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAPHY
FILE REFERENCE: P2015R1
CURRENT APPLICATION NUMBER: US/10/877,532
CURRENT FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: US 60/490,500
PRIOR FILING DATE: 2003-07-28
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 6
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-10-877-532-6

Query Match          100.0%; Score 93; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 MIHPDSETRYNQKFKD 17
        |||
        50 MIHPDSETRYNQKFKD 66

RESULT 6
US-10-423-299-4
Sequence 4, Application US/10423299
Publication No. US20030229212A1
GENERAL INFORMATION:
APPLICANT: FAHRNER, ROBERT
APPLICANT: FOLLMAN, DEBORAH
APPLICANT: LEBRETON, BENEDICTE
APPLICANT: VAN REIS, ROBERT
TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
FILE REFERENCE: 39766-0121A
CURRENT APPLICATION NUMBER: US/10/423,299
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/375,953
PRIOR FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 451

```

TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized
US-10-423-299-4

Query Match 100.0%; Score 93; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHPSDSTRYNOKFXD 17
|||||
Db 50 MIHPSDSTRYNOKFXD 66

RESULT 7
US-10-727-737-34
Sequence 34, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-727-737-34

Query Match 96.8%; Score 90; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHPSDSTRYNOKFXD 17
|||||
Db 1 MIHPSDSTRYNOKFXD 17

RESULT 8
US-10-727-737-36
Sequence 36, Application US/10727737
Publication No. US20040146507A1

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-727-737-36

Query Match 96.8%; Score 90; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHPSDSTRYNOKFXD 17
|||||
Db 1 MIHPSDSTRYNOKFXD 17

RESULT 9
US-10-727-737-37
Sequence 37, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737

FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-727-737-37

Query Match 96.8%; Score 90; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.9e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHPSDSETRYNOKEFD 17
Db 1 MHPSDNETRYNOKEFD 17

RESULT 10
US-10-727-737-38
Sequence 38, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-727-737-38

Query Match 95.7%; Score 89; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.7e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MHPSDSETRYNOKEFD 17
Db 1 MHPSDQETRYNOKEFD 17

RESULT 11
US-10-727-737-30
Sequence 30, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-727-737-30

Query Match 93.5%; Score 87; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 5.6e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHPSDSETRYNOKEFD 17
Db 1 MHPSDAETRYNOKEFD 17

RESULT 12
US-10-727-737-39
Sequence 39, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.

```

      TITLE OF INVENTION: Antibody Mutants
      NUMBER OF SEQUENCES: 79
      CORRESPONDENCE ADDRESSES:
      ADDRESSEE: Genentech, Inc.
      STREET: 1 DNA Way
      CITY: South San Francisco
      STATE: California
      COUNTRY: USA
      ZIP: 94080

      COMPUTER READABLE FORM:
      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Winpatin (Genentech)

      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/727,737
      FILING DATE: 03-Dec-2003
      CLASSIFICATION: <Unknown>

      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/975,329B
      FILING DATE: 20-Nov-1997
      APPLICATION NUMBER: 60/031945
      FILING DATE: 27-Nov-1996
      ATTORNEY/AGENT INFORMATION:
      NAME: Lee, Wendy M.
      REGISTRATION NUMBER: 40,378
      REFERENCE/DOCKET NUMBER: P1064R1
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 650/225-1994
      TELEFAX: 650/952-9881
      INFORMATION FOR SEQ ID NO: 39:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 17 amino acids
      TYPE: Amino Acid
      TOPOLOGY: Linear

      SEQUENCE DESCRIPTION: SEQ ID NO: 39:
      US-10-727-737-39

      Query Match      93.5%; Score 87; DB 4; Length 17;
      Best Local Similarity 94.1%; Pred. No. 5,6e-07;
      Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

      Cy      1 MHPSDSETRVNOQKPKD 17
              ||||| ||||| |||||
      Db      1 MHPSDSATRYNOQKPKD 17

RESULT 13
US-10-727-737-40
; Sequence 40, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
;             Jarden, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
; US-10-727-737-39

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1      APPLICATION NUMBER: US/08/975,329B
2      FILING DATE: 20-NOV-1997
3      APPLICATION NUMBER: 60/031945
4      FILING DATE: 27-NOV-1996
5      ATTORNEY/AGENT INFORMATION:
6      NAME: Lee, Wendy M.
7      REGISTRATION NUMBER: 40,378
8      REFERENCE/DOCKET NUMBER: PI064R1
9      TELECOMMUNICATION INFORMATION:
10     TELEPHONE: 650/225-1994
11     TELEFAX: 650/952-9881
12     INFORMATION FOR SEQ ID NO: 40:
13     SEQUENCE CHARACTERISTICS:
14     LENGTH: 17 amino acids
15     TYPE: Amino Acid
16     TOPOLOGY: Linear
17     SEQUENCE DESCRIPTION: SEQ ID NO: 40:
18     US-10-727-737-40
19
20 Query Match      93.5%; Score 87; DB 4; Length 17;
21 Best Local Similarity 94.1%; Pred. No. 5.6e-07;
22 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0
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24 Oy      1 MHPDSETRYNOKFKD 17
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Query Match 93.5%; Score 87; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0;

QY 1 MHPSDSETRYNOKFXD 17
| | | | | | | | | | | | | | | | | | |
DB 1 MHPSDSETRYNOKFXD 17

RESULT 15

US-10-727-737-42
; Sequence 42, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Prestia, Leonard G.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-727-737-42
Query Match 93.5%; Score 87; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0;
QY 1 MHPSDSETRYNOKFXD 17
| | | | | | | | | | | | | | | | | | |
DB 1 MHPSDSETRYNOKFXD 17

RESULT 16
US-10-727-737-43
; Sequence 43, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Prestia, Leonard G.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-727-737-43

Query Match 93.5%; Score 87; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0;

QY 1 MHPSDSETRYNOKFXD 17
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DB 1 MHPSDSETRYNOKFXD 17

RESULT 17

US-10-727-737-44
; Sequence 44, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Prestia, Leonard G.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945

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; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lee, Wendy M.
;   REGISTRATION NUMBER: 40,378
;   REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-1994
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 44:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 17 amino acids
;     TYPE: Amino Acid
;     TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-727-737-44

Query Match          93.5%; Score 87; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MIHPDSESTRYNOKFK 16
Db      1 MIHPDSESTRYNOKFK 16

RESULT 18
US-10-727-737-35
; Sequence 35, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Antibody Mutants
;   NUMBER OF SEQUENCES: 79
;   CORRESPONDENCE ADDRESS:
;     ADDRESS: Genentech, Inc.
;     STREET: 1 DNA Way
;     CITY: South San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/727,737
;   FILING DATE: 03-Dec-2003
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/975,329B
;   FILING DATE: 20-Nov-1997
;   APPLICATION NUMBER: 60/031945
;   FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Lee, Wendy M.
;   REGISTRATION NUMBER: 40,378
;   REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-1994
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 35:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 17 amino acids
;     TYPE: Amino Acid
;     TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-727-737-35

Query Match          91.4%; Score 85; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 MIHPDSESTRYNOKFKD 17
Db      1 MIHPDSESTRYNOKFKD 17

RESULT 19
US-10-842-011-10
; Sequence 10, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
;   APPLICANT: Protein Design Labs
;   TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CSI ANTIBODIES
;   FILE REFERENCE: 05882.0110.NPUS04
;   CURRENT APPLICATION NUMBER: US/10/842,011
;   CURRENT FILING DATE: 2004-05-07
;   NUMBER OF SEQ ID NOS: 93
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
; US-10-842-011-10

Query Match          91.4%; Score 85; DB 5; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MIHPDSESTRYNOKFKD 17
Db      1 MIHPDSESTRYNOKFKD 17

RESULT 20
US-10-842-011-3
; Sequence 3, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
;   APPLICANT: Protein Design Labs
;   TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CSI ANTIBODIES
;   FILE REFERENCE: 05882.0110.NPUS04
;   CURRENT APPLICATION NUMBER: US/10/842,011
;   CURRENT FILING DATE: 2004-05-07
;   NUMBER OF SEQ ID NOS: 93
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
; US-10-842-011-3

Query Match          91.4%; Score 85; DB 5; Length 120;
Best Local Similarity 94.1%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MIHPDSESTRYNOKFKD 17
Db      50 MIHPDSESTRYNOKFKD 66

RESULT 21
US-09-795-798-4
; Sequence 4, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
;   APPLICANT: Presta, Leonard G.
;   TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
;   NUMBER OF SEQUENCES: 24
;   CORRESPONDENCE ADDRESS:
;     ADDRESS: Genentech, Inc.
;     STREET: 1 DNA Way
;     CITY: South San Francisco
```

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-795-798-4
Query Match 91.4%; Score 85; DB 3; Length 121;
Best Local Similarity 94.1%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MHPDSETRYNOKFXD 17
DB 50 MHPDSETRYNOKFXD 66
RESULT 22
US-10-727-737-4
Sequence 4, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-727-737-4
Query Match 91.4%; Score 85; DB 4; Length 121;
Best Local Similarity 94.1%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MHPDSETRYNOKFXD 17
DB 50 MHPDSETRYNOKFXD 66
RESULT 23
US-10-727-737-33
Sequence 33, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-727-737-33
Query Match 90.3%; Score 84; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MHPDSETRYNOKFXD 17
DB 1 MHPDSETRYNOKFXD 17

RESULT 24
US-10-727-737-32
; Sequence 32, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-727-737-32
Query Match 89.2%; Score 83; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNQKFKD 17
DB 1 MIHPDSETRYNQKFKD 17
RESULT 25
US-10-435-614-13
; Sequence 13, Application US/10435614
; Publication No. US20040005647A1
; GENERAL INFORMATION:
; APPLICANT: DENARDO, SALLY J.
; APPLICANT: WINTHROP, MICHELLE D.
; APPLICANT: DENARDO, GERALD L.
; TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING
; FILE REFERENCE: 3097-000220US
; CURRENT APPLICATION NUMBER: US/10/435,614
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/112,788
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/280,721
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-435-614-13
Query Match 88.2%; Score 82; DB 4; Length 118;
Best Local Similarity 88.2%; Pred. No. 3e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNQKFKD 17
DB 50 MIHPDSETRYNQKFKD 66
RESULT 26
US-09-144-886-55
; Sequence 55, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.1170S0
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Botn/A clone
; OTHER INFORMATION: S25 region VH epitope 1
US-09-144-886-55
Query Match 88.2%; Score 82; DB 3; Length 120;
Best Local Similarity 82.4%; Pred. No. 3.1e-05;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNQKFKD 17
DB 50 MIHPDSETRYNQKFKD 66
RESULT 27
US-10-632-706-52
; Sequence 52, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 4077-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-52

Query Match 88.2%; Score 82; DB 4; Length 120;
Best Local Similarity 82.4%; Pred. No. 3.1e-05;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPDSETRYNQKFXD 17
|||||:|||||:
Db 50 MHPDSETRYNQKFXD 66

RESULT 28

US-10-435-614-21
; Sequence 21, Application US/10435614
; Publication No. US20040005647A1

GENERAL INFORMATION:

APPLICANT: DENARDO, SALLY J.
APPLICANT: WINTHROP, MICHELLE D.
APPLICANT: DENARDO, GERALD L.
TITLE OF INVENTION: ANTI-MWC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING
FILE REFERENCE: 309T-000220US
CURRENT APPLICATION NUMBER: US/10/435,614
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: 10/112,788
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,721
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.2
SEQ ID NO 21
LENGTH: 177
TYPE: PRT
ORGANISM: Mus Musculus
US-10-435-614-21

Query Match 88.2%; Score 82; DB 4; Length 177;
Best Local Similarity 88.2%; Pred. No. 4.7e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHPDSETRYNQKFXD 17
|||||:|||||:
Db 52 MHPDSETRYNQKFXD 68

RESULT 29

US-10-727-737-29
; Sequence 29, Application US/10727737
; Publication No. US20040146507A1

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996

ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid

TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-727-737-29

Query Match 86.0%; Score 80; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHPDSETRYNQKFXD 17
|||||:|||||:
Db 1 MHPDSETRYNQKFXD 17

RESULT 30

US-10-727-737-31
; Sequence 31, Application US/10727737
; Publication No. US20040146507A1

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-727-737-31

Query Match 86.0%; Score 80; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHPDSETRYNQKFXD 17

Db 1 MIAPSDAETRYNOKFKD 17

RESULT 31
US-09-948-004-33
; Sequence 33, Application US/09948004
; Publication No. US20030017979A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-948-004-33

Query Match 86.0%; Score 80; DB 3; Length 19;
Best Local Similarity 88.2%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MIHPSDSETRYNOKFKD 17
Db 2 MIHPSDSETRYNOKFKD 18

RESULT 32
US-10-672-932-33
; Sequence 33, Application US/10672932
; Publication No. US20050191702A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/10/672,932
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/948,004
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-10-672-932-33

Query Match 86.0%; Score 80; DB 5; Length 19;
Best Local Similarity 88.2%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MIHPSDSETRYNOKFKD 17
Db 2 MIHPSDSETRYNOKFKD 18

RESULT 33
US-09-948-004-16
; Sequence 16, Application US/09948004
; Publication No. US20030017979A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in

; TITLE OF INVENTION: Immunological disorders
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-16

Query Match 86.0%; Score 80; DB 3; Length 117;
Best Local Similarity 88.2%; Pred. No. 6.3e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MIHPSDSETRYNOKFKD 17
Db 60 MIHPSDSETRYNOKFKD 76

RESULT 34
US-10-672-932-16
; Sequence 16, Application US/10672932
; Publication No. US20050191702A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/10/672,932
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/948,004
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-672-932-16

Query Match 86.0%; Score 80; DB 5; Length 117;
Best Local Similarity 88.2%; Pred. No. 6.3e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MIHPSDSETRYNOKFKD 17
Db 60 MIHPSDSETRYNOKFKD 76

RESULT 35
US-09-144-886-53
; Sequence 53, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-53

Query Match 86.0%; Score 80; DB 3; Length 125;
Best Local Similarity 88.2%; Pred. No. 6.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIHPSDETRYNOKFND 17
|||||:|||||
Db 50 MIHPSDETRLNOKFND 66

RESULT 36
US-10-632-706-50
; Sequence 50, Application US/10632706
; Publication No. US20040175355A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 50
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-50

Query Match 86.0%; Score 80; DB 4; Length 125;
Best Local Similarity 88.2%; Pred. No. 6.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIHPSDETRYNOKFND 17
|||||:|||||
Db 50 MIHPSDETRLNOKFND 66

RESULT 37
US-09-948-004-14
; Sequence 14, Application US/09948004
; Publication No. US20030017979A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-14

Query Match 86.0%; Score 80; DB 3; Length 138;
Best Local Similarity 88.2%; Pred. No. 7.5e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIHPSDETRYNOKFND 17
|||||:|||||
Db 69 MIHPSDETRLNOKFND 85

RESULT 38
US-10-672-932-14
; Sequence 14, Application US/10672932
; Publication No. US20050191702A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/10/672,932
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/948,004
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-672-932-14

Query Match 86.0%; Score 80; DB 5; Length 138;
Best Local Similarity 88.2%; Pred. No. 7.5e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIHPSDETRYNOKFND 17
|||||:|||||
Db 69 MIHPSDETRLNOKFND 85

RESULT 39
US-09-948-004-18
; Sequence 18, Application US/09948004
; Publication No. US20030017979A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/09/948,004
; CURRENT FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-948-004-18

Query Match 86.0%; Score 80; DB 3; Length 495;
Best Local Similarity 88.2%; Pred. No. 0.00031;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MIHPSDETRYNOKFND 17
|||||:|||||
Db 172 MIHPSDETRLNOKFND 188

RESULT 40
US-10-672-932-18
; Sequence 18, Application US/10672932
; Publication No. US20050191702A1
; GENERAL INFORMATION:
; APPLICANT: MACK, Matthias
; TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
; FILE REFERENCE: E 2411 EP
; CURRENT APPLICATION NUMBER: US/10/672,932
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/948,004
; PRIOR FILING DATE: 2001-09-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1


```

; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-61

Query Match          79.6%; Score 74; DB 5; Length 96;
Best Local Similarity 86.7%; Pred. No. 0.00047;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 IHPSDSETRYNOKFK 16
        |||||:|||||
        50 IHPSDSDTYNOKFK 64

RESULT 45
US-09-144-886-51
; Sequence 51, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-51

Query Match          79.6%; Score 74; DB 3; Length 125;
Best Local Similarity 76.5%; Pred. No. 0.00062;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 MIHPSDSETRYNOKFKD 17
        |||||:|||||
        50 MIHPSNSEIRFNOKFKD 66

Db      50 MIHPSNSEIRFNOKFKD 66

RESULT 46
US-10-632-706-48
; Sequence 48, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 125
; TYPE: PRT
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```

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-48

Query Match          79.6%; Score 74; DB 4; Length 125;
Best Local Similarity 76.5%; Pred. No. 0.00062;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 MIHPSDSETRYNOKFKD 17
        |||||:|||||
        50 MIHPSNSEIRFNOKFKD 66

Db      50 MIHPSNSEIRFNOKFKD 66

RESULT 47
US-10-727-737-28
; Sequence 28, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-10-727-737-28

Query Match          78.5%; Score 73; DB 4; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 MIHPSDSETRYNOKFKD 17
        |||||:|||||
        1 MIHPSASATAYNOKFKD 17

Db      1 MIHPSASATAYNOKFKD 17

RESULT 48
US-10-435-614-11
; Sequence 11, Application US/10435614
; Publication No. US20040005647A1
; GENERAL INFORMATION:
```

```
; APPLICANT: DENARDO, SALLY J.
; APPLICANT: WINTHROP, MICHELLE D.
; APPLICANT: DENARDO, GERALD L.
; TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING
; FILE REFERENCE: 309T-000220US
; CURRENT APPLICATION NUMBER: US/10/435,614
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/112,788
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/280,721
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-435-614-11
```

```
Query Match          78.5%; Score 73; DB 4; Length 118;
Best Local Similarity 82.4%; Pred. No. 0.00085;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 MHPDSESTRYNQKFD 17
        |||||||
        50 MIDPDSSETHYNQMFKD 66
```

```
RESULT 49
US-10-789-090-9
; Sequence 9, Application US/10789090
; Publication No. US2004023970A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Law, Debbie
; TITLE OF INVENTION: ANTIBODIES AGAINST SLC15A2 AND USES THEREOF
; FILE REFERENCE: 05882.0192.NPUS01
; CURRENT APPLICATION NUMBER: US/10/789,090
; CURRENT FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-789-090-9
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```
Query Match          78.5%; Score 73; DB 5; Length 118;
Best Local Similarity 82.4%; Pred. No. 0.00085;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 MHPDSESTRYNQKFD 17
        |||||||
        50 MIDPDSSETHYNQMFKD 66
```

```
RESULT 50
US-10-435-614-20
; Sequence 20, Application US/10435614
; Publication No. US20040005647A1
; GENERAL INFORMATION:
; APPLICANT: DENARDO, SALLY J.
; APPLICANT: WINTHROP, MICHELLE D.
; APPLICANT: DENARDO, GERALD L.
; TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING
; FILE REFERENCE: 309T-000220US
; CURRENT APPLICATION NUMBER: US/10/435,614
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/112,788
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/280,721
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 22
```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-435-614-20
```

```
Query Match          78.5%; Score 73; DB 4; Length 260;
Best Local Similarity 82.4%; Pred. No. 0.002;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 MHPDSESTRYNQKFD 17
        |||||||
        52 MIDPDSSETHYNQMFKD 68
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Search completed: January 17, 2006, 12:13:01
Job time : 83.6818 secs
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:59:34 ; Search time 5.66667 Seconds
(without alignments)
28.363 Million cell updates/sec

Title: US-10-665-658-11
Perfect score: 93
Sequence: 1 MHHSDESTRYNQKFD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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4: /cgn2_6/ptodata/2/pubppaa/ECT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	93	100.0	17	6	US-10-665-658-11 Sequence 11, Appl
2	93	100.0	17	6	US-10-665-658-32 Sequence 32, Appl
3	93	100.0	121	6	US-10-665-658-5 Sequence 5, Appl
4	93	100.0	121	7	US-11-107-028-50 Sequence 50, Appl
5	90	96.8	17	6	US-10-665-658-40 Sequence 40, Appl
6	90	96.8	17	6	US-10-665-658-42 Sequence 42, Appl
7	90	96.8	17	6	US-10-665-658-43 Sequence 43, Appl
8	89	95.7	17	6	US-10-665-658-44 Sequence 44, Appl
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10	87	93.5	17	6	US-10-665-658-45 Sequence 45, Appl
11	87	93.5	17	6	US-10-665-658-46 Sequence 46, Appl
12	87	93.5	17	6	US-10-665-658-47 Sequence 47, Appl
13	87	93.5	17	6	US-10-665-658-48 Sequence 48, Appl
14	87	93.5	17	6	US-10-665-658-49 Sequence 49, Appl
15	87	93.5	17	6	US-10-665-658-50 Sequence 50, Appl
16	85	91.4	17	6	US-10-665-658-41 Sequence 41, Appl
17	85	91.4	121	6	US-10-665-658-41 Sequence 41, Appl
18	85	91.4	121	7	US-11-107-028-52 Sequence 52, Appl
19	84	90.3	17	6	US-10-665-658-39 Sequence 39, Appl
20	83	89.2	17	6	US-10-665-658-38 Sequence 38, Appl
21	80	86.0	17	6	US-10-665-658-35 Sequence 35, Appl
22	80	86.0	17	6	US-10-665-658-37 Sequence 37, Appl
23	77	82.8	17	6	US-10-665-658-33 Sequence 33, Appl
24	73	78.5	17	6	US-10-665-658-34 Sequence 34, Appl
25	70	75.3	121	6	US-10-507-662-25 Sequence 25, Appl

26	70	75.3	121	6	US-10-507-662-26 Sequence 26, Appl
27	69	74.2	17	6	US-10-665-658-23 Sequence 23, Appl
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30	63	67.7	120	7	US-11-097-812-68 Sequence 68, Appl
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32	59	63.4	447	7	US-11-102-621-131 Sequence 131, Appl
33	59	63.4	447	7	US-11-102-621-132 Sequence 132, Appl
34	59	63.4	447	7	US-11-102-621-133 Sequence 133, Appl
35	59	63.4	447	7	US-11-102-621-134 Sequence 134, Appl
36	58	62.4	118	6	US-10-507-662-32 Sequence 32, Appl
37	58	62.4	248	6	US-10-512-184-36 Sequence 36, Appl
38	58	62.4	442	7	US-11-102-621-124 Sequence 124, Appl
39	58	62.4	442	7	US-11-102-621-125 Sequence 125, Appl
40	58	62.4	442	7	US-11-102-621-126 Sequence 126, Appl
41	58	62.4	442	7	US-11-102-621-127 Sequence 127, Appl
42	58	62.4	442	7	US-11-102-621-128 Sequence 128, Appl
43	58	62.4	446	7	US-11-102-621-119 Sequence 119, Appl
44	58	62.4	446	7	US-11-102-621-120 Sequence 120, Appl
45	58	62.4	446	7	US-11-102-621-121 Sequence 121, Appl
46	58	62.4	446	7	US-11-102-621-122 Sequence 122, Appl
47	58	62.4	446	7	US-11-102-621-123 Sequence 123, Appl
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49	57	61.3	119	7	US-11-221-900-10 Sequence 10, Appl
50	57	61.3	119	7	US-11-221-900-12 Sequence 12, Appl
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52	57	61.3	119	7	US-11-221-900-14 Sequence 14, Appl
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58	54	58.1	17	7	US-11-120-338-11 Sequence 11, Appl
59	54	58.1	17	7	US-11-106-820-11 Sequence 11, Appl
60	54	58.1	114	7	US-11-055-163-18 Sequence 18, Appl
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62	54	58.1	121	7	US-11-107-028-35 Sequence 35, Appl
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65	54	58.1	122	7	US-11-120-338-7 Sequence 7, Appl
66	54	58.1	122	7	US-11-120-338-8 Sequence 8, Appl
67	54	58.1	122	7	US-11-107-028-30 Sequence 30, Appl
68	54	58.1	122	7	US-11-107-028-39 Sequence 39, Appl
69	54	58.1	122	7	US-11-107-028-41 Sequence 41, Appl
70	54	58.1	122	7	US-11-106-820-7 Sequence 7, Appl
71	54	58.1	122	7	US-11-106-820-8 Sequence 8, Appl
72	54	58.1	253	7	US-11-106-820-20 Sequence 20, Appl
73	54	58.1	451	7	US-11-120-338-22 Sequence 22, Appl
74	54	58.1	452	7	US-11-120-338-14 Sequence 14, Appl
75	54	58.1	452	7	US-11-120-338-15 Sequence 15, Appl
76	54	58.1	452	7	US-11-107-028-32 Sequence 32, Appl
77	54	58.1	452	7	US-11-107-028-33 Sequence 33, Appl
78	54	58.1	452	7	US-11-106-820-26 Sequence 26, Appl
79	54	58.1	452	7	US-11-106-820-28 Sequence 28, Appl
80	54	58.1	471	7	US-11-106-820-25 Sequence 25, Appl
81	54	58.1	471	7	US-11-106-820-27 Sequence 27, Appl
82	53	57.0	17	6	US-10-932-334-2 Sequence 2, Appl
83	53	57.0	17	6	US-10-489-866-22 Sequence 22, Appl
84	53	57.0	17	7	US-11-069-834-6 Sequence 6, Appl
85	53	57.0	108	6	US-10-932-334-57 Sequence 57, Appl
86	53	57.0	108	6	US-11-097-812-27 Sequence 27, Appl
87	53	57.0	116	6	US-10-489-866-19 Sequence 19, Appl
88	53	57.0	116	6	US-11-097-812-19 Sequence 19, Appl
89	53	57.0	118	6	US-10-507-662-33 Sequence 33, Appl
90	53	57.0	123	6	US-10-932-334-87 Sequence 87, Appl
91	53	57.0	124	6	US-10-932-334-7 Sequence 7, Appl
92	53	57.0	124	6	US-10-932-334-70 Sequence 70, Appl
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94	53	57.0	135	6	US-10-489-866-28 Sequence 28, Appl
95	53	57.0	143	6	US-10-932-334-52 Sequence 52, Appl
96	53	57.0	245	7	US-11-054-515-1902 Sequence 1902, Ap
97	53	57.0	247	7	US-11-084-717-21 Sequence 21, Appl
98	53	57.0	247	7	US-11-179-244-21 Sequence 21, Appl

99	53	57.0	543	6	US-10-495-664-3	Sequence 3, Appl1	172	48	51.6	251	7	US-11-054-515-1066	Sequence 1066, Ap
100	52	55.9	119	7	US-11-054-669-13	Sequence 123, App	173	48	51.6	251	7	US-11-054-515-1067	Sequence 1067, Ap
101	52	55.9	122	6	US-10-932-334-73	Sequence 73, Appl	174	48	51.6	251	7	US-11-054-515-1080	Sequence 1080, Ap
102	52	55.9	123	6	US-10-932-334-88	Sequence 88, Appl	175	48	51.6	251	7	US-11-054-515-1081	Sequence 1081, Ap
103	52	55.9	123	6	US-10-932-334-92	Sequence 92, Appl	176	48	51.6	251	7	US-11-054-515-1083	Sequence 1083, Ap
104	52	55.9	124	6	US-10-932-334-13	Sequence 13, Appl	177	48	51.6	251	7	US-11-102-621-136	Sequence 136, App
105	51	54.8	17	7	US-11-120-338-20	Sequence 20, Appl	178	48	51.6	446	7	US-11-102-621-137	Sequence 137, App
106	51	54.8	116	7	US-11-055-163-17	Sequence 17, Appl	179	48	51.6	446	7	US-11-102-621-138	Sequence 138, App
107	51	54.8	117	6	US-10-932-334-76	Sequence 76, Appl	180	48	51.6	446	7	US-11-102-621-139	Sequence 139, App
108	51	54.8	117	6	US-11-149-943-61	Sequence 61, Appl	181	48	51.6	446	7	US-11-102-621-140	Sequence 140, App
109	51	54.8	118	6	US-10-507-662-35	Sequence 35, Appl	182	47	50.5	111	7	US-11-097-812-205	Sequence 205, App
110	51	54.8	120	7	US-11-097-812-18	Sequence 18, Appl	183	47	50.5	120	6	US-10-932-334-71	Sequence 71, Appl
111	51	54.8	122	7	US-11-120-338-24	Sequence 24, Appl	184	47	50.5	120	6	US-10-932-334-72	Sequence 72, Appl
112	51	54.8	123	7	US-11-112-240-14	Sequence 14, Appl	185	47	50.5	247	7	US-11-054-515-3240	Sequence 3240, Ap
113	51	54.8	123	7	US-11-112-304A-14	Sequence 14, Appl	186	47	50.5	251	7	US-11-054-515-871	Sequence 871, App
114	51	54.8	451	7	US-11-120-338-25	Sequence 25, Appl	187	46	49.5	116	7	US-11-097-812-21	Sequence 31, Appl
115	51	54.8	452	7	US-11-120-338-17	Sequence 17, Appl	188	46	49.5	247	7	US-11-054-515-2103	Sequence 2103, Ap
116	51	54.8	452	7	US-11-107-028-43	Sequence 43, Appl	189	46	49.5	249	7	US-11-054-515-1891	Sequence 1891, Ap
117	51	54.8	452	7	US-11-107-028-45	Sequence 45, Appl	190	45	48.4	114	7	US-11-102-743-9	Sequence 9, Appl1
118	51	54.8	452	7	US-11-107-028-46	Sequence 46, Appl	191	45	48.4	116	7	US-11-096-074-50	Sequence 50, Appl
119	51	54.8	452	7	US-11-107-028-47	Sequence 47, Appl	192	45	48.4	116	7	US-11-096-822-50	Sequence 50, Appl
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121	51	54.8	452	7	US-11-106-820-45	Sequence 45, Appl	194	45	48.4	247	7	US-11-084-717-25	Sequence 25, Appl
122	50	53.8	17	7	US-11-051-453-76	Sequence 76, Appl	195	45	48.4	247	7	US-11-179-244-23	Sequence 23, Appl
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124	50	53.8	98	7	US-11-054-669-45	Sequence 45, Appl	197	45	48.4	247	7	US-11-179-244-35	Sequence 35, Appl
125	50	53.8	98	7	US-11-084-554-56	Sequence 56, Appl	198	44	47.3	17	6	US-10-502-145-30	Sequence 30, Appl
126	50	53.8	98	7	US-11-051-453-81	Sequence 81, Appl	199	44	47.3	17	7	US-11-009-939-14	Sequence 14, Appl
127	50	53.8	98	7	US-11-061-848-24	Sequence 24, Appl	200	44	47.3	17	7	US-11-193-512-41	Sequence 41, Appl
128	50	53.8	114	7	US-11-065-943-47	Sequence 47, Appl	201	44	47.3	17	7	US-11-051-453-64	Sequence 64, Appl
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130	50	53.8	118	6	US-11-112-240-26	Sequence 26, Appl	203	44	47.3	119	7	US-11-051-453-54	Sequence 54, Appl
131	50	53.8	118	7	US-11-112-304A-26	Sequence 26, Appl	204	44	47.3	121	6	US-10-502-145-17	Sequence 17, Appl
132	50	53.8	119	6	US-10-834-397-26	Sequence 26, Appl	205	44	47.3	121	6	US-10-932-334-81	Sequence 81, Appl
133	50	53.8	120	6	US-10-834-397-40	Sequence 40, Appl	206	44	47.3	138	7	US-11-051-453-56	Sequence 56, Appl
134	50	53.8	120	6	US-10-834-397-67	Sequence 67, Appl	207	44	47.3	140	7	US-11-193-512-27	Sequence 27, Appl
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137	50	53.8	258	7	US-11-054-515-1537	Sequence 1537, Ap	210	44	47.3	140	7	US-11-193-512-78	Sequence 78, Appl
138	50	53.8	474	7	US-11-000-463-284	Sequence 284, App	211	44	47.3	140	7	US-11-193-512-83	Sequence 83, Appl
139	49	52.7	17	6	US-10-507-662-51	Sequence 51, Appl	212	44	47.3	142	7	US-11-158-505-16	Sequence 36, Appl
140	49	52.7	17	6	US-10-880-238-119	Sequence 129, App	213	44	47.3	242	7	US-11-054-515-2084	Sequence 2084, Ap
141	49	52.7	17	7	US-11-108-135-2	Sequence 2, Appl1	214	44	47.3	246	7	US-11-054-515-2079	Sequence 2079, Ap
142	49	52.7	100	6	US-10-793-626-2550	Sequence 2550, Ap	215	44	47.3	251	7	US-11-054-515-1390	Sequence 1390, Ap
143	49	52.7	118	6	US-10-507-662-36	Sequence 36, Appl	216	43	46.2	17	6	US-10-839-799-116	Sequence 116, App
144	49	52.7	121	6	US-10-507-662-62	Sequence 62, Appl	217	43	46.2	17	7	US-11-105-268-2	Sequence 2, Appl1
145	49	52.7	121	7	US-11-108-135-24	Sequence 24, Appl	218	43	46.2	17	7	US-11-096-046-43	Sequence 43, Appl
146	49	52.7	121	7	US-11-108-135-28	Sequence 28, Appl	219	43	46.2	22	7	US-11-149-943-10	Sequence 10, Appl
147	49	52.7	138	7	US-11-089-872-3	Sequence 3, Appl1	220	43	46.2	98	7	US-11-054-669-11	Sequence 11, Appl
148	49	52.7	253	7	US-11-054-515-1418	Sequence 1418, Ap	221	43	46.2	117	6	US-10-839-799-132	Sequence 132, App
149	49	52.7	253	7	US-11-054-515-1672	Sequence 1672, Ap	222	43	46.2	119	7	US-11-105-268-21	Sequence 21, Appl
150	48	51.6	111	7	US-11-097-812-17	Sequence 17, Appl	223	43	46.2	136	6	US-10-839-799-29	Sequence 29, Appl
151	48	51.6	111	7	US-11-097-812-20	Sequence 20, Appl	224	43	46.2	136	6	US-10-839-799-99	Sequence 99, Appl
152	48	51.6	111	7	US-11-097-812-21	Sequence 21, Appl	225	43	46.2	248	7	US-11-054-515-1386	Sequence 1386, Ap
153	48	51.6	111	7	US-11-097-812-25	Sequence 25, Appl	226	43	46.2	248	7	US-11-054-515-1388	Sequence 1388, Ap
154	48	51.6	111	7	US-11-097-812-30	Sequence 30, Appl	227	43	46.2	249	7	US-11-054-515-918	Sequence 918, App
155	48	51.6	111	7	US-11-097-812-32	Sequence 32, Appl	228	43	46.2	249	7	US-11-054-515-926	Sequence 926, App
156	48	51.6	111	7	US-11-097-812-34	Sequence 34, Appl	229	43	46.2	251	7	US-11-054-515-1351	Sequence 1351, Ap
157	48	51.6	111	7	US-11-097-812-36	Sequence 36, Appl	230	43	46.2	251	7	US-11-054-515-1459	Sequence 1459, Ap
158	48	51.6	120	6	US-10-932-334-78	Sequence 78, Appl	231	43	46.2	269	6	US-10-839-799-109	Sequence 109, App
159	48	51.6	120	6	US-11-149-943-59	Sequence 59, Appl	232	43	46.2	448	7	US-11-158-505-8	Sequence 8, Appl1
160	48	51.6	249	7	US-11-054-515-950	Sequence 950, App	233	43	46.2	448	7	US-11-158-505-16	Sequence 16, Appl
161	48	51.6	249	7	US-11-054-515-1312	Sequence 1312, Ap	234	43	46.2	448	7	US-11-158-505-24	Sequence 24, Appl
162	48	51.6	251	7	US-11-054-515-840	Sequence 840, App	235	43	46.2	448	7	US-11-158-505-32	Sequence 32, Appl
163	48	51.6	251	7	US-11-054-515-874	Sequence 874, App	236	43	46.2	467	7	US-11-158-505-5	Sequence 5, Appl1
164	48	51.6	251	7	US-11-054-515-876	Sequence 876, App	237	43	46.2	467	7	US-11-158-505-7	Sequence 7, Appl1
165	48	51.6	251	7	US-11-054-515-1046	Sequence 1046, Ap	238	43	46.2	467	7	US-11-158-505-13	Sequence 13, Appl
166	48	51.6	251	7	US-11-054-515-1047	Sequence 1047, Ap	239	43	46.2	467	7	US-11-158-505-15	Sequence 15, Appl
167	48	51.6	251	7	US-11-054-515-1053	Sequence 1053, Ap	240	43	46.2	467	7	US-11-158-505-21	Sequence 21, Appl
168	48	51.6	251	7	US-11-054-515-1058	Sequence 1058, Ap	241	43	46.2	467	7	US-11-158-505-23	Sequence 23, Appl
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171	48	51.6	251	7	US-11-054-515-1063	Sequence 1063, Ap	244	43	46.2	467	7	US-11-158-505-72	Sequence 72, Appl

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246	43	46.2	695	7	US-11-096-046-26	Sequence 26, Appl	319	39	41.9	17	6	US-10-507-662-4	Sequence 27, Appl
247	42	45.2	17	7	US-11-105-268-10	Sequence 10, Appl	320	39	41.9	73	7	US-11-051-461-27	Sequence 27, Appl
248	42	45.2	22	7	US-11-149-943-5	Sequence 5, Appl	321	39	41.9	87	7	US-11-051-481-26	Sequence 26, Appl
249	42	45.2	22	7	US-11-149-943-7	Sequence 7, Appl	322	39	41.9	118	7	US-11-105-268-7	Sequence 7, Appl
250	42	45.2	98	7	US-11-054-669-5	Sequence 5, Appl	323	39	41.9	119	7	US-11-097-812-63	Sequence 63, Appl
251	42	45.2	98	7	US-11-054-669-7	Sequence 7, Appl	324	39	41.9	119	7	US-11-097-812-64	Sequence 64, Appl
252	42	45.2	98	7	US-11-084-554-17	Sequence 17, Appl	325	39	41.9	119	7	US-11-097-812-65	Sequence 65, Appl
253	42	45.2	98	7	US-11-084-554-20	Sequence 20, Appl	326	39	41.9	119	7	US-11-097-812-70	Sequence 70, Appl
254	42	45.2	98	7	US-11-061-848-18	Sequence 18, Appl	327	39	41.9	119	7	US-11-097-812-75	Sequence 75, Appl
255	42	45.2	118	6	US-10-932-334-75	Sequence 75, Appl	328	39	41.9	119	7	US-11-097-812-77	Sequence 77, Appl
256	42	45.2	118	7	US-11-112-240-10	Sequence 10, Appl	329	39	41.9	119	7	US-11-097-812-80	Sequence 80, Appl
257	42	45.2	118	7	US-11-112-240-10	Sequence 10, Appl	330	39	41.9	119	7	US-11-097-812-80	Sequence 80, Appl
258	42	45.2	120	6	US-10-932-334-77	Sequence 77, Appl	331	39	41.9	120	7	US-11-096-074-2	Sequence 2, Appl
259	42	45.2	120	6	US-10-932-334-79	Sequence 79, Appl	332	39	41.9	120	7	US-11-107-028-17	Sequence 17, Appl
260	42	45.2	120	7	US-11-105-268-15	Sequence 15, Appl	333	39	41.9	120	7	US-11-095-822-2	Sequence 2, Appl
261	42	45.2	120	7	US-11-105-268-17	Sequence 17, Appl	334	39	41.9	121	7	US-11-107-028-16	Sequence 16, Appl
262	42	45.2	125	7	US-11-096-074-58	Sequence 58, Appl	335	39	41.9	121	7	US-11-107-028-18	Sequence 18, Appl
263	42	45.2	125	7	US-11-095-822-58	Sequence 58, Appl	336	39	41.9	121	7	US-11-107-028-18	Sequence 18, Appl
264	42	45.2	243	7	US-11-054-515-1947	Sequence 1947, Ap	337	39	41.9	121	7	US-11-107-028-20	Sequence 20, Appl
265	42	45.2	245	7	US-11-054-515-1919	Sequence 1919, Ap	338	39	41.9	121	7	US-11-107-028-20	Sequence 20, Appl
266	42	45.2	245	7	US-11-054-515-1946	Sequence 1946, Ap	339	39	41.9	124	7	US-11-096-074-14	Sequence 14, Appl
267	42	45.2	247	7	US-11-054-515-1899	Sequence 1899, Ap	340	39	41.9	124	7	US-11-096-074-14	Sequence 14, Appl
268	42	45.2	247	7	US-11-054-515-2076	Sequence 2076, Ap	341	39	41.9	126	6	US-10-507-662-20	Sequence 20, Appl
269	42	45.2	248	6	US-10-512-184-32	Sequence 32, Appl	342	39	41.9	126	6	US-10-507-662-21	Sequence 20, Appl
270	42	45.2	248	7	US-11-054-515-1	Sequence 1, Appl	343	39	41.9	143	7	US-11-096-074-6	Sequence 6, Appl
271	42	45.2	248	7	US-11-054-515-1178	Sequence 1178, Ap	344	39	41.9	143	7	US-11-096-074-12	Sequence 12, Appl
272	42	45.2	248	7	US-11-054-515-2091	Sequence 2091, Ap	345	39	41.9	143	7	US-11-096-074-12	Sequence 12, Appl
273	42	45.2	249	7	US-11-106-820-16	Sequence 16, Appl	346	39	41.9	143	7	US-11-096-074-16	Sequence 16, Appl
274	42	45.2	249	7	US-11-054-515-1290	Sequence 1290, Ap	347	39	41.9	143	7	US-11-096-074-16	Sequence 16, Appl
275	42	45.2	250	7	US-11-054-515-1299	Sequence 1299, Ap	348	39	41.9	143	7	US-11-095-822-6	Sequence 6, Appl
276	42	45.2	250	7	US-11-054-515-2074	Sequence 2074, Ap	349	39	41.9	143	7	US-11-095-822-10	Sequence 10, Appl
277	42	45.2	252	7	US-11-054-515-1874	Sequence 1874, Ap	350	39	41.9	143	7	US-11-095-822-12	Sequence 12, Appl
278	42	45.2	252	7	US-11-054-515-1875	Sequence 1875, Ap	351	39	41.9	143	7	US-11-095-822-12	Sequence 12, Appl
279	42	45.2	253	7	US-11-054-515-1875	Sequence 1875, Ap	352	39	41.9	143	7	US-11-095-822-15	Sequence 15, Appl
280	42	45.2	254	7	US-11-054-515-1893	Sequence 1893, Ap	353	39	41.9	143	7	US-11-095-822-18	Sequence 18, Appl
281	42	45.2	254	7	US-11-054-515-1893	Sequence 1893, Ap	354	39	41.9	248	7	US-11-054-515-185	Sequence 1785, Ap
282	42	45.2	254	7	US-11-054-515-1961	Sequence 1961, Ap	355	39	41.9	249	7	US-11-054-515-1820	Sequence 1620, Ap
283	42	45.2	254	7	US-11-054-515-1983	Sequence 1983, Ap	356	39	41.9	251	7	US-11-054-515-1084	Sequence 1084, Ap
284	42	45.2	254	7	US-11-054-515-2082	Sequence 2082, Ap	357	39	41.9	251	7	US-11-054-515-1760	Sequence 1760, Ap
285	42	45.2	255	7	US-11-054-515-857	Sequence 857, Ap	358	39	41.9	252	7	US-11-054-515-1129	Sequence 1129, Ap
286	42	45.2	255	7	US-11-054-515-1156	Sequence 1156, Ap	359	39	41.9	252	7	US-11-054-515-1658	Sequence 1658, Ap
287	42	45.2	255	7	US-11-054-515-1849	Sequence 1849, Ap	360	39	41.9	253	7	US-11-054-515-1684	Sequence 1684, Ap
288	42	45.2	256	7	US-11-054-515-1967	Sequence 1967, Ap	361	39	41.9	255	7	US-11-054-515-2087	Sequence 2087, Ap
289	42	45.2	257	7	US-11-054-515-1596	Sequence 1596, Ap	362	39	41.9	256	7	US-11-054-515-8	Sequence 8, Appl
290	42	45.2	258	7	US-11-054-515-2090	Sequence 2090, Ap	363	39	41.9	256	7	US-11-054-515-1253	Sequence 1253, Ap
291	42	45.2	317	6	US-10-512-184-69	Sequence 69, Appl	364	39	41.9	256	7	US-11-054-515-1279	Sequence 1279, Ap
292	41	44.1	16	7	US-11-125-837-11	Sequence 11, Appl	365	39	41.9	260	7	US-11-054-515-1039	Sequence 1039, Ap
293	41	44.1	17	7	US-11-097-812-91	Sequence 91, Appl	366	39	41.9	293	7	US-11-116-939-10	Sequence 10, Appl
294	41	44.1	22	7	US-11-149-943-6	Sequence 6, Appl	367	39	41.9	412	7	US-11-116-939-11	Sequence 11, Appl
295	41	44.1	22	7	US-11-149-943-50	Sequence 50, Appl	368	39	41.9	824	7	US-11-116-939-11	Sequence 11, Appl
296	41	44.1	98	7	US-11-054-669-6	Sequence 6, Appl	369	38	40.9	17	6	US-10-507-662-52	Sequence 52, Appl
297	41	44.1	98	7	US-11-084-554-19	Sequence 19, Appl	370	38	40.9	17	6	US-10-507-662-52	Sequence 52, Appl
298	41	44.1	119	7	US-11-097-812-72	Sequence 72, Appl	371	38	40.9	17	6	US-10-880-238-107	Sequence 107, Appl
299	41	44.1	119	7	US-11-097-812-81	Sequence 81, Appl	372	38	40.9	22	7	US-11-096-046-22	Sequence 22, Appl
300	41	44.1	138	7	US-11-125-837-22	Sequence 22, Appl	373	38	40.9	17	6	US-11-149-943-1	Sequence 1, Appl
301	41	44.1	232	7	US-11-025-712-10	Sequence 10, Appl	374	38	40.9	98	7	US-11-054-669-1	Sequence 16, Appl
302	41	44.1	248	7	US-11-054-515-2088	Sequence 2088, Ap	375	38	40.9	98	7	US-11-084-554-16	Sequence 16, Appl
303	41	44.1	249	7	US-11-054-515-1957	Sequence 1957, Ap	376	38	40.9	117	7	US-11-054-669-120	Sequence 120, Appl
304	41	44.1	251	7	US-11-054-515-1380	Sequence 1380, Ap	377	38	40.9	120	6	US-10-507-662-61	Sequence 61, Appl
305	41	44.1	253	7	US-11-054-515-1358	Sequence 1358, Ap	378	38	40.9	120	6	US-10-834-397-36	Sequence 36, Appl
306	41	44.1	259	7	US-11-054-515-1567	Sequence 1567, Ap	379	38	40.9	120	6	US-10-834-397-59	Sequence 59, Appl
307	41	44.1	754	6	US-11-025-712-12	Sequence 12, Appl	380	38	40.9	124	7	US-11-040-159-8	Sequence 8, Appl
308	41	44.1	754	6	US-10-793-626-1296	Sequence 1296, Ap	381	38	40.9	124	7	US-11-096-046-2	Sequence 2, Appl
309	40	43.0	17	7	US-11-097-812-168	Sequence 168, Appl	382	38	40.9	124	7	US-11-096-046-4	Sequence 4, Appl
310	40	43.0	117	6	US-10-834-397-22	Sequence 22, Appl	383	38	40.9	125	7	US-11-096-074-57	Sequence 57, Appl
311	40	43.0	120	7	US-11-097-812-153	Sequence 153, Appl	384	38	40.9	125	7	US-11-095-822-57	Sequence 57, Appl
312	40	43.0	225	7	US-11-054-515-1451	Sequence 1451, Ap	385	38	40.9	238	7	US-11-054-515-1907	Sequence 1907, Ap
313	40	43.0	248	7	US-11-054-515-1361	Sequence 1361, Ap	386	38	40.9	241	7	US-11-054-515-1948	Sequence 1948, Ap
314	40	43.0	248	7	US-11-054-515-2094	Sequence 2094, Ap	387	38	40.9	241	7	US-11-054-515-2008	Sequence 2008, Ap
315	40	43.0	252	7	US-11-054-515-1646	Sequence 1646, Ap	388	38	40.9	241	7	US-11-054-515-2032	Sequence 2032, Ap
316	40	43.0	252	7	US-11-054-515-1695	Sequence 1695, Ap	389	38	40.9	242	7	US-11-054-515-2021	Sequence 2021, Ap
317	40	43.0	254	7	US-11-054-515-1001	Sequence 1001, Ap	390	38	40.9	242	7	US-11-054-515-2046	Sequence 2046, Ap

391	38	40.9	242	7	US-11-054-515-2106	Sequence 2106, Ap	464	37	39.8	256	7	US-11-054-515-1621	Sequence 1621, Ap
392	38	40.9	243	7	US-11-054-515-2009	Sequence 2009, Ap	465	37	39.8	562	7	US-11-065-943-36	Sequence 36, Appl
393	38	40.9	243	7	US-11-054-515-2012	Sequence 2012, Ap	466	36	38.7	17	6	US-10-507-662-46	Sequence 46, Appl
394	38	40.9	243	7	US-11-054-515-2014	Sequence 2014, Ap	467	36	38.7	73	7	US-11-051-481-31	Sequence 31, Appl
395	38	40.9	243	7	US-11-054-515-2063	Sequence 2063, Ap	468	36	38.7	87	7	US-11-051-481-30	Sequence 30, Appl
396	38	40.9	243	7	US-11-054-515-2107	Sequence 2107, Ap	469	36	38.7	115	6	US-10-932-334-80	Sequence 80, Appl
397	38	40.9	243	7	US-11-054-515-2109	Sequence 2109, Ap	470	36	38.7	121	7	US-11-096-074-60	Sequence 60, Appl
398	38	40.9	244	7	US-11-054-515-1908	Sequence 1908, Ap	471	36	38.7	121	7	US-11-095-822-60	Sequence 60, Appl
399	38	40.9	244	7	US-11-054-515-2011	Sequence 2011, Ap	472	36	38.7	123	7	US-11-096-074-56	Sequence 56, Appl
400	38	40.9	244	7	US-11-054-515-2026	Sequence 2026, Ap	473	36	38.7	124	7	US-11-107-028-10	Sequence 10, Appl
401	38	40.9	244	7	US-11-054-515-2037	Sequence 2037, Ap	474	36	38.7	124	7	US-11-107-028-11	Sequence 11, Appl
402	38	40.9	245	7	US-11-054-515-1714	Sequence 1714, Ap	475	36	38.7	124	7	US-11-107-028-12	Sequence 12, Appl
403	38	40.9	245	7	US-11-054-515-1950	Sequence 1950, Ap	476	36	38.7	124	7	US-11-107-028-17	Sequence 17, Appl
404	38	40.9	245	7	US-11-054-515-2004	Sequence 2004, Ap	477	36	38.7	126	6	US-10-507-662-19	Sequence 19, Appl
405	38	40.9	245	7	US-11-054-515-2042	Sequence 2042, Ap	478	36	38.7	248	7	US-11-054-515-0071	Sequence 1011, Ap
406	38	40.9	245	7	US-11-054-515-2116	Sequence 2116, Ap	479	36	38.7	249	7	US-11-054-515-1730	Sequence 1730, Ap
407	38	40.9	247	7	US-11-054-515-1729	Sequence 1729, Ap	480	36	38.7	250	7	US-11-054-515-1370	Sequence 1370, Ap
408	38	40.9	248	7	US-11-054-515-1721	Sequence 1721, Ap	481	36	38.7	251	7	US-11-054-515-311	Sequence 311, App
409	38	40.9	249	7	US-11-054-515-1635	Sequence 1635, Ap	482	36	38.7	251	7	US-11-054-515-1059	Sequence 1059, Ap
410	38	40.9	249	7	US-11-054-515-1970	Sequence 1970, Ap	483	36	38.7	251	7	US-11-054-515-1592	Sequence 1592, Ap
411	38	40.9	250	7	US-11-054-515-1722	Sequence 1722, Ap	484	36	38.7	253	7	US-11-054-515-1895	Sequence 1895, Ap
412	38	40.9	250	7	US-11-054-515-1723	Sequence 1723, Ap	485	36	38.7	253	7	US-11-054-515-1951	Sequence 1951, Ap
413	38	40.9	251	7	US-11-054-515-254	Sequence 254, App	486	36	38.7	253	7	US-11-054-515-2098	Sequence 2098, Ap
414	38	40.9	251	7	US-11-054-515-271	Sequence 271, App	487	36	38.7	253	7	US-11-054-515-2101	Sequence 2101, Ap
415	38	40.9	251	7	US-11-054-515-945	Sequence 945, App	488	36	38.7	254	7	US-11-054-515-673	Sequence 673, App
416	38	40.9	251	7	US-11-054-515-1688	Sequence 1688, Ap	489	36	38.7	254	7	US-11-054-515-888	Sequence 888, App
417	38	40.9	251	7	US-11-054-515-1776	Sequence 1776, Ap	490	36	38.7	254	7	US-11-054-515-1087	Sequence 1087, Ap
418	38	40.9	251	7	US-11-054-515-1806	Sequence 1806, Ap	491	36	38.7	254	7	US-11-054-515-1087	Sequence 1087, Ap
419	38	40.9	253	7	US-11-054-515-1936	Sequence 1936, Ap	492	36	38.7	254	7	US-11-054-515-1088	Sequence 1088, Ap
420	38	40.9	253	7	US-11-054-515-1301	Sequence 1301, Ap	493	36	38.7	452	7	US-11-166-284-79	Sequence 79, Appl
421	38	40.9	256	7	US-11-054-515-1640	Sequence 1640, Ap	494	35	38.2	1095	6	US-10-793-626-3154	Sequence 3154, Ap
422	38	40.9	654	7	US-11-046-668-4	Sequence 4, Appli	495	35	37.6	22	7	US-11-149-943-3	Sequence 3, Appli
423	38	40.9	654	7	US-11-046-668-27	Sequence 27, Appl	496	35	37.6	98	7	US-10-467-657-3320	Sequence 4350, Ap
424	38	40.9	666	7	US-11-096-046-25	Sequence 25, Appl	497	35	37.6	99	7	US-11-054-669-93	Sequence 23, Appli
425	38	40.9	667	7	US-11-096-046-25	Sequence 28, Appl	498	35	37.6	119	6	US-10-477-980-2	Sequence 2, Appli
426	38	40.9	667	7	US-11-096-046-28	Sequence 29, Appl	499	35	37.6	236	7	US-11-086-289-4	Sequence 4, Appli
427	38	40.9	667	7	US-11-096-046-29	Sequence 30, Appl	500	35	37.6	241	7	US-11-054-515-2031	Sequence 2031, Ap
428	38	40.9	683	7	US-11-046-668-2	Sequence 2, Appli	501	35	37.6	243	7	US-11-054-515-1927	Sequence 1927, Ap
429	38	40.9	17	7	US-11-173-071-6	Sequence 6, Appli	502	35	37.6	246	7	US-11-054-515-1691	Sequence 1691, Ap
430	37	39.8	17	7	US-11-097-812-94	Sequence 94, Appl	503	35	37.6	247	7	US-11-054-515-948	Sequence 948, App
431	37	39.8	17	7	US-11-097-812-162	Sequence 162, App	504	35	37.6	247	7	US-11-054-515-111	Sequence 111, App
432	37	39.8	22	7	US-11-149-943-2	Sequence 2, Appli	505	35	37.6	249	7	US-11-054-515-919	Sequence 919, App
433	37	39.8	98	7	US-11-054-669-2	Sequence 2, Appli	506	35	37.6	250	7	US-11-054-515-54	Sequence 54, Appl
434	37	39.8	117	7	US-11-054-669-119	Sequence 119, App	507	35	37.6	250	7	US-11-054-515-58	Sequence 58, Appl
435	37	39.8	119	6	US-10-507-662-22	Sequence 22, Appl	508	35	37.6	250	7	US-11-054-515-50	Sequence 50, Appl
436	37	39.8	119	7	US-11-054-669-124	Sequence 124, App	509	35	37.6	250	7	US-11-054-515-59	Sequence 59, Appl
437	37	39.8	119	7	US-11-097-812-71	Sequence 71, App	510	35	37.6	250	7	US-11-054-515-51	Sequence 51, Appl
438	37	39.8	119	7	US-11-097-812-73	Sequence 73, Appl	511	35	37.6	250	7	US-11-054-515-52	Sequence 52, Appl
439	37	39.8	119	7	US-11-097-812-74	Sequence 74, Appl	512	35	37.6	250	7	US-11-054-515-53	Sequence 53, Appl
440	37	39.8	119	7	US-11-097-812-76	Sequence 76, Appl	513	35	37.6	250	7	US-11-054-515-54	Sequence 54, Appl
441	37	39.8	120	7	US-11-173-071-2	Sequence 2, Appli	514	35	37.6	250	7	US-11-054-515-56	Sequence 56, Appl
442	37	39.8	120	7	US-11-096-074-59	Sequence 59, Appl	515	35	37.6	250	7	US-11-054-515-57	Sequence 57, Appl
443	37	39.8	120	7	US-11-097-812-135	Sequence 135, App	516	35	37.6	250	7	US-11-054-515-58	Sequence 58, Appl
444	37	39.8	120	7	US-11-097-812-143	Sequence 143, App	517	35	37.6	250	7	US-11-054-515-59	Sequence 59, Appl
445	37	39.8	120	7	US-11-097-812-144	Sequence 144, App	518	35	37.6	250	7	US-11-054-515-62	Sequence 62, Appl
446	37	39.8	120	7	US-11-095-822-59	Sequence 59, Appl	519	35	37.6	250	7	US-11-054-515-63	Sequence 63, Appl
447	37	39.8	128	7	US-11-173-071-12	Sequence 12, Appl	520	35	37.6	250	7	US-11-054-515-66	Sequence 66, Appl
448	37	39.8	128	7	US-11-173-071-14	Sequence 14, Appl	521	35	37.6	250	7	US-11-054-515-69	Sequence 69, Appl
449	37	39.8	128	7	US-11-054-515-1896	Sequence 1896, Ap	522	35	37.6	250	7	US-11-054-515-73	Sequence 73, Appl
450	37	39.8	128	7	US-11-054-515-2089	Sequence 2089, Ap	523	35	37.6	250	7	US-11-054-515-74	Sequence 74, Appl
451	37	39.8	128	7	US-11-054-515-1328	Sequence 1328, Ap	524	35	37.6	250	7	US-11-054-515-75	Sequence 75, Appl
452	37	39.8	248	7	US-11-054-515-959	Sequence 959, App	525	35	37.6	250	7	US-11-054-515-76	Sequence 76, Appl
453	37	39.8	248	7	US-11-054-515-1331	Sequence 1331, Ap	526	35	37.6	250	7	US-11-054-515-77	Sequence 77, Appl
454	37	39.8	249	7	US-11-054-515-2033	Sequence 2033, Ap	527	35	37.6	250	7	US-11-054-515-78	Sequence 78, Appl
455	37	39.8	250	7	US-11-054-515-932	Sequence 932, App	528	35	37.6	250	7	US-11-054-515-80	Sequence 80, Appl
456	37	39.8	250	7	US-11-054-515-2093	Sequence 2093, App	529	35	37.6	250	7	US-11-054-515-81	Sequence 81, Appl
457	37	39.8	250	7	US-11-054-515-2097	Sequence 2097, App	530	35	37.6	250	7	US-11-054-515-100	Sequence 100, App
458	37	39.8	251	7	US-11-054-515-960	Sequence 960, App	531	35	37.6	250	7	US-11-054-515-107	Sequence 107, App
459	37	39.8	251	7	US-11-054-515-1005	Sequence 1005, Ap	532	35	37.6	250	7	US-11-054-515-110	Sequence 110, App
460	37	39.8	251	7	US-11-054-515-1071	Sequence 1071, Ap	533	35	37.6	251	7	US-11-054-515-9	Sequence 9, Appli
461	37	39.8	251	7	US-11-054-515-1336	Sequence 1336, Ap	534	35	37.6	251	7	US-11-054-515-10	Sequence 10, Appl
462	37	39.8	251	7	US-11-054-515-2001	Sequence 2001, Ap	535	35	37.6	251	7	US-11-054-515-11	Sequence 11, Appl
463	37	39.8	252	7	US-11-054-515-1698	Sequence 1698, Ap	536	35	37.6	251	7	US-11-054-515-12	Sequence 12, Appl

537	35	37.6	251	7	US-11-054-515-13	Sequence 13, App1	610	35	37.6	251	7	US-11-054-515-119	Sequence 119, App
538	35	37.6	251	7	US-11-054-515-14	Sequence 14, App1	611	35	37.6	251	7	US-11-054-515-120	Sequence 120, App
539	35	37.6	251	7	US-11-054-515-15	Sequence 15, App1	612	35	37.6	251	7	US-11-054-515-121	Sequence 121, App
540	35	37.6	251	7	US-11-054-515-16	Sequence 16, App1	613	35	37.6	251	7	US-11-054-515-122	Sequence 122, App
541	35	37.6	251	7	US-11-054-515-17	Sequence 17, App1	614	35	37.6	251	7	US-11-054-515-123	Sequence 123, App
542	35	37.6	251	7	US-11-054-515-18	Sequence 18, App1	615	35	37.6	251	7	US-11-054-515-125	Sequence 125, App
543	35	37.6	251	7	US-11-054-515-19	Sequence 19, App1	616	35	37.6	251	7	US-11-054-515-126	Sequence 126, App
544	35	37.6	251	7	US-11-054-515-20	Sequence 20, App1	617	35	37.6	251	7	US-11-054-515-127	Sequence 127, App
545	35	37.6	251	7	US-11-054-515-21	Sequence 21, App1	618	35	37.6	251	7	US-11-054-515-128	Sequence 128, App
546	35	37.6	251	7	US-11-054-515-22	Sequence 22, App1	619	35	37.6	251	7	US-11-054-515-129	Sequence 129, App
547	35	37.6	251	7	US-11-054-515-23	Sequence 23, App1	620	35	37.6	251	7	US-11-054-515-130	Sequence 130, App
548	35	37.6	251	7	US-11-054-515-24	Sequence 24, App1	621	35	37.6	251	7	US-11-054-515-131	Sequence 131, App
549	35	37.6	251	7	US-11-054-515-25	Sequence 25, App1	622	35	37.6	251	7	US-11-054-515-132	Sequence 132, App
550	35	37.6	251	7	US-11-054-515-26	Sequence 26, App1	623	35	37.6	251	7	US-11-054-515-133	Sequence 133, App
551	35	37.6	251	7	US-11-054-515-27	Sequence 27, App1	624	35	37.6	251	7	US-11-054-515-134	Sequence 134, App
552	35	37.6	251	7	US-11-054-515-28	Sequence 28, App1	625	35	37.6	251	7	US-11-054-515-135	Sequence 135, App
553	35	37.6	251	7	US-11-054-515-29	Sequence 29, App1	626	35	37.6	251	7	US-11-054-515-136	Sequence 136, App
554	35	37.6	251	7	US-11-054-515-30	Sequence 30, App1	627	35	37.6	251	7	US-11-054-515-137	Sequence 137, App
555	35	37.6	251	7	US-11-054-515-31	Sequence 31, App1	628	35	37.6	251	7	US-11-054-515-138	Sequence 138, App
556	35	37.6	251	7	US-11-054-515-32	Sequence 32, App1	629	35	37.6	251	7	US-11-054-515-139	Sequence 139, App
557	35	37.6	251	7	US-11-054-515-33	Sequence 33, App1	630	35	37.6	251	7	US-11-054-515-141	Sequence 141, App
558	35	37.6	251	7	US-11-054-515-34	Sequence 34, App1	631	35	37.6	251	7	US-11-054-515-142	Sequence 142, App
559	35	37.6	251	7	US-11-054-515-35	Sequence 35, App1	632	35	37.6	251	7	US-11-054-515-143	Sequence 143, App
560	35	37.6	251	7	US-11-054-515-36	Sequence 36, App1	633	35	37.6	251	7	US-11-054-515-144	Sequence 144, App
561	35	37.6	251	7	US-11-054-515-37	Sequence 37, App1	634	35	37.6	251	7	US-11-054-515-145	Sequence 145, App
562	35	37.6	251	7	US-11-054-515-38	Sequence 38, App1	635	35	37.6	251	7	US-11-054-515-146	Sequence 146, App
563	35	37.6	251	7	US-11-054-515-39	Sequence 39, App1	636	35	37.6	251	7	US-11-054-515-147	Sequence 147, App
564	35	37.6	251	7	US-11-054-515-40	Sequence 40, App1	637	35	37.6	251	7	US-11-054-515-148	Sequence 148, App
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684	35	37.6	251	7	US-11-054-515-197	Sequence 197, App	756	35	37.6	251	7	US-11-054-515-276	Sequence 276, App
685	35	37.6	251	7	US-11-054-515-198	Sequence 198, App	757	35	37.6	251	7	US-11-054-515-277	Sequence 277, App
686	35	37.6	251	7	US-11-054-515-199	Sequence 199, App	758	35	37.6	251	7	US-11-054-515-278	Sequence 278, App
687	35	37.6	251	7	US-11-054-515-200	Sequence 200, App	759	35	37.6	251	7	US-11-054-515-279	Sequence 279, App
688	35	37.6	251	7	US-11-054-515-201	Sequence 201, App	760	35	37.6	251	7	US-11-054-515-280	Sequence 280, App
689	35	37.6	251	7	US-11-054-515-202	Sequence 202, App	761	35	37.6	251	7	US-11-054-515-281	Sequence 281, App
690	35	37.6	251	7	US-11-054-515-203	Sequence 203, App	762	35	37.6	251	7	US-11-054-515-282	Sequence 282, App
691	35	37.6	251	7	US-11-054-515-204	Sequence 204, App	763	35	37.6	251	7	US-11-054-515-283	Sequence 283, App
692	35	37.6	251	7	US-11-054-515-205	Sequence 205, App	764	35	37.6	251	7	US-11-054-515-284	Sequence 284, App
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698	35	37.6	251	7	US-11-054-515-211	Sequence 211, App	770	35	37.6	251	7	US-11-054-515-290	Sequence 290, App
699	35	37.6	251	7	US-11-054-515-212	Sequence 212, App	771	35	37.6	251	7	US-11-054-515-291	Sequence 291, App
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701	35	37.6	251	7	US-11-054-515-214	Sequence 214, App	773	35	37.6	251	7	US-11-054-515-293	Sequence 293, App
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708	35	37.6	251	7	US-11-054-515-221	Sequence 221, App	780	35	37.6	251	7	US-11-054-515-300	Sequence 300, App
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710	35	37.6	251	7	US-11-054-515-223	Sequence 223, App	782	35	37.6	251	7	US-11-054-515-302	Sequence 302, App
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831	34	36.6	17	6	US-10-880-238-111	Sequence 11, App	904	33	35.5	248	7	US-11-054-515-1668	Sequence 1668, Ap
832	34	36.6	17	6	US-10-880-238-113	Sequence 113, App	905	33	35.5	248	7	US-11-054-515-1670	Sequence 1670, Ap
833	34	36.6	17	7	US-11-097-812-93	Sequence 93, Appl	906	33	35.5	248	7	US-11-054-515-1679	Sequence 1679, Ap
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836	34	36.6	109	6	US-10-771-257-26	Sequence 26, Appl	909	33	35.5	248	7	US-11-054-515-1823	Sequence 1823, Ap
837	34	36.6	109	7	US-11-127-677-26	Sequence 26, Appl	910	33	35.5	250	7	US-11-054-515-859	Sequence 859, App
838	34	36.6	119	7	US-11-097-812-66	Sequence 66, Appl	911	33	35.5	250	7	US-11-054-515-1484	Sequence 1484, Ap
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845	34	36.6	125	7	US-11-054-515-1943	Sequence 1943, Ap	918	33	35.5	251	7	US-11-054-515-883	Sequence 883, App
846	34	36.6	243	7	US-11-054-515-2064	Sequence 2064, Ap	919	33	35.5	251	7	US-11-054-515-885	Sequence 885, App
847	34	36.6	246	7	US-11-054-515-1996	Sequence 1996, Ap	920	33	35.5	251	7	US-11-054-515-875	Sequence 875, App
848	34	36.6	248	6	US-10-454-437-364	Sequence 364, App	921	33	35.5	251	7	US-11-054-515-879	Sequence 879, App
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851	34	36.6	248	7	US-11-054-515-1700	Sequence 1700, Ap	924	33	35.5	251	7	US-11-054-515-887	Sequence 887, App
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855	34	36.6	249	7	US-11-054-515-2085	Sequence 2085, Ap	928	33	35.5	251	7	US-11-054-515-962	Sequence 962, App
856	34	36.6	249	7	US-11-054-515-2150	Sequence 2120, Ap	929	33	35.5	251	7	US-11-054-515-968	Sequence 968, App
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859	34	36.6	254	7	US-11-054-515-1807	Sequence 1807, Ap	932	33	35.5	251	7	US-11-054-515-986	Sequence 986, App
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863	34	36.6	401	6	US-10-641-678-33	Sequence 33, Appl	936	33	35.5	251	7	US-11-054-515-1057	Sequence 1057, Ap
864	34	36.6	405	6	US-10-517-939-132	Sequence 132, App	937	33	35.5	251	7	US-11-054-515-1062	Sequence 1062, Ap
865	34	36.6	638	6	US-10-793-626-1468	Sequence 1468, Ap	938	33	35.5	251	7	US-11-054-515-1064	Sequence 1064, Ap
866	34	36.6	677	6	US-10-982-545-12	Sequence 12, Appl	939	33	35.5	251	7	US-11-054-515-1068	Sequence 1068, Ap
867	34	36.6	993	7	US-11-132-764-7	Sequence 7, Appl	940	33	35.5	251	7	US-11-054-515-1072	Sequence 1072, Ap
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869	33	35.5	107	7	US-11-105-268-16	Sequence 16, Appl	942	33	35.5	251	7	US-11-054-515-1074	Sequence 1074, Ap
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871	33	35.5	109	7	US-11-041-471-8	Sequence 8, Appl	944	33	35.5	251	7	US-11-054-515-1077	Sequence 1077, Ap
872	33	35.5	120	7	US-11-195-585-5	Sequence 5, Appl	945	33	35.5	251	7	US-11-054-515-1078	Sequence 1078, Ap
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874	33	35.5	122	7	US-11-105-268-29	Sequence 29, Appl	947	33	35.5	251	7	US-11-054-515-1085	Sequence 1085, Ap
875	33	35.5	129	7	US-11-051-453-52	Sequence 52, Appl	948	33	35.5	251	7	US-11-054-515-1086	Sequence 1086, Ap
876	33	35.5	132	7	US-11-100-338-51	Sequence 51, Appl	949	33	35.5	251	7	US-11-054-515-1103	Sequence 1103, Ap
877	33	35.5	145	6	US-10-721-763-29	Sequence 29, Appl	950	33	35.5	251	7	US-11-054-515-1106	Sequence 1106, Ap
878	33	35.5	152	7	US-11-128-900-18	Sequence 18, Appl	951	33	35.5	251	7	US-11-054-515-1107	Sequence 1107, Ap
879	33	35.5	152	7	US-11-128-900-95	Sequence 95, Appl	952	33	35.5	251	7	US-11-054-515-1133	Sequence 1133, Ap
880	33	35.5	232	7	US-11-173-564-2	Sequence 2, Appl	953	33	35.5	251	7	US-11-054-515-1143	Sequence 1143, Ap
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883	33	35.5	247	7	US-11-054-515-1903	Sequence 1903, Ap	956	33	35.5	251	7	US-11-054-515-1172	Sequence 1172, Ap
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885	33	35.5	248	7	US-11-054-515-877	Sequence 877, App	958	33	35.5	251	7	US-11-054-515-1187	Sequence 1187, Ap
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887	33	35.5	248	7	US-11-054-515-965	Sequence 965, App	960	33	35.5	251	7	US-11-054-515-1338	Sequence 1338, Ap
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889	33	35.5	248	7	US-11-054-515-984	Sequence 984, App	962	33	35.5	251	7	US-11-054-515-1343	Sequence 1343, Ap
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891	33	35.5	248	7	US-11-054-515-1181	Sequence 1181, Ap	964	33	35.5	251	7	US-11-054-515-1355	Sequence 1355, Ap
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ALIGNMENTS

RESULT 1

US-10-665-658-11

Sequence 11, Application US/10665658

Publication No. US20050276801A1

GENERAL INFORMATION:

APPLICANT: Jardiou, Paula M.

Presta, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658

FILING DATE: 19-Sep-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971

FILING DATE: 27-NOV-1996

APPLICATION NUMBER: 08/974899

FILING DATE: 20-NOV-1997

APPLICATION NUMBER: 09/420745

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APPLICATION NUMBER: 09/975798

FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:

NAME: Tan, Lee K.

REGISTRATION NUMBER: 39,447

REFERENCE/DOCKET NUMBER: P1014R1C1D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-4462

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-665-658-11

Query Match 100.0%; Score 93; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIHPSDSTRYNOKFXD 17
|||||
Db 1 MIHPSDSTRYNOKFXD 17

RESULT 2

US-10-665-658-32

Sequence 32, Application US/10665658

Publication No. US20050276801A1

GENERAL INFORMATION:

APPLICANT: Jardiou, Paula M.

Presta, Leonard G.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

NUMBER OF SEQUENCES: 71

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ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658

FILING DATE: 19-Sep-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971

FILING DATE: 27-NOV-1996

APPLICATION NUMBER: 08/974899

FILING DATE: 20-NOV-1997

APPLICATION NUMBER: 09/420745

FILING DATE: 20-OCT-1999

APPLICATION NUMBER: 09/975798

FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:

NAME: Tan, Lee K.

REGISTRATION NUMBER: 39,447

REFERENCE/DOCKET NUMBER: P1014R1C1D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-4462

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: Amino Acid

TOPOLOGY: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-10-665-658-32

Query Match 100.0%; Score 93; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIHPSDSTRYNOKFXD 17
|||||
Db 1 MIHPSDSTRYNOKFXD 17

RESULT 3
US-10-665-658-5
Sequence 5, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-665-658-5
Query Match 100.0%; Score 93; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MIHPSDETRYNOKFXD 17
|||||
Db 50 MIHPSDETRYNOKFXD 66
RESULT 4
US-11-107-028-50
Sequence 50, Application US/11107028
Publication No. US20050276803A1
GENERAL INFORMATION:
APPLICANT: CHAN, ANDREW C.
APPLICANT: GONG, QIAN
APPLICANT: MARTIN, FLAVIUS
TITLE OF INVENTION: Method for Augmenting B Cell Depletion
FILE REFERENCE: P2112R1
CURRENT APPLICATION NUMBER: US/11/107,028
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/563,263
PRIOR FILING DATE: 2004-04-16

NUMBER OF SEQ ID NOS: 52
SEQ ID NO 50
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-107-028-50
Query Match 100.0%; Score 93; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MIHPSDETRYNOKFXD 17
|||||
Db 50 MIHPSDETRYNOKFXD 66
RESULT 5
US-10-665-658-40
Sequence 40, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-665-658-40
Query Match 96.8%; Score 90; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.8e-09;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 MIHPSDETRYNOKFXD 17
|||||

Db 1 MIHPADSETRYNOKEFD 17

RESULT 6
US-10-665-658-42
Sequence 42, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-665-658-42

Query Match 96.8%; Score 90; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.8e-09;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKEFD 17
Db 1 MIHPDSETRYNOKEFD 17

RESULT 7
US-10-665-658-43
Sequence 43, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971

US-10-665-658-43

Query Match 96.8%; Score 90; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.8e-09;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MIHPDSETRYNOKEFD 17
Db 1 MIHPDSETRYNOKEFD 17

RESULT 8
US-10-665-658-44
Sequence 44, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971

FILED DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-665-658-44

Query Match 95.7%; Score 89; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 6.9e-09;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOXKFD 17
DB 1 MHPSDSETRYNOXKFD 17

RESULT 9
US-10-665-658-36
Sequence 36, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
PRESTA, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-665-658-36

Query Match 93.5%; Score 87; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.5e-08;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOXKFD 17
DB 1 MHPSDSETRYNOXKFD 17

RESULT 10
US-10-665-658-45
Sequence 45, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
PRESTA, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-665-658-45

Query Match 93.5%; Score 87; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHPSDSETRYNOXKFD 17
DB 1 MHPSDSETRYNOXKFD 17

RESULT 11
US-10-665-658-46
; Sequence 46, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-Oct-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-Feb-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1CID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-665-658-46
Query Match 93.5%; Score 87; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNAKFKD 17
Db 1 MIHPDSETRYNAKFKD 17

RESULT 12
US-10-665-658-47
; Sequence 47, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-Nov-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-Oct-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-Feb-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-665-658-47
Query Match 93.5%; Score 87; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNAKFKD 17
Db 1 MIHPDSETRYNAKFKD 17

RESULT 13
US-10-665-658-48
; Sequence 48, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899

FILED DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-665-658-48

Query Match 93.5%; Score 87; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIHPDSETRYNQKFD 17
| | | | | | | | | | | | | | | | | | |
DB 1 MIHPDSETRYNQKFD 17

RESULT 14
US-10-665-658-49
Sequence 49, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardiou, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids

TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-665-658-49

Query Match 93.5%; Score 87; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIHPDSETRYNQKFD 17
| | | | | | | | | | | | | | | | | | |
DB 1 MIHPDSETRYNQKFD 17

RESULT 15
US-10-665-658-50
Sequence 50, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardiou, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-665-658-50

Query Match 93.5%; Score 87; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIHPDSETRYNQKFD 16
| | | | | | | | | | | | | | | | | | |
DB 1 MIHPDSETRYNQKFD 16

RESULT 16

US-10-665-658-41
; Sequence 41, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; TYPE: Amino Acid
; LENGTH: 17 amino acids
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-665-658-41
Query Match 91.4%; Score 85; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 3.1e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNOKEFD 17
Db 1 MIHPDSETRYNOKEFD 17
RESULT 17
US-10-665-658-4
; Sequence 4, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-665-658-4
Query Match 91.4%; Score 85; DB 6; Length 121;
Best Local Similarity 94.1%; Pred. No. 2.4e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNOKEFD 17
Db 50 MIHPDSETRYNOKEFD 66

RESULT 18
US-11-107-028-52
; Sequence 52, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO: 52
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-107-028-52
Query Match 91.4%; Score 85; DB 7; Length 121;
Best Local Similarity 94.1%; Pred. No. 2.4e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIHPDSETRYNOKEFD 17
Db 50 MIHPDSETRYNOKEFD 66
RESULT 19

US-10-665-658-39
; Sequence 39, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-Oct-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-Feb-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-665-658-39
Query Match 90.3%; Score 84; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.5e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIHPSDSETRYNOKEFD 17
Db 1 MIHPSDSETRYNOKEFD 17
RESULT 20
US-10-665-658-38
; Sequence 38, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-Oct-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-Feb-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-665-658-38
Query Match 89.2%; Score 83; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 6.6e-08;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIHPSDSETRYNOKEFD 17
Db 1 MIHPSDSETRYNOKEFD 17
RESULT 21
US-10-665-658-35
; Sequence 35, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 09/420745

FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014RIC1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-665-658-35

Query Match 86.0%; Score 80; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MHPDSETRYNOKEFD 17
|||:|||||
Db 1 MHPADSETRYNOKEFD 17

RESULT 22
US-10-665-658-37
; Sequence 37, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014RIC1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-665-658-37

Query Match 86.0%; Score 80; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 2e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MHPDSETRYNOKEFD 17
|||:|||||
Db 1 MHPADSETRYNOKEFD 17

RESULT 23
US-10-665-658-33
; Sequence 33, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014RIC1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-665-658-33

Query Match 82.8%; Score 77; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 6.2e-07;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MHPDSETRYNOKEFD 17
|||:|||||
Db 1 MHPADSETRYNOKEFD 17

RESULT 24
US-10-665-658-34
; Sequence 34, Application US/10665658

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; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-665-658-34
;
; Query Match 78.5%; Score 73; DB 6; Length 17;
; Best Local Similarity 82.4%; Pred. No. 2.8e-06;
; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; QY 1 MIHPDSETRYNOXPKD 17
; ||||| |||||
; DB 1 MIHPASATATYNOXPKD 17
;
; RESULT 25
; US-10-507-662-25
; Sequence 25, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
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; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-25
;
; Query Match 75.3%; Score 70; DB 6; Length 121;
; Best Local Similarity 82.4%; Pred. No. 6.8e-05;
; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; QY 1 MIHPDSETRYNOXPKD 17
; ||||| |||||
; DB 50 MIHPISSETRLNPKXKD 66
;
; RESULT 26
; US-10-507-662-26
; Sequence 26, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-26
;
; Query Match 75.3%; Score 70; DB 6; Length 121;
; Best Local Similarity 82.4%; Pred. No. 6.8e-05;
; Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; QY 1 MIHPDSETRYNOXPKD 17
; ||||| |||||
; DB 50 MIHPISSETRLNPKXKD 66
;
; RESULT 27
; US-10-665-658-23
; Sequence 23, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 60/031971
```

FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-665-658-23

Query Match 74.2%; Score 69; DB 6; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.3e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHPDSETRYNOXFKD 17
|||:|||||
DB 1 MHPDSETRYNOXFKD 17

RESULT 28
US-10-665-658-24
Sequence 24, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardiou, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESSES:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-665-658-24

Query Match 74.2%; Score 69; DB 6; Length 121;
Best Local Similarity 76.5%; Pred. No. 9.8e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHPDSETRYNOXFKD 17
|||:|||||
DB 50 MHPDSETRYNOXFKD 66

RESULT 29
US-11-097-812-89
Sequence 89, Application US/11097812
Publication No. US20050281828A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
Kretz-Rommel, Anke
TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
CURRENT APPLICATION NUMBER: US/11/097,812
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 11/016,647
PRIOR FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PCT/US04/06570
PRIOR FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: US 60/548,395
PRIOR FILING DATE: 2004-02-28
PRIOR APPLICATION NUMBER: US 60/529,500
PRIOR FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: US 60/451,816
PRIOR FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn version 3.2
SEQ ID NO 89
LENGTH: 17
TYPE: PRT
ORGANISM: mouse
US-11-097-812-89

Query Match 67.7%; Score 63; DB 7; Length 17;
Best Local Similarity 70.6%; Pred. No. 0.00012;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHPDSETRYNOXFKD 17
|||:|||||
DB 1 MHPDSETRYNOXFKD 17

RESULT 30
US-11-097-812-68
Sequence 68, Application US/11097812
Publication No. US20050281828A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
Kretz-Rommel, Anke
APPLICANT: Dakappagari, Naveen
TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
CURRENT APPLICATION NUMBER: US/11/097,812
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 11/016,647
PRIOR FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PCT/US04/06570
PRIOR FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 68
; LENGTH: 120
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-68

Query Match 67.7%; Score 63; DB 7; Length 120;
Best Local Similarity 70.6%; Pred. No. 0.00093;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IHPSDETRYNQKFD 17
Db 50 MIDPNSERARLNQKFD 66

RESULT 31
US-11-102-621-130
; Sequence 130, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 130
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-130

Query Match 63.4%; Score 59; DB 7; Length 447;
Best Local Similarity 68.8%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IHPSDETRYNQKFD 17
Db 51 IDPSDEVHYNQDFKD 66

RESULT 32
US-11-102-621-131
; Sequence 131, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300

; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 131
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-131

Query Match 63.4%; Score 59; DB 7; Length 447;
Best Local Similarity 68.8%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IHPSDETRYNQKFD 17
Db 51 IDPSDEVHYNQDFKD 66

RESULT 33
US-11-102-621-132
; Sequence 132, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 132
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-132

Query Match 63.4%; Score 59; DB 7; Length 447;
Best Local Similarity 68.8%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IHPSDETRYNQKFD 17
Db 51 IDPSDEVHYNQDFKD 66

RESULT 34
US-11-102-621-133
; Sequence 133, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 133
; LENGTH: 447

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-133

Query Match      63.4%; Score 59; DB 7; Length 447;
Best Local Similarity 68.8%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 IHPDSETRYNOKFXD 17
      ||||| |||||
Db      51 IDPSDGEVHYNDPFXD 66

RESULT 35
US-11-102-621-134
; Sequence 134, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsunushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 134
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-134

Query Match      63.4%; Score 59; DB 7; Length 447;
Best Local Similarity 68.8%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 IHPDSETRYNOKFXD 17
      ||||| |||||
Db      51 IDPSDGEVHYNDPFXD 66

RESULT 36
US-10-507-662-32
; Sequence 32, Application US/10507662
; Publication No. US20050255102A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
; FILE REFERENCE: A136PCT
; CURRENT APPLICATION NUMBER: US/10/507,662
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: 60/364,991
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/426,286
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-507-662-32

Query Match      62.4%; Score 58; DB 6; Length 118;
Best Local Similarity 56.2%; Pred. No. 0.0059;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Qy      2 IHPDSETRYNOKFXD 17
      ||:|: ||:|: ||:|:
Db      51 IYPGNQNTKYNEKFXD 66

RESULT 37
US-10-512-184-36
; Sequence 36, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: seqv SS2 with
; OTHER INFORMATION: specificity against Sclerotinia sclerotiorum;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

Query Match      62.4%; Score 58; DB 6; Length 248;
Best Local Similarity 66.7%; Pred. No. 0.013;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      2 IHPDSETRYNOKFX 16
      ||:|: ||:|: ||:|:
Db      53 IYPGNSDTSYNOKFX 67

RESULT 38
US-11-102-621-124
; Sequence 124, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsunushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-124

Query Match      62.4%; Score 58; DB 7; Length 442;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IHPDSETRYNOKFXD 17
      ||:|: ||:|: ||:|:
Db      51 IHPSTGYTRYNOKFXD 66

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RESULT 39
US-11-102-621-125
; Sequence 125, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Teurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-125

Query Match          62.4%; Score 58; DB 7; Length 442;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPSDSETRYNOXFKD 17
Db      51 INPSTGYTEYNOKFKD 66

RESULT 40
US-11-102-621-126
; Sequence 126, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Teurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-126

Query Match          62.4%; Score 58; DB 7; Length 442;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPSDSETRYNOXFKD 17
Db      51 INPSTGYTEYNOKFKD 66

RESULT 41
US-11-102-621-127
; Sequence 127, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Teurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-127

Query Match          62.4%; Score 58; DB 7; Length 442;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPSDSETRYNOXFKD 17
Db      51 INPSTGYTEYNOKFKD 66

RESULT 42
US-11-102-621-128
; Sequence 128, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Teurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-128

Query Match          62.4%; Score 58; DB 7; Length 442;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPSDSETRYNOXFKD 17
Db      51 INPSTGYTEYNOKFKD 66

RESULT 43
US-11-102-621-119
; Sequence 119, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Teurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 119
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-119

Query Match          62.4%; Score 58; DB 7; Length 442;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPSDSETRYNOXFKD 17
Db      51 INPSTGYTEYNOKFKD 66
```

```

; TITLE OF INVENTION: ALTERATION OF PERN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 119
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-119

Query Match          62.4%; Score 58; DB 7; Length 446;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IHPDSETRYNQKFXD 17
       ||| ||| ||| |||
       51 INPSTGYTEYNQKFXD 66

RESULT 44
US-11-102-621-120
; Sequence 120, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsunushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF PERN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-120

Query Match          62.4%; Score 58; DB 7; Length 446;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IHPDSETRYNQKFXD 17
       ||| ||| ||| |||
       51 INPSTGYTEYNQKFXD 66

RESULT 45
US-11-102-621-121
; Sequence 121, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsunushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF PERN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
```

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; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 121
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-121

Query Match          62.4%; Score 58; DB 7; Length 446;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IHPDSETRYNQKFXD 17
       ||| ||| ||| |||
       51 INPSTGYTEYNQKFXD 66

RESULT 46
US-11-102-621-122
; Sequence 122, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsunushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF PERN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-122

Query Match          62.4%; Score 58; DB 7; Length 446;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IHPDSETRYNQKFXD 17
       ||| ||| ||| |||
       51 INPSTGYTEYNQKFXD 66

RESULT 47
US-11-102-621-123
; Sequence 123, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsunushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF PERN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
```



```

; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-123

Query Match          62.4%; Score 58; DB 7; Length 446;
Best Local Similarity 68.8%; Pred. No. 0.024;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPDSETRYNOQKFXD 17
       ||| |||||
Db      51 INPSTGYTNYNOQKFXD 66

RESULT 48
US-10-512-184-50
; Sequence 50, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - scfv ss2 - cmvc/His6.
US-10-512-184-50

Query Match          62.4%; Score 58; DB 6; Length 615;
Best Local Similarity 66.7%; Pred. No. 0.034;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 IHPDSETRYNOQKFX 16
       ||| |||||
Db      394 ITPGNSDSTYNOQKFX 408

RESULT 49
US-11-221-900-10
; Sequence 10, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: TOLT:004USC1
; CURRENT APPLICATION NUMBER: US/11/221,900
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/267,286
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 08/557,050
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 119
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-221-900-10

Query Match          61.3%; Score 57; DB 7; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.0087;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPDSETRYNOQKFXD 17
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Db      51 INPSRGYTNNOQKFXD 66

RESULT 50
US-11-221-900-12
; Sequence 12, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: TOLT:004USC1
; CURRENT APPLICATION NUMBER: US/11/221,900
; CURRENT FILING DATE: 2005-09-09
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; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-221-900-12

Query Match          61.3%; Score 57; DB 7; Length 119;
Best Local Similarity 68.8%; Pred. No. 0.0087;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPDSETRYNOQKFXD 17
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Db      51 INPSRGYTNNOQKFXD 66
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Search completed: January 17, 2006, 12:13:32
Job time : 6.66667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:46:53 ; Search time 75.0909 Seconds
(without alignments)
70.215 Million cell updates/sec

Title: US-10-665-658-12
Perfect score: 72
Sequence: 1 GIFYGTYFDY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

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- 2: geneseqp1990s:*
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- 6: geneseqp2003as:*
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- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	72	100.0	12	3	AAW82339 Humanised
3	72	100.0	12	8	ADG39000 Humanised
4	72	100.0	116	2	AAW29452 Human Igg
5	72	100.0	116	3	AAW77755 Human Igg
6	72	100.0	116	3	AAW830312 Human Igg
7	72	100.0	116	6	ABU13789 Human Igg
8	72	100.0	116	6	ABU59502 Human Igg
9	72	100.0	116	7	AAW39085 Human Igg
10	72	100.0	121	2	AAW62013 Heavy cha
11	72	100.0	121	2	AAW62019 Heavy cha
12	72	100.0	121	2	AAW63542 Murine MH
13	72	100.0	121	2	AAW63531 Murine MH
14	72	100.0	121	2	AAW63532 Murine MH
15	72	100.0	121	3	AAW82348 Humanised
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18	72	100.0	121	8	ADG39012 Rhesusise
19	72	100.0	121	8	ADG38992 Mouse ant
20	72	100.0	121	8	ADG38993 Humanised
21	72	100.0	121	8	ADG38993 Humanised
22	72	100.0	121	8	ADG38993 Humanised
23	72	100.0	121	8	ADG38993 Humanised
24	72	100.0	121	8	ADG38993 Humanised

25	72	100.0	121	9	ADG80646 Humanized
26	72	100.0	451	8	ADG11670 anti-CD11
27	65	90.3	11	8	ADG03408 Humanised
28	60	83.3	11	8	ADG03414 Humanised
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30	56	77.8	11	8	ADG03412 Humanised
31	56	77.8	11	8	ADG03411 Humanised
32	55	76.4	122	8	ADG03415 Humanised
33	54	75.0	120	2	AAW38454 CD11a hea
34	54	75.0	120	2	AAW93002 Monoclonal
35	54	75.0	120	2	AAW93004 Humanised
36	54	75.0	232	7	ADP72730 Divalent
37	54	75.0	241	7	ADP72729 Monovalent
38	54	75.0	255	7	ADP72734 His-Cage
39	52	72.2	206	5	ADK34542 Novel hum
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46	44.5	61.8	13	8	ADG17151 Murine an
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53	44	61.1	124	1	AAW70990 Sequence
54	44	61.1	124	1	AAW06350 M13 VPRC
55	44	61.1	124	2	AAW06350 NEWM VH e
56	44	61.1	139	7	AD125190 Humanised
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58	44	61.1	269	8	ADP94354 Humanised
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61	44	61.1	344	4	AAW66954 ScFV PRAS
62	44	61.1	402	2	AAW56485 ScFV PRAS
63	44	61.1	428	2	AAW56484 ScFV PRAS
64	44	61.1	428	2	AAW56482 Single ch
65	44	61.1	435	2	AAW56483 ScFV PRAS
66	44	61.1	443	2	AAW42025 Single ch
67	43	59.7	33	2	AAW20207 H. pylori
68	43	59.7	121	2	AAW0808 H. pylori
69	43	59.7	152	2	AAW61004 Streptococ
70	43	59.7	227	6	ABU02540 S. pneumo
71	43	59.7	234	5	ABP27712 Streptococ
72	43	59.7	234	6	ABU46430 Protein e
73	43	59.7	234	6	ABU46436 Protein e
74	43	59.7	236	9	ADG48234 Streptococ
75	43	59.7	236	9	ADG48234 Streptococ
76	43	59.7	238	5	ADG48234 Streptococ
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102	40.5	56.2	117	7	ADC27445	Adc27445 TMERF2#20	175	39	54.2	320	5	AAU95673
103	40.5	56.2	117	7	ADR87271	Adr87271 Anti-Liv-	176	39	54.2	320	5	AAU85328
104	40	55.6	55	6	ABU56893	Abu56893 BONT/A Hc	177	39	54.2	320	6	ABU11154
105	40	55.6	121	8	ADR38649	Adr38649 Mouse hea	178	39	54.2	320	7	AAE39677
106	40	55.6	122	8	ADH17833	Adh17833 Murine an	179	39	54.2	320	7	ADC86075
107	40	55.6	122	8	ADM11464	Adm11464 Murine an	180	39	54.2	320	7	ADG83418
108	40	55.6	306	8	ADN17809	Adn17809 Bacterial	181	39	54.2	347	4	AAU24696
109	40	55.6	351	8	ADS21855	Ads21855 Bacterial	182	39	54.2	347	5	ABP95863
110	40	55.6	542	6	ABU27388	Abu27388 Protein e	183	39	54.2	347	5	AAU85316
111	40	55.6	543	6	ABR38852	Ab38852 A. niger	184	39	54.2	351	2	AAU07015
112	39.5	54.9	19	5	ABP46963	Abp46963 Human Bly	185	39	54.2	352	6	ABU30630
113	39.5	54.9	19	7	ADG97790	Adg97790 ecry VHCD	186	39	54.2	352	6	AAE30476
114	39.5	54.9	254	7	ABP44972	Abp44972 Human Bly	187	39	54.2	362	2	AAU11468
115	39.5	54.9	254	7	ADG95799	Adg95799 Single ch	188	39	54.2	451	8	ADN97505
116	39.5	54.9	258	8	ADN23635	Adn23635 Bacterial	189	39	54.2	475	5	AAU70762
117	39	54.2	10	3	AAU79428	Aay79428 Tie2 rece	190	39	54.2	480	6	ABU35108
118	39	54.2	10	3	ABE01003	AbE01003 Human IPI	191	39	54.2	486	8	ADL05827
119	39	54.2	63	8	ADR90757	Adr90757 CDR's fro	192	39	54.2	512	8	ADN97497
120	39	54.2	94	4	ABG26685	Abg26685 Novel hum	193	39	54.2	517	8	ADN97495
121	39	54.2	118	9	ADH5026	Adh5026 Monoclonal	194	39	54.2	519	8	ADN97493
122	39	54.2	119	3	AAU79424	Aay79424 Tie2 rece	195	39	54.2	532	2	AAW35565
123	39	54.2	121	5	ABJ04928	Abj04928 Human Igg	196	39	54.2	548	8	ADN17887
124	39	54.2	122	5	ABJ04927	Abj04927 Human Igg	197	39	54.2	552	8	ADN97513
125	39	54.2	123	7	ADP03872	Adp03872 Murine-ex	198	39	54.2	586	2	AAU23621
126	39	54.2	123	7	ABE01014	AbE01014 Human IPI	199	39	54.2	590	8	ADQ65530
127	39	54.2	126	7	ADK18786	Adk18786 Anti-huma	200	39	54.2	621	3	AAU19285
128	39	54.2	126	7	ADK18822	Adk18822 Anti-huma	201	39	54.2	621	8	ADH01236
129	39	54.2	126	7	ADK18882	Adk18882 Anti-huma	202	39	54.2	677	8	ADN21140
130	39	54.2	126	7	ADK18601	Adk18601 Anti-huma	203	39	54.2	712	8	ADN97543
131	39	54.2	126	8	ADL25420	Adl25420 Human mb	204	39	54.2	713	8	ADN97489
132	39	54.2	131	6	ABR54874	Ab54874 Igg kappa	205	39	54.2	725	5	ABP41188
133	39	54.2	131	6	ABE19250	AbE19250 Igg heavy	206	39	54.2	729	5	ABG96303
134	39	54.2	142	2	AAW09816	Aaw09816 PelB-VH47	207	39	54.2	852	5	ABR47422
135	39	54.2	269	4	AAW09819	Aaw09819 3DX gFv P	208	39	54.2	852	6	ABR47422
136	39	54.2	274	2	AAW09818	Aaw09818 VH4715-11	209	39	54.2	1059	7	ADH45524
137	39	54.2	282	2	AAW09818	Aaw09818 VH4715-11	210	39	54.2	1059	7	ADH45524
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139	39	54.2	289	2	AAW35564	Aaw35564 HindIII-E	212	39	54.2	1062	8	ADU76277
140	39	54.2	309	7	ADL98006	Adl98006 Herdicia	213	39	54.2	1065	5	ABG96304
141	39	54.2	309	7	ADL98006	Adl98006 Human oif	214	39	54.2	1065	5	ABR47423
142	39	54.2	317	4	AAU71435	Aau71435 Human oif	215	39	54.2	1065	6	ADL18608
143	39	54.2	317	4	AAU71435	Aau71435 Human oif	216	39	54.2	1065	7	ADH45526
144	39	54.2	317	5	ABE06652	AbE06652 G protein	217	39	54.2	1065	7	ADH45526
145	39	54.2	317	5	AAU95671	Aau95671 Human oif	218	39	54.2	1065	7	ADH45526
146	39	54.2	317	5	ADH85675	Adh85675 Human GPC	219	39	54.2	1065	8	ADU75542
147	39	54.2	318	4	AAU71464	Aau71464 Human oif	220	39	54.2	1065	8	ABE17662
148	39	54.2	318	4	AAU724710	Aau724710 Human oif	221	39	54.2	1065	9	ABG96302
149	39	54.2	318	5	ABE06650	AbE06650 G protein	222	39	54.2	1069	5	ABR47424
150	39	54.2	318	5	ABE06651	AbE06651 G protein	223	39	54.2	1069	5	ABR47424
151	39	54.2	318	5	ABP95861	AbP95861 Human GPC	224	39	54.2	1090	5	ABG96305
152	39	54.2	318	5	AAU95735	Aau95735 Human oif	225	39	54.2	1090	5	ABG96305
153	39	54.2	318	5	AAU85330	Aau85330 G-coupled	226	39	54.2	1090	5	ABG96305
154	39	54.2	318	6	ABU11215	Abu11215 Human G-P	227	39	54.2	1090	5	ABG96305
155	39	54.2	318	7	ADH85677	Adh85677 Human GPC	228	39	54.2	1090	5	ABG96305
156	39	54.2	319	4	AAU71989	Aau71989 Human oif	229	39	54.2	1090	5	ABG96305
157	39	54.2	319	4	AAU10311	Aau10311 G-protein	230	39	54.2	1090	5	ABG96305
158	39	54.2	319	4	AAU24550	Aau24550 Human oif	231	39	54.2	1090	5	ABG96305
159	39	54.2	319	4	AAU07096	Aau07096 Human odo	232	39	54.2	1090	5	ABG96305
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161	39	54.2	319	5	AAU85170	Aau85170 G-coupled	234	39	54.2	1090	5	ABG96305
162	39	54.2	319	5	AAU85170	Aau85170 G-coupled	235	39	54.2	1090	5	ABG96305
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165	39	54.2	319	8	ADH41859	Adh41859 Novel hum	238	39	54.2	1090	5	ABG96305
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244	38.5	53.5	276	5	AAE15791	Mouse Nit	317	38	52.8	960	6	ABM70214	Photorhab
245	38.5	53.5	432	5	ABBA9171	Listeria	318	38	52.8	960	8	ADP18624	Photorhab
246	38.5	53.5	432	6	ABU32904	Protein e	319	38	52.8	960	8	ADR21527	Photorhab
247	38.5	53.5	447	8	ADQ17121	Humanised	320	38	52.8	962	8	ADR21531	Xenorhab
248	38	52.8	12	9	ADM77387	Human pla	321	38	52.8	962	6	ABBA7814	Native Xp
249	38	52.8	18	5	AAU70375	Mouse hea	322	38	52.8	966	6	ABM69154	Photorhab
250	38	52.8	58	5	ABP01736	Human ORF	323	38	52.8	971	6	AAV95687	Cosmid cH
251	38	52.8	120	6	ABG74719	Murine hu	324	38	52.8	999	4	ABM70223	Photorhab
252	38	52.8	120	6	ABG74712	Murine hu	325	38	52.8	999	4	ABM65291	Drosophil
253	38	52.8	120	6	ABG74703	Murine Mu	326	38	52.8	1016	8	ADR20367	Recombina
254	38	52.8	120	6	ABR83159	Mu007 ant	327	38	52.8	1016	8	ADR21496	Xenorhab
255	38	52.8	120	7	ABR83160	Abt83159 Hu007 ant	328	38	52.8	1043	2	AAW18306	Photorhab
256	38	52.8	120	7	ABR83152	Hu007 ant	329	38	52.8	1043	2	AAW56569	Toxin Tec
257	38	52.8	123	3	AAQ05124	Streptococ	330	38	52.8	1043	6	ADR21577	Photorhab
258	38	52.8	132	2	AAW03183	Gly's 13	331	38	52.8	1044	6	ABM69055	Photorhab
259	38	52.8	132	2	ABP27484	Streptococ	332	38	52.8	1871	7	ADM77484	Murine Db6
260	38	52.8	200	8	ADL71884	Streptococ	333	38	52.8	4249	8	ADR39912	Murine Pk
261	38	52.8	212	4	AAQ71993	Human olf	334	37.5	52.1	13	9	AEA24326	Anti-HAAM
262	38	52.8	212	4	AAQ72337	Human OR-	335	37.5	52.1	13	9	AEA24461	Anti-HAAM
263	38	52.8	215	8	ADU60622	Puffer fi	336	37.5	52.1	132	9	AEA24276	Anti-HAAM
264	38	52.8	223	8	AAQ71583	Human olf	337	37.5	52.1	178	5	ADZ57715	Germiline
265	38	52.8	275	4	AAQ71583	Human OR-	338	37.5	52.1	178	5	ABU51719	Helicobac
266	38	52.8	291	4	AAQ72580	Human OR-	339	37.5	52.1	254	8	ADQ67052	Novel hum
267	38	52.8	320	5	ABP61146	Human GPC	340	37.5	52.1	266	9	AEA24295	Anti-HAAM
268	38	52.8	320	7	ADC79350	Human G p	341	37.5	52.1	341	2	AAW98546	H. pylori
269	38	52.8	324	2	AAV34528	Porphorym	342	37.5	52.1	341	6	ABU30769	Protein e
270	38	52.8	335	8	ADP57618	Plant pol	343	37.5	52.1	341	7	ADE86739	Ribonucle
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274	38	52.8	423	5	ABBA8413	Listeria	347	37	51.4	13	5	AAW70634	Second ge
275	38	52.8	430	4	AAU35657	Haemophil	348	37	51.4	13	5	ABP61203	Anti-VEGF
276	38	52.8	430	6	ABU30614	Protein e	349	37	51.4	14	2	AAW70699	Anti-VEGF
277	38	52.8	443	6	ADJ33252	Enterococ	350	37	51.4	14	5	ABP61268	Humanised
278	38	52.8	450	6	ABG74713	Murine hu	351	37	51.4	17	9	AEA40774	Anti-VEGF
279	38	52.8	450	8	ABR83153	Hu007 ant	352	37	51.4	19	5	AAU70381	Mouse hea
280	38	52.8	456	8	ADN21162	Bacterial	353	37	51.4	19	8	ADG31772	Affinity
281	38	52.8	468	7	ADH68683	Enterococ	354	37	51.4	26	8	ADG31828	Anti-VEGF
282	38	52.8	523	2	AAH34097	Partial a	355	37	51.4	82	5	ABP01556	Human ORF
283	38	52.8	523	9	AEA55073	Mouse fac	356	37	51.4	102	4	ABG13921	Novel hum
284	38	52.8	540	4	AAQ72588	Human OR-	357	37	51.4	117	4	AAO04324	Human pol
285	38	52.8	542	7	ADC31036	Human nov	358	37	51.4	117	7	ADP09953	Antibody
286	38	52.8	551	8	ADN20656	Bacterial	359	37	51.4	117	7	ADP10058	VEGF anti
287	38	52.8	552	8	ADN20566	Bacterial	360	37	51.4	118	2	AAW70686	Anti-VEGF
288	38	52.8	607	5	ABR52408	Protein r	361	37	51.4	118	2	AAW70688	Anti-VEGF
289	38	52.8	631	7	ADH34696	CE7-speci	362	37	51.4	118	2	AAW70688	Anti-VEGF
290	38	52.8	662	5	ABR52423	Protein r	363	37	51.4	118	3	AAH13385	Anti-VEGF
291	38	52.8	682	6	ABP72716	Human pro	364	37	51.4	118	3	AAH13384	Anti-VEGF
292	38	52.8	698	7	ADC39230	Novel hum	365	37	51.4	118	3	AAH13383	Anti-VEGF
293	38	52.8	699	5	ABR52422	Protein r	366	37	51.4	118	5	ABP61253	Humanised
294	38	52.8	703	6	ABJ26648	Human pro	367	37	51.4	118	5	ABP61255	Humanised
295	38	52.8	703	6	ADC39232	Novel hum	368	37	51.4	118	5	ABP61257	Humanised
296	38	52.8	747	5	ABR52421	Protein r	369	37	51.4	122	3	AAV96802	Streptococ
297	38	52.8	800	5	ABP40810	Staphyloc	370	37	51.4	123	7	AAV42965	Kabat id
298	38	52.8	800	8	ADN08146	Staphyloc	371	37	51.4	123	8	ADG31769	V(H) doma
299	38	52.8	800	8	ADN08146	Staphyloc	372	37	51.4	123	8	AEA40494	Anti-VEGF
300	38	52.8	806	5	ABR52420	Protein r	373	37	51.4	123	9	AEA40541	Anti-VEGF
301	38	52.8	915	5	ABG32653	P. lumine	374	37	51.4	126	7	ADK18603	Anti-huma
302	38	52.8	915	5	ADK18628	Photorhab	375	37	51.4	126	7	ADK18889	Anti-huma
303	38	52.8	916	6	ABM70231	Photorhab	376	37	51.4	126	7	ADK18790	Anti-huma
304	38	52.8	930	6	ADN61349	Paenibaci	377	37	51.4	126	7	ADK18825	Anti-huma
305	38	52.8	930	6	ADN61349	Paenibaci	378	37	51.4	126	8	ADL25424	Human mAb
306	38	52.8	937	6	ABM67982	Photorhab	379	37	51.4	135	7	AAV42974	Kabat id
307	38	52.8	938	8	ADP18628	Photorhab	380	37	51.4	137	2	AAW03724	Anti-huma
308	38	52.8	938	8	ADP18628	Photorhab	381	37	51.4	149	6	ABO04846	Human epi
309	38	52.8	939	6	ABM70226	Photorhab	382	37	51.4	149	6	AEA17758	Hydridoma
310	38	52.8	940	7	ADG73071	Pseudomon	383	37	51.4	158	8	ADN48200	Thermococ
311	38	52.8	940	7	ADL12126	Pseudomon	384	37	51.4	158	8	ADN46914	Thermococ
312	38	52.8	949	8	ADP18626	Photorhab	385	37	51.4	162	4	AAV73049	Olfactory
313	38	52.8	949	8	ADP18626	Photorhab	386	37	51.4	177	6	ABU19609	Protein e
314	38	52.8	953	8	ADN61355	Paenibaci	387	37	51.4	212	6	ABU44457	Protein e
315	38	52.8	953	8	ADR21523	Paenibaci	388	37	51.4	233	3	ADW05083	Humanized
316	38	52.8	954	2	AAV33728	Photorhab	389	37	51.4	237	5	ABP45930	Human Bly

390	37	51.4	237	7	ADG96757	Adg96757 Single ch	463	37	51.4	735	6	ABR65570	Abt65570 Human sec
391	37	51.4	243	8	ADN36307	Adn36307 Hamster a	464	37	51.4	735	6	ABU99510	Abu99510 Human sec
392	37	51.4	254	5	ADN51953	Adn51953 Plasmid p	465	37	51.4	735	6	ABU82749	Abu82749 Human PRO
393	37	51.4	294	8	ADS30672	Ads30672 Bacterial	466	37	51.4	735	6	ABU89870	Abu89870 Novel hum
394	37	51.4	313	4	AA67054	Aa67054 Human imm	467	37	51.4	735	6	ABR68119	Abt68119 Human sec
395	37	51.4	318	4	AA67166	Aa67166 Human olf	468	37	51.4	735	6	ABU96172	Abu96172 Novel hum
396	37	51.4	318	4	AA672405	Aa672405 Human OR-	469	37	51.4	735	6	ABU92603	Abu92603 Human sec
397	37	51.4	331	6	AA667970	Aa667970 Photorhab	470	37	51.4	735	6	ABO06680	AbO06680 Human sec
398	37	51.4	334	3	AA651994	Aa651994 Human sec	471	37	51.4	735	6	ABO02732	AbO02732 Human sec
399	37	51.4	334	3	AA651993	Aa651993 Gene 38 h	472	37	51.4	735	6	ABR74886	Abt74886 Human sec
400	37	51.4	345	6	AB030604	Ab030604 Protein e	473	37	51.4	735	6	ABR94648	Abt94648 Human sec
401	37	51.4	349	7	ADC32682	Adc32682 Human nov	474	37	51.4	735	6	ABO25197	AbO25197 Novel hum
402	37	51.4	367	2	AAW94087	Aaw94087 F. hepatic	475	37	51.4	735	6	ABU85621	Abu85621 Human PRO
403	37	51.4	367	2	AAW94087	Aaw94087 F. hepatic	476	37	51.4	735	6	ABU98781	Abu98781 Novel hum
404	37	51.4	413	4	AAW58457	Aaw58457 Flavobact	477	37	51.4	735	6	ABU97996	Abu97996 Novel hum
405	37	51.4	413	6	ABU70885	Abu70885 Human adi	478	37	51.4	735	6	ABU91702	Abu91702 Novel hum
406	37	51.4	445	6	ABU29913	Abu29913 Protein e	479	37	51.4	735	6	ABU72203	Abu72203 Novel hum
407	37	51.4	476	5	ABE45845	Aeb45845 Human mon	480	37	51.4	735	6	ABU89395	Abu89395 Human PRO
408	37	51.4	476	5	ABE45845	Aeb45845 Human mon	481	37	51.4	735	6	ABU86236	Abu86236 Human sec
409	37	51.4	476	8	ADO14129	Ado14129 Plasmid p	482	37	51.4	735	6	ABU67449	Abu67449 Human sec
410	37	51.4	476	8	ADO90730	Ado90730 Anti-VEGF	483	37	51.4	735	6	ABU80477	Abu80477 Human PRO
411	37	51.4	476	8	ADO90733	Ado90733 Anti-VEGF	484	37	51.4	735	6	ABR93395	Abt93395 Human sec
412	37	51.4	482	8	ADOC94885	Adc94885 E. faeciu	485	37	51.4	735	6	ABR98785	Abt98785 Human sec
413	37	51.4	495	5	ABE30540	Abp30540 Streptococ	486	37	51.4	735	6	ABO16308	AbO16308 Human sec
414	37	51.4	513	8	ADU69671	Adu69671 S agalact	487	37	51.4	735	6	ABR92208	Abt92208 Human sec
415	37	51.4	513	8	ADY89805	Ady89805 Streptococ	488	37	51.4	735	6	ABO18849	AbO18849 Human sec
416	37	51.4	513	8	ADY81058	Ady81058 Streptococ	489	37	51.4	735	6	ABR78270	Abt78270 Human sec
417	37	51.4	513	8	ADY83197	Ady83197 Streptococ	490	37	51.4	735	6	ABU85006	Abu85006 Novel hum
418	37	51.4	518	5	ABP27099	Abp27099 Streptococ	491	37	51.4	735	6	ABO00145	AbO00145 Novel hum
419	37	51.4	529	4	ABB60241	Abb60241 Drosophil	492	37	51.4	735	6	ABO11477	AbO11477 Human sec
420	37	51.4	542	8	ADS23395	Ads23395 Bacterial	493	37	51.4	735	6	ABO02122	AbO02122 Human sec
421	37	51.4	542	8	ADS21201	Ads21201 Bacterial	494	37	51.4	735	6	ABU88696	Abu88696 Novel hum
422	37	51.4	549	8	ABM84770	Abm84770 Human dia	495	37	51.4	735	6	ABU83391	Abu83391 Human sec
423	37	51.4	555	8	ABO75310	AbO75310 Pseudomon	496	37	51.4	735	6	ABO06192	AbO06192 Novel hum
424	37	51.4	564	8	ADN19053	Adn19053 Bacterial	497	37	51.4	735	6	ABR59228	Abt59228 Human sec
425	37	51.4	564	8	ADN19353	Adn19353 Bacterial	498	37	51.4	735	6	ABO02920	AbO02920 Human sec
426	37	51.4	567	8	ADN18890	Adn18890 Bacterial	499	37	51.4	735	6	ABO19154	AbO19154 Novel hum
427	37	51.4	567	8	ADS43780	Ads43780 Bacterial	500	37	51.4	735	6	ABO11172	AbO11172 Human sec
428	37	51.4	572	8	ABM84768	Abm84768 Human dia	501	37	51.4	735	6	ABR66790	Abt66790 Human sec
429	37	51.4	572	8	ABM84768	Abm84768 Human dia	502	37	51.4	735	6	ABO13709	AbO13709 Human sec
430	37	51.4	589	8	ABM84772	Abm84772 Human dia	503	37	51.4	735	6	ABU84883	Abu84883 Human sec
431	37	51.4	597	4	ADS23667	Ads23667 Bacterial	504	37	51.4	735	6	ABU84883	Abu84883 Human sec
432	37	51.4	600	7	ABM84771	Abm84771 Human inc	505	37	51.4	735	6	ABO07460	AbO07460 Human PRO
433	37	51.4	613	2	AAW93823	Aaw93823 E. coli G	506	37	51.4	735	6	ABO03647	AbO03647 Human sec
434	37	51.4	613	2	AAW93823	Aaw93823 E. coli G	507	37	51.4	735	6	ABR67095	Abt67095 Human sec
435	37	51.4	613	2	AAW93828	Aaw93828 Human GUS	508	37	51.4	735	6	ABO15698	AbO15698 Human sec
436	37	51.4	613	3	AAE28407	Aae28407 Escherich	509	37	51.4	735	6	ABU55979	Abt55979 Human sec
437	37	51.4	633	4	AAE62276	Aae62276 Mutant he	510	37	51.4	735	6	ABU61081	Abu61081 Human PRO
438	37	51.4	633	4	AAE62276	Aae62276 Mutant he	511	37	51.4	735	6	ABU65307	Abu65307 Human PRO
439	37	51.4	636	7	ADC30950	Adc30950 Human nov	512	37	51.4	735	6	ABU95252	Abu95252 Novel hum
440	37	51.4	648	9	ABE18195	Aeb18195 African G	513	37	51.4	735	6	ABU71155	Abu71155 Human PRO
441	37	51.4	651	4	AAE02443	Aae02443 Human bet	514	37	51.4	735	6	ABO07765	AbO07765 Human PRO
442	37	51.4	651	7	ADD45481	Add45481 Human Pro	515	37	51.4	735	6	ABR70006	Abt70006 Human sec
443	37	51.4	651	7	ADDE5748	Adde5748 Human Pro	516	37	51.4	735	6	ABR69339	Abt69339 Human sec
444	37	51.4	651	8	ADP12392	Adp12392 Protein e	517	37	51.4	735	6	ABO01480	AbO01480 Human PRO
445	37	51.4	651	8	ADQ89808	Adq89808 Antagonis	518	37	51.4	735	6	ABU81282	Abu81282 Human PRO
446	37	51.4	651	9	ADX06032	Adx06032 Cyclin-de	519	37	51.4	735	6	ABR60079	Abt60079 Human sec
447	37	51.4	651	9	ABE18196	Aeb18196 Human bet	520	37	51.4	735	6	ABR67814	Abt67814 Human sec
448	37	51.4	651	9	ABE18196	Aeb18196 Dog beta-	521	37	51.4	735	6	ABR65202	Abt65202 Human sec
449	37	51.4	686	8	AAW25719	Aaw25719 Human alp	522	37	51.4	735	6	ABR68424	Abt68424 Human sec
450	37	51.4	689	8	ADQ09744	Adq09744 Human gen	523	37	51.4	735	6	ABR71836	Abt71836 Human sec
451	37	51.4	708	6	ABU40900	Abu40900 Protein e	524	37	51.4	735	6	ABU85316	Abu85316 Human PRO
452	37	51.4	715	7	ADF05006	Adf05006 Bacterial	525	37	51.4	735	6	ABU89006	Abu89006 Human sec
453	37	51.4	722	6	AAE33322	Aae33322 L. mexica	526	37	51.4	735	6	ABU83086	Abu83086 Human sec
454	37	51.4	722	8	ADP47503	Adp47503 Human bet	527	37	51.4	735	6	ABU94942	Abu94942 Novel hum
455	37	51.4	722	8	ADJ58609	Adj58609 Fusison pr	528	37	51.4	735	6	ABU90490	Abu90490 Novel hum
456	37	51.4	735	3	AAAY1695	Aay1695 Human PRO	529	37	51.4	735	6	ABU84001	Abu84001 Human sec
457	37	51.4	735	3	AAAB44251	Aaab44251 Human PRO	530	37	51.4	735	6	ABU93652	Abu93652 Novel hum
458	37	51.4	735	6	AAU29067	Aau29067 Human PRO	531	37	51.4	735	6	ABR64897	Abt64897 Human sec
459	37	51.4	735	6	ABU58443	Abu58443 Human PRO	532	37	51.4	735	6	ABR68729	Abt68729 Human sec
460	37	51.4	735	6	ABU87991	Abu87991 Novel hum	533	37	51.4	735	6	ABO06545	AbO06545 Human sec
461	37	51.4	735	6	ABU84306	Abu84306 Human sec	534	37	51.4	735	6	ABR99090	Abt99090 Human sec
462	37	51.4	735	6	ABR66180	Abt66180 Human sec	535	37	51.4	735	6		

536	37	51.4	735	6	ABU56974	Human	PRO	609	37	51.4	735	6	ABM03606	Human	sec
537	37	51.4	735	6	ABU85926	Novel	hum	610	37	51.4	735	6	ABM35057	Human	sec
538	37	51.4	735	6	ABU82213	Novel	hum	611	37	51.4	735	6	ABM26294	Human	sec
539	37	51.4	735	6	ABU87224	Human	PRO	612	37	51.4	735	6	ABO48076	Human	sec
540	37	51.4	735	6	ABU83696	Human	sec	613	37	51.4	735	6	ABR92818	Human	sec
541	37	51.4	735	6	ABO08070	Human	PRO	614	37	51.4	735	6	ABO24579	Human	sec
542	37	51.4	735	6	ABU81781	Novel	hum	615	37	51.4	735	6	ABM11590	Human	sec
543	37	51.4	735	6	ABU65945	Novel	hum	616	37	51.4	735	6	ABM02691	Human	sec
544	37	51.4	735	6	ABR59774	Human	sec	617	37	51.4	735	6	ABM15987	Human	sec
545	37	51.4	735	6	ABU93962	Novel	hum	618	37	51.4	735	6	ABO27548	Human	sec
546	37	51.4	735	6	ABU80350	Human	sec	619	37	51.4	735	6	ABM29039	Human	sec
547	37	51.4	735	6	ABU99815	Novel	hum	620	37	51.4	735	6	ABM07015	Human	sec
548	37	51.4	735	6	ABR66485	Human	sec	621	37	51.4	735	6	ABM21109	Human	sec
549	37	51.4	735	6	ABR90903	Human	sec	622	37	51.4	735	6	ABM09455	Human	sec
550	37	51.4	735	6	ABU94330	Human	PRO	623	37	51.4	735	6	ABO41325	Human	sec
551	37	51.4	735	6	ABU79212	Human	PRO	624	37	51.4	735	6	ABO36140	Human	PRO
552	37	51.4	735	6	ABU86541	Human	sec	625	37	51.4	735	6	ABO43669	Human	PRO
553	37	51.4	735	6	ABU86846	Novel	hum	626	37	51.4	735	6	ABM76369	Human	sec
554	37	51.4	735	6	ABU94635	Human	PRO	627	37	51.4	735	6	ABM76065	Human	sec
555	37	51.4	735	6	ABO04562	Human	PRO	628	37	51.4	735	6	ABM25684	Human	sec
556	37	51.4	735	6	ABR70311	Human	sec	629	37	51.4	735	6	ABO25989	Human	sec
557	37	51.4	735	6	ABU98476	Human	PRO	630	37	51.4	735	6	ABO03342	Human	sec
558	37	51.4	735	6	ABR65875	Human	sec	631	37	51.4	735	6	ABO02427	Human	sec
559	37	51.4	735	6	ABR64592	Human	sec	632	37	51.4	735	6	ABR90598	Human	sec
560	37	51.4	735	6	ABU79517	Human	PRO	633	37	51.4	735	6	ABR73666	Human	sec
561	37	51.4	735	6	ABU92908	Human	sec	634	37	51.4	735	6	ABO16918	Human	sec
562	37	51.4	735	6	ABU95867	Human	PRO	635	37	51.4	735	6	ABR94343	Human	sec
563	37	51.4	735	6	ABU91087	Novel	hum	636	37	51.4	735	6	ABR71226	Human	sec
564	37	51.4	735	6	ABU90180	Novel	hum	637	37	51.4	735	6	ABR93123	Human	sec
565	37	51.4	735	6	ABO09595	Human	sec	638	37	51.4	735	6	ABR93428	Human	sec
566	37	51.4	735	6	ABO10867	Human	sec	639	37	51.4	735	6	ABR87853	Human	sec
567	37	51.4	735	6	ABR70921	Human	sec	640	37	51.4	735	6	ABO27853	Human	sec
568	37	51.4	735	6	ABU87529	Human	PRO	641	37	51.4	735	6	ABO29988	Human	sec
569	37	51.4	735	6	ABU91397	Human	sec	642	37	51.4	735	6	ABO33197	Human	PRO
570	37	51.4	735	6	ABU84611	Human	sec	643	37	51.4	735	6	ABM04885	Human	sec
571	37	51.4	735	6	ABR69701	Human	sec	644	37	51.4	735	6	ABM08845	Human	sec
572	37	51.4	735	6	ABU80078	Human	PRO	645	37	51.4	735	6	ABO36445	Human	sec
573	37	51.4	735	6	ABU93347	Human	PRO	646	37	51.4	735	6	ABO35530	Human	PRO
574	37	51.4	735	6	ABO09900	Human	sec	647	37	51.4	735	6	ABO39495	Human	sec
575	37	51.4	735	6	ABO08985	Human	sec	648	37	51.4	735	6	ABM10370	Human	sec
576	37	51.4	735	6	ABU10553	Human	sec	649	37	51.4	735	6	ABM11895	Human	sec
577	37	51.4	735	6	ABU95562	Human	PRO	650	37	51.4	735	6	ABO52041	Human	PRO
578	37	51.4	735	6	ABU66771	Novel	hum	651	37	51.4	735	6	ABO52346	Human	PRO
579	37	51.4	735	6	ABR70616	Human	sec	652	37	51.4	735	6	ABO23664	Human	sec
580	37	51.4	735	6	ABO04967	Novel	hum	653	37	51.4	735	6	ABR97150	Human	sec
581	37	51.4	735	6	ABO08375	Human	sec	654	37	51.4	735	6	ABR86938	Human	sec
582	37	51.4	735	6	ABO05582	Human	sec	655	37	51.4	735	6	ABR86388	Human	sec
583	37	51.4	735	6	ABR73971	Human	sec	656	37	51.4	735	6	ABM10980	Human	sec
584	37	51.4	735	6	ABR95563	Human	sec	657	37	51.4	735	6	ABM28124	Human	sec
585	37	51.4	735	6	ABR80860	Human	sec	658	37	51.4	735	6	ABO32123	Human	sec
586	37	51.4	735	6	ABR81165	Human	sec	659	37	51.4	735	6	ABM15250	Human	sec
587	37	51.4	735	6	ABM00861	Human	sec	660	37	51.4	735	6	ABM06405	Human	sec
588	37	51.4	735	6	ABR88463	Human	sec	661	37	51.4	735	6	ABM04216	Human	sec
589	37	51.4	735	6	ABM77284	Human	sec	662	37	51.4	735	6	ABM22329	Human	sec
590	37	51.4	735	6	ABO28768	Human	sec	663	37	51.4	735	6	ABO07625	Human	sec
591	37	51.4	735	6	ABO31513	Human	sec	664	37	51.4	735	6	ABO40715	Human	sec
592	37	51.4	735	6	ABM07930	Human	sec	665	37	51.4	735	6	ABM35362	Human	sec
593	37	51.4	735	6	ABO40410	Human	sec	666	37	51.4	735	6	ABO52651	Human	PRO
594	37	51.4	735	6	ABO35835	Human	PRO	667	37	51.4	735	6	ABR97455	Human	sec
595	37	51.4	735	6	ABO43974	Human	PRO	668	37	51.4	735	6	ABR80555	Human	sec
596	37	51.4	735	6	ADA77840	Human	sec	669	37	51.4	735	6	ABM01166	Human	sec
597	37	51.4	735	6	ABM24769	Human	sec	670	37	51.4	735	6	ABR88768	Human	sec
598	37	51.4	735	6	ABO03037	Human	sec	671	37	51.4	735	6	ABM13420	Human	sec
599	37	51.4	735	6	ABR90293	Human	sec	672	37	51.4	735	6	ABM18427	Human	sec
600	37	51.4	735	6	ABM17207	Human	sec	673	37	51.4	735	6	ABR97455	Human	sec
601	37	51.4	735	6	ABR94953	Human	sec	674	37	51.4	735	6	ABR80555	Human	sec
602	37	51.4	735	6	ABR95258	Human	sec	675	37	51.4	735	6	ABM01166	Human	sec
603	37	51.4	735	6	ABO21496	Human	sec	676	37	51.4	735	6	ABR88768	Human	sec
604	37	51.4	735	6	ABR97760	Human	sec	677	37	51.4	735	6	ABM13420	Human	sec
605	37	51.4	735	6	ABR87548	Human	sec	678	37	51.4	735	6	ABM20804	Human	sec
606	37	51.4	735	6	ABM77589	Human	sec	679	37	51.4	735	6	ABO41935	Human	sec
607	37	51.4	735	6	ABM27819	Human	sec	680	37	51.4	735	6	ABO42545	Human	sec
608	37	51.4	735	6	ABM06100	Human	sec	681	37	51.4	735	6	ABM10065	Human	sec

682	37	51.4	735	6	ABO38580	Human	sec	755	37	51.4	735	6	ABM04521	Adm04521	Human	sec
683	37	51.4	735	6	ABM32820	Human	sec	756	37	51.4	735	6	ABM06710	Adm06710	Human	sec
684	37	51.4	735	6	ABM22634	Human	sec	757	37	51.4	735	6	ABM09150	Adm09150	Human	sec
685	37	51.4	735	6	ABM74845	Human	sec	758	37	51.4	735	6	ABO39190	Adm039190	Human	sec
686	37	51.4	735	6	ABM79632	Human	sec	759	37	51.4	735	6	ABM75455	Adm75455	Human	sec
687	37	51.4	735	6	ADA24613	Novel	hum	760	37	51.4	735	6	ABM25379	Adm25379	Human	sec
688	37	51.4	735	6	ABR96235	Human	sec	761	37	51.4	735	6	ABM19889	Adm19889	Human	sec
689	37	51.4	735	6	ABM02386	Human	sec	762	37	51.4	735	6	ABO46795	Adm046795	Human	PRO
690	37	51.4	735	6	ABR86538	Human	sec	763	37	51.4	735	6	ABO47100	Adm047100	Human	PRO
691	37	51.4	735	6	ABR86633	Human	sec	764	37	51.4	735	6	ADA83157	Adm83157	Human	sec
692	37	51.4	735	6	ABM16597	Human	sec	765	37	51.4	735	6	ABR71531	Adm71531	Human	sec
693	37	51.4	735	6	ABM29649	Human	sec	766	37	51.4	735	6	ABR72141	Adm72141	Human	sec
694	37	51.4	735	6	ABO29073	Human	sec	767	37	51.4	735	6	ABR98480	Adm98480	Human	sec
695	37	51.4	735	6	ABM23854	Human	sec	768	37	51.4	735	6	ABO06850	Adm06850	Human	sec
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697	37	51.4	735	6	ABM22024	Human	sec	770	37	51.4	735	6	ABR73361	Adm73361	Human	sec
698	37	51.4	735	6	ABO37665	Human	sec	771	37	51.4	735	6	ABR76455	Adm76455	Human	sec
699	37	51.4	735	6	ABM28429	Human	sec	772	37	51.4	735	6	ABR73056	Adm73056	Human	sec
700	37	51.4	735	6	ABM28734	Human	sec	773	37	51.4	735	6	ABM18122	Adm18122	Human	sec
701	37	51.4	735	6	ABM66378	Human	sec	774	37	51.4	735	6	ABO20581	Adm020581	Human	sec
702	37	51.4	735	6	ABM75760	Human	sec	775	37	51.4	735	6	ABO25324	Adm025324	Human	PRO
703	37	51.4	735	6	ABM34040	Human	sec	776	37	51.4	735	6	ABO25629	Adm025629	Human	PRO
704	37	51.4	735	6	ABM34345	Human	sec	777	37	51.4	735	6	ABR94038	Adm94038	Human	sec
705	37	51.4	735	6	ABO19652	Novel	hum	778	37	51.4	735	6	ABR79945	Adm79945	Human	sec
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708	37	51.4	735	6	ABO22106	Human	sec	781	37	51.4	735	6	ABO30598	Adm030598	Human	sec
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710	37	51.4	735	6	ABR96540	Human	sec	783	37	51.4	735	6	ABM27209	Adm27209	Human	sec
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712	37	51.4	735	6	ABR99700	Human	sec	785	37	51.4	735	6	ABM05490	Adm05490	Human	sec
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716	37	51.4	735	6	ABM23549	Human	sec	789	37	51.4	735	6	ABO37970	Adm037970	Human	sec
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718	37	51.4	735	6	ABO38275	Human	sec	791	37	51.4	735	6	ABM66683	Adm66683	Human	sec
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720	37	51.4	735	6	ABM20499	Human	sec	793	37	51.4	735	6	ABM19584	Adm19584	Human	sec
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722	37	51.4	735	6	ABO18613	Human	sec	795	37	51.4	735	6	ABO49601	Adm049601	Human	sec
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725	37	51.4	735	6	ABO22971	Human	PRO	798	37	51.4	735	6	ABR88158	Adm88158	Human	sec
726	37	51.4	735	6	ABR92513	Human	sec	799	37	51.4	735	6	ABM26904	Adm26904	Human	sec
727	37	51.4	735	6	ABR81470	Human	sec	800	37	51.4	735	6	ABM03301	Adm03301	Human	sec
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734	37	51.4	735	6	ABM07320	Human	sec	807	37	51.4	735	7	ABR95868	Adm95868	Human	sec
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738	37	51.4	735	6	ABO35525	Human	PRO	811	37	51.4	735	7	ABO24274	Adm024274	Human	sec
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743	37	51.4	735	6	ABO51431	Human	PRO	816	37	51.4	735	7	ABM12505	Adm12505	Human	sec
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747	37	51.4	735	6	ABM16902	Human	sec	820	37	51.4	735	7	ABM18974	Adm18974	Human	sec
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749	37	51.4	735	6	ABO20886	Human	sec	822	37	51.4	735	7	ABO46490	Adm046490	Human	PRO
750	37	51.4	735	6	ABR96845	Human	sec	823	37	51.4	735	7	ABO48991	Adm048991	Human	sec
751	37	51.4	735	6	ABM12200	Human	sec	824	37	51.4	735	7	ABR69034	Adm69034	Human	sec
752	37	51.4	735	6	ABM16292	Human	sec	825	37	51.4	735	7	ABR89073	Adm89073	Human	sec
753	37	51.4	735	6	ABM24159	Human	sec	826	37	51.4	735	7	ABR72446	Adm72446	Human	sec
754	37	51.4	735	6	ABM14640	Human	sec	827	37	51.4	735	7	ABR74276	Adm74276	Human	sec

828	37	51.4	735	7	ABO18544	Human sec	901	37	51.4	735	7	ADCC62106	Adc62106	Human sec
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843	37	51.4	735	7	ABO03952	Human sec	916	37	51.4	735	7	ADG59991	Adg59991	Human sec
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856	37	51.4	735	7	ABM08235	Human sec	929	37	51.4	735	8	ADG40465	Adg40465	Human sec
857	37	51.4	735	7	ABO40105	Human sec	930	37	51.4	735	8	ADG23409	Adg23409	Human sec
858	37	51.4	735	7	ABM74540	Human sec	931	37	51.4	735	8	ADG33392	Adg33392	Human sec
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878	37	51.4	735	7	ABO37360	Human sec	951	37	51.4	735	8	ADG50871	Adg50871	Human sec
879	37	51.4	735	7	ABM75150	Human sec	952	37	51.4	735	8	ADG62271	Adg62271	Human sec
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882	37	51.4	735	7	ADA82523	Human sec	955	37	51.4	735	8	ADU64497	Adu64497	Human sec
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888	37	51.4	735	7	ABM32394	Human sec	961	37	51.4	735	8	ADN37853	Adn37853	Human sec
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891	37	51.4	735	7	ADBR76296	Human sec	964	37	51.4	735	9	ADG51969	Adg51969	Human sec
892	37	51.4	735	7	ADBC43722	Human sec	965	37	51.4	735	9	ADG39959	Adg39959	Human sec
893	37	51.4	735	7	ADBC1482	Human sec	966	37	51.4	738	8	ADG67219	Adg67219	Human sec
894	37	51.4	735	7	ADBC3446	Human sec	967	37	51.4	738	9	ADZ15122	Adz15122	Human sec
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896	37	51.4	735	7	ADCC6870	Human sec	969	37	51.4	749	8	ADR09606	Adr09606	Human sec
897	37	51.4	735	7	ADCC2730	Human sec	970	37	51.4	897	6	ABU40481	Abu40481	Human sec
898	37	51.4	735	7	ADCC6795	Human sec	971	37	51.4	897	7	ADT03964	Adt03964	Human sec
899	37	51.4	735	7	ADCC41115	Human sec	972	37	51.4	903	2	AAW25715	Aaw25715	Human sec
900	37	51.4	735	7	ADCC67170	Human sec	973	37	51.4					Mouse alp

974	37	51.4	906	8	ADQ39961	Adq39961 Human myo
975	37	51.4	909	2	AAR50092	AAR50092 Humanised
976	37	51.4	909	5	ABJ05540	ABJ05540 Breast ca
977	37	51.4	909	6	ABU56614	ABU56614 Lung canc
978	37	51.4	909	7	ADN80514	ADN80514 Ovarian c
979	37	51.4	909	8	ADN38780	ADN38780 Cancer/an
980	37	51.4	909	8	ADJ32434	ADJ32434 Human ADA
981	37	51.4	909	8	ADQ39960	ADQ39960 Human myo
982	37	51.4	909	8	ADR67220	ADR67220 Human bla
983	37	51.4	909	9	ADZ15120	ADZ15120 Human ADA
984	37	51.4	909	9	ADZ09876	ADZ09876 Human bre
985	37	51.4	909	9	AEA00128	AEA00128 Human TAT
986	37	51.4	909	9	AEA00648	AEA00648 Human TAT
987	37	51.4	7094	8	ABY03145	ABY03145 Bovine co
988	36.5	50.7	119	2	AAR79861	AAR79861 Anti-EGFR
989	36.5	50.7	119	2	AAR79863	AAR79863 Anti-EGFR
990	36	50.0	12	5	ABP46196	ABP46196 Human Bly
991	36	50.0	12	7	ADG97023	ADG97023 scFV VHCD
992	36	50.0	16	9	AEA14212	AEA14212 VEGF rela
993	36	50.0	17	9	AEA40758	AEA40758 Anti-VEGF
994	36	50.0	19	5	AAN70372	AAN70372 Human hea
995	36	50.0	31	2	AAR21422	AAR21422 Matrix pe
996	36	50.0	52	2	AAR12876	AAR12876 Non-colla
997	36	50.0	52	2	AAR12874	AAR12874 Non-colla
998	36	50.0	52	2	AAR12877	AAR12877 Non-colla
999	36	50.0	52	2	AAR12872	AAR12872 Non-colla
1000	36	50.0	52	2	AAR12875	AAR12875 Non-colla

ALIGNMENTS

RESULT 1

AAW62012 standard; peptide; 12 AA.

AAW62012;

01-OCT-1998 (first entry)

Heavy chain variable region complementarity determining region 3.

Complementarity determining region; heavy chain variable region;
 humanised antibody; MM24F(ab)-8; anti-CD11a antibody;
 human CD11a I domain; MM24 epitope; alpha subunit;
 lymphocyte function-associated antigen 1; LFA-1; immunoassay;
 in vivo imaging; diagnosis; CD11a-associated disease.

Mus sp.

Homo sapiens.

WO9823761-A1.

04-JUN-1998.

20-OCT-1997; 97WO-US019041.

27-NOV-1996; 96US-00757205.

(GERTH) GENENTECH INC.

Jardieu PM, Presta LG;

WPI, 1998-322737/28.

New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
 also to treat conditions such as immunological or inflammatory disease.

Claim 6; Page 2; 66pp; English.

AAW62010-12 represent complementarity determining regions of the heavy
 chain variable region of humanised antibody MM24F(ab)-8. The fragments
 were used to make a humanised anti-CD11a antibody that binds specifically

CC to the human CD11a I domain (MM24 epitope). CD11a refers to the alpha
 CC subunit of lymphocyte function-associated antigen 1 (LFA-1) from any
 CC mammal. The humanised anti-CD11a antibodies are used to determine
 CC presence of CD11a in usual immunoassays or by in vivo imaging,
 CC particularly for diagnosis of CD11a-associated diseases (typically immune
 CC responses and inflammation such as psoriasis, Crohn's disease, rheumatoid
 CC arthritis, transplant rejection, leukaemia, etc

SQ Sequence 12 AA;

Query Match 100.0%; Score 72; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIVFYGTTPDY 12
 DB 1 GIVFYGTTPDY 12

RESULT 2

AAV82339 standard; peptide; 12 AA.

AAV82339;

22-JUN-2000 (first entry)

Humanised anti-CD11a antibody heavy chain CDR3 SEQ ID NO:12.

Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 antitumour; antiviral; inflammation; immunological response; LFA-1;
 lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 viral infection; transplant rejection; graft rejection.

Mus sp.

Homo sapiens.

US6037454-A.

14-MAR-2000.

20-NOV-1997; 97US-00974899.

27-NOV-1996; 96US-0031971P.

(GERTH) GENENTECH INC.

Jardieu PM, Presta LG;

WPI, 2000-282241/24.

New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 inflammation and transplant rejection, contains human heavy variable
 region complementarity determining regions.

Claim 1; Col 57-58; 38pp; English.

The present invention describes a humanised anti-CD11a antibody (Ab) that
 binds specifically to the human CD11a I-domain. The Ab has anti-
 inflammatory, immunosuppressant, antitumour and antiviral activities. The
 Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 involved in leucocyte adhesion associated with inflammatory and
 immunological responses. The Ab are used: (i) optionally when coupled to
 a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 inflammatory bowel disease, eczema, systemic lupus erythematosus,
 rhinitis, leukaemia, viral infections and many others, also for
 inhibiting graft rejection; (ii) when labeled, to detect CD11a;
 tumor pretreatment; (iv) for delivery of enzymes that convert prodrugs
 to active anticancer agent; and (v) for affinity chromatography. The Ab
 retain about the same activity in adhesion and mixed lymphocyte response
 assays as the murine antibodies from which they are derived. The murine

CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
CC between Jurkat cells (expressing LFA-1) and normal epidermal
CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
CC sequence represents the heavy chain variable region CDR3 of the humanised
CC anti-CD11a Ab
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 72; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYTTPDY 12
DB 1 GIFYGTYTTPDY 12

RESULT 3
ADG39000
ID ADG39000 standard; peptide; 12 AA.
XX
AC ADG39000;
XX
DT 26-FEB-2004 (first entry)
XX
DE Humanised Mouse anti-CD11a antibody heavy chain variable region CDR3.
XX
KM Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
KM VH; cluster of differentiation 11a; mixed lymphocyte response assay;
KM Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
KM ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
KM psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
KM rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KM diabetes mellitus; prodrug activating enzyme; humanised;
KM complementarity determining region; CDR.
XX
OS Synthetic.
OS Mus sp.
XX
PN US2003207336-A1.
XX
PD 06-NOV-2003.
XX
PF 28-FEB-2001; 2001US-00795798.
XX
PR 27-NOV-1996; 96US-0031971P.
XX
PR 20-NOV-1997; 97US-00974899.
XX
PR 20-OCT-1999; 99US-00420745.
XX
PA (GENTH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 2004-051511/05.
XX
PT Humanized anti-CD11a antibody useful for treating lymphocyte function-
PT associated antigen mediated disorder e.g. psoriasis; Crohn's disease,
PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
XX
PS Claim 6; SEQ ID NO 12; 43bp; English.
XX
XX The invention relates to a Humanised anti-cluster of differentiation
CC (CD11a) antibody having specificity to human CD11a I-domain or CD11a with
CC a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
CC inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
CC response assay or for preventing adhesion of Jurkat cells to normal human
CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
CC -1. Also included are a kit comprising the antibody and instructions for
CC use to detect the CD11a protein, an isolated nucleic acid encoding the
CC antibody, a vector comprising the nucleic acid, a host cell comprising
CC the vector and producing the antibody by culturing the cell so that the
CC antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The

CC antibody is useful for determining the presence of CD11a protein and for
CC treating lymphocyte function-associated antigen 1 mediated disorder such
CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
CC and diabetes mellitus. The antibody is useful when conjugated to a
CC prodrug activating enzyme, or as an affinity purification agent. The
CC present sequence is a CDR (complementarity determining region) of the
CC heavy chain variable region (VH) of the humanised mouse anti-CD11a I
CC domain monoclonal antibody MHM24.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 72; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYTTPDY 12
DB 1 GIFYGTYTTPDY 12

RESULT 4
AAV29452
ID AAV29452 standard; protein; 116 AA.
XX
AC AAV29452;
XX
DT 05-OCT-1999 (first entry)
XX
DE Human IgG1 subgroup III heavy chain variable domain.
XX
KM Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
KM diagnosis; inflammatory disorder; conjugate; immunoglobulin;
KM fusion protein.
XX
XX Homo sapiens.
XX
OS
XX
PN WO9937779-A1.
XX
PD 29-JUL-1999.
XX
PF 19-JAN-1999; 99WO-US001081.
XX
PR 22-JAN-1998; 98US-00012116.
XX
PR 20-FEB-1998; 98WO-US003337.
XX
PR 24-JUL-1998; 98US-00121952.
XX
PR 24-JUL-1998; 98US-00122513.
XX
PA (GENTH) GENENTECH INC.
XX
PI Hael V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z, Zapata GA;
XX
DR WPI; 1999-469134/39.
XX
PT New conjugates of nonproteinaceous polymers with antibody fragments, used
PT for treating inflammatory disorders.
XX
PS Disclosure; Fig 29; 360pp; English.
XX
XX The present invention describes a novel conjugate having one or more
CC antibody fragments covalently attached to one or more nonproteinaceous
CC polymer molecules, where the apparent size of the conjugate is at least
CC about 500 kDa. Conjugates of antibody fragments which bind the human
CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC treating inflammatory disorders e.g. acute lung injury, ischemic
CC reperfusion disorder, and autoimmune diseases. They can also be used for
CC treating e.g. inflammatory skin diseases including psoriasis and atopic
CC dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases.
CC The conjugates can also be used as reagents in an animal model system for
CC in vivo study of the biological functions of the antigen recognised by
CC the conjugate. The present sequence represents the human IgG1 subgroup
CC III heavy chain variable domain form the present invention
XX

SQ Sequence 116 AA;

Query Match 100.0%; Score 72; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GIFYGTTYFDY 12
 |||||
 100 GIFYGTTYFDY 111

RESULT 5

AA77755
 ID AA77755 standard; protein; 116 AA.

AC AA77755;

DT 06-JUN-2000 (first entry)

DE Human IgG1 subgroup III heavy chain variable domain.

XX Interleukin-8, IL-8; monoclonal antibody; Mab; anti-IL-8; 6G4.2.SV11N35A;
 KW inflammatory disorder; adult respiratory distress syndrome; chimeric;
 KW affinity purification; 6G4.2.5.

XX Homo sapiens.

OS US6025158-A.

PM 15-FEB-2000.

PD 20-FEB-1998; 98US-00027449.

PF 21-FEB-1997; 97US-0038664P.

PR 22-JAN-1998; 98US-0074330P.

PA (GETH) GENENTECH INC.

PI Presta LG, Leong SR, Gonzalez TN;

DR WPI; 2000-181809/16.

PT New nucleic acid molecule encodes a polypeptide which is an anti-interleukin-8 monoclonal antibody or antibody fragment useful for the production of anti-interleukin-8 monoclonal antibodies or fragments.

PS Example; Fig 29; 188bp; English.

XX The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody (Mab). The anti-IL-8 Mab comprises a sequence containing the CDRs (complementarity determining regions) of the humanized anti-IL-8 6G4.2.SV11N35A light chain; and amino acids 24-253 of the humanized anti-IL-8 6G4.2.SV11N35A heavy chain. The anti-IL-8 Mabs and fragments can be used in diagnosis, for affinity purification of IL-8 from recombinant cell culture or natural sources and for the treatment of inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic acids encoding the anti-IL-8 Mab can be associated in a vector with another gene encoding another protein or protein fragment to produce a fusion protein which can make isolation and/or purification of the protein an easier process

SQ Sequence 116 AA;

Query Match 100.0%; Score 72; DB 3; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GIFYGTTYFDY 12
 |||||
 100 GIFYGTTYFDY 111

RESULT 6

AAB30312
 ID AAB30312 standard; protein; 116 AA.

AC AAB30312;

DT 12-FEB-2001 (first entry)

DE Human IgG1 subgroup III heavy chain V region SEQ ID NO: 50.

KW Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
 KW adult respiratory distress syndrome; multiple organ failure;
 KW bacterial pneumonia; inflammatory bowel disease.

XX Homo sapiens.

OS US6133426-A.

PM 17-OCT-2000.

PD 20-FEB-1998; 98US-00026985.

PF 21-FEB-1997; 97US-0038664P.

PR 22-JAN-1998; 98US-0074330P.

PA (GETH) GENENTECH INC.

PI Presta LG, Leong SR, Gonzalez TN;

DR WPI; 2000-686027/67.

PT Humanized anti-interleukin 8 monoclonal antibody variant useful for treating inflammatory disorders, such as adult respiratory distress syndrome, hypovolemic shock and ulcerative colitis.

PS Disclosure; Col 163-164; 240bp; English.

XX The present invention provides a number of humanised monoclonal anti-IL-8 antibodies which can be used in the diagnosis and treatment of inflammatory disorders, including adult respiratory distress syndrome, septic shock, multiple organ failure, bacterial pneumonia and inflammatory bowel disease. The present sequence comprises one of the antibodies of the invention

SQ Sequence 116 AA;

Query Match 100.0%; Score 72; DB 3; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GIFYGTTYFDY 12
 |||||
 100 GIFYGTTYFDY 111

RESULT 7

ABU13789
 ID ABU13789 standard; protein; 116 AA.

AC ABU13789;

DT 25-FEB-2003 (first entry)

DE Human IgG1 subgroup III heavy chain variable domain.

XX Antibody; monoclonal antibody; 5.12.14; 6G4.2.5; interleukin-8; mab;
 KW antiinflammatory; respiratory; acute lung injury; polyethylene glycol;
 KW PEG; lung injury; adult respiratory distress syndrome; ARDS; asthma;
 KW inflammatory disease; inflammatory bowel disease; psoriasis; sclerosis;
 KW ischaemic reperfusion disorder; stroke; multiple sclerosis; meningitis;
 KW osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis;
 KW alcoholic hepatitis; cystic fibrosis; human.

OS Homo sapiens.

PX	US6469532-BL.
PN	
XX	
PD	22-OCT-2002.
PF	20-JAN-1999;
PR	98US-00234340.
PR	22-JAN-1998;
PR	98US-0074330P.
PR	20-FEB-1998;
PR	98US-0075467P.
PR	24-JUL-1998;
PR	98US-0094003P.
PR	24-JUL-1998;
PR	98US-0094013P.
PA	(GETH) GENENTECH INC.
PI	Hseil V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
XX	
DR	WPI; 2003-138230/13.
PT	Treating acute lung injury in mammal by administering to mammal a 500 kD
PT	conjugate comprising F(ab') ₂ antibody fragment that binds to human
PT	interleukin-8, covalently attached to one or two polyethylene glycol
PT	molecules.
XX	
PS	Example G; Fig 29; 259pp; English.
XX	
CC	The invention relates to treating acute lung injury in a mammal,
CC	comprising administering to the mammal an effective amount of a conjugate
CC	of a single antibody fragment covalently attached to 1 or 2 polyethylene
CC	glycol (PEG) molecules, where the antibody fragment is a F(ab') ₂
CC	comprising: (a) first chain that is either a light chain or a heavy chain
CC	; (b) a first opposite chain that is either a heavy chain opposite the
CC	first light chain or a light chain opposite the first heavy chain; (c) a
CC	second light chain that is either a light chain or a heavy chain; and (d) a
CC	second opposite chain that is either a heavy chain opposite the second
CC	light chain or a light chain opposite the second heavy chain; where every
CC	PEG molecule is covalently attached to a first cysteine residue in the
CC	first or second chain that would ordinarily form a disulfide bridge with
CC	a second cysteine residue in the first or second opposite chain, where
CC	the disulfide bridge is avoided by substitution of another amino acid
CC	residue for the second cysteine residue in the first or second opposite
CC	chain, where the F(ab') ₂ comprises an antigen binding site that binds to
CC	human interleukin-8 (IL-8), and where the apparent size of the conjugate
CC	is at least about 500 kD. The antigen binding sites may be derived from
CC	murine monoclonal antibodies 5.12.14 or 6G4.2.5. The method is useful for
CC	treating lung injury, including adult respiratory distress syndrome
CC	(ARDS) in a mammal and inflammatory diseases (such as asthma,
CC	inflammatory bowel disease, psoriasis and sclerosis), ischemic
CC	reperfusion disorders, stroke, multiple sclerosis, meningitis,
CC	osteoarthritis, septic shock, autoimmune disease (e.g., rheumatoid
CC	arthritis), alcoholic hepatitis, cystic fibrosis and many other diseases
CC	and disorders listed in the specification. The present sequence
CC	represents a human antibody sequence included for comparison with the
CC	mouse humanised monoclonal antibody sequences
XX	
SQ	Sequence 116 AA;
OY	Query Match 100.0%; Score 72; DB 6; Length 116;
DB	Best Local Similarity 100.0%; Pred. No. 0.0017; Indels 0; Gaps 0
MATCHES	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
1	GIFYGYTFDY 12
100	GIFYGYTFDY 111
RESULT 8	
ID	ABU59502
AC	ABU59502 standard; protein; 116 AA.
XX	
DT	22-APR-2003 (first entry)
XX	

DE	Human IgG1 subgroup III heavy chain variable domain.
XX	
KM	Interleukin-8; IL-8; humanised antibody; antibody; 5.12.14; 6G4.2.5;
KW	inflammatory disorder; psoriasis; atopic dermatitis; sclerosis;
KW	systemic scleroderma; inflammatory bowel disease; Crohn's disease;
KW	ulcerative colitis; ischaemia; reperfusion; myocardial infarction;
KW	stroke; adult respiratory distress syndrome; rheumatoid arthritis;
KW	alcoholic hepatitis; acute lung injury; asthma; cerebral oedema;
KW	myocardial ischaemia; cranial trauma; aphasia; Behcet's disease;
KW	demyelinating diseases; polymyositis; multiple sclerosis; meningitis;
KW	autoimmune disease; Sjogren's syndrome; vasculitis; septicæmia;
KW	central nervous system inflammatory disorder; sepsis; sarcoidosis;
KW	inflamation of the lung; human.
OS	Homo sapiens.
XX	
PN	US6458355-B1.
XX	
PD	01-OCT-2002.
XX	
PF	24-JUL-1998; 98US-00121952.
XX	
PR	22-JAN-1998; 98US-0074330P.
PR	20-FEB-1998; 98US-0075467P.
XX	
PA	(GENTH) GENENTECH INC.
PI	Hseil V, Koumenis I, Leong S, Presta L, Shahrokhi Z, Zapata G;
DR	WPI; 2003-208759/20.
XX	
PT	Treating inflammatory disorder in a mammal, involves administering a
PT	conjugate of polyethylene glycol and a single antibody fragment
PT	comprising antigen binding site that binds to human interleukin-8, to
PT	mammal.
XX	
PS	Example 3G; Fig 29; 259pp; English.
XX	
CC	The invention relates to treating an inflammatory disorder in a mammal,
CC	comprising administering to the mammal, an effective amount of a
CC	conjugate of a single antibody fragment (e.g. the heavy or light chains
CC	of the humanised mouse monoclonal antibodies 5.12.14 and 6G4.2.5, which
CC	also have their intramolecular disulphide bridges ablated by substitution
CC	(mutations) covalently attached to one or two polyethylene glycol (PEG)
CC	molecules. The antibodies comprise an antigen binding site that binds to
CC	human interleukin-8 (IL-8), and the apparent size of the conjugate is at
CC	least 500 kDa. The method is useful for treating an inflammatory disorder
CC	e.g., ischemic reperfusion disorder such as surgical tissue reperfusion
CC	injury, myocardial ischaemia or myocardial infarction, or hypovolemic
CC	shock, in a mammal e.g. human . The method is useful for treating
CC	inflammatory disorders including psoriasis, atopic dermatitis, systemic
CC	scleroderma and sclerosis, responses associated with inflammatory bowel
CC	disease, ischemic reperfusion disorders, myocardial ischemic
CC	conditions, cerebral oedema secondary to stroke, cranial trauma,
CC	asphyxia, adult respiratory distress syndrome, acute-lung injury,
CC	Behcet's disease, dematomyositis, polymyositis, multiple sclerosis,
CC	dermatitis, meningitis, encephalitis, uveitis, osteoarthritis, lupus
CC	nephritis, autoimmune diseases such as rheumatoid arthritis, Sjogren's
CC	syndrome, vasculitis, central nervous system inflammatory disorder,
CC	multiple organ injury syndrome secondary to septicæmia or trauma,
CC	alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex,
CC	mediated diseases including glomerulonephritis, sepsis, sarcoidosis,
CC	immunopathologic responses to tissue/organ transplantation, inflammations
CC	of the lung, inflammatory bowel disease such as ulcerative colitis and
CC	asthma. The present sequence represents the light or heavy chain of human
CC	IgG ₁ , used to design the humanising mutations in the two mouse antibodies
XX	
SO	Sequence 116 AA;
Query Match	100.0%; Score 72; DB 6; Length 116;
Best Local Similarity	100.0%; Pred. No. 0.0017;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GIFYGTYFPDY 12
 |||||
 Db 100 GIFYGTYFPDY 111

RESULT 9
 AAE39085
 ID AAE39085 standard; protein; 116 AA.
 XX
 AC AAE39085;
 XX
 DT 18-DEC-2003 (first entry)
 XX

DE Human IgG1 subgroup III heavy chain variable domain.

XX Interleukin-8 mediated disease; adult respiratory distress syndrome; IL;
 KW bacterial pneumonia; inflammatory bowel disease; hypovolemic shock; ARDS;
 KW ulcerative colitis; ischemic reperfusion injury; myocardial infarction;
 KW acute lung injury; inflammatory disease; asthma; antibody; human; VH;
 KW heavy chain variable domain.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 26..35

XX /note= "Complementarity determining region (CDR) #1"

XX Region 50..66

XX /note= "Complementarity determining region (CDR) #2"

XX Region 100..111

XX /note= "Complementarity determining region (CDR) #3"

XX US2003021790-A1.

XX 30-JAN-2003.

XX 29-NOV-2000; 2000US-00726258.

XX 22-JAN-1998; 98US-0074330P.

XX 20-FEB-1998; 98US-0075467P.

XX 24-JUL-1998; 98US-0094003P.

XX 20-JAN-1998; 98US-0094013P.

XX 20-JAN-1999; 99US-00234182.

XX (GETH) GENENTECH INC.

XX Hsai V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 XX WPI; 2003-605694/57.

XX Novel conjugates comprising antibody fragments covalently attached to
 PT nonproteinaceous polymer molecules, useful for treating inflammatory
 PT diseases, acute lung injury, ischemic reperfusion injury, pneumonia and
 PT asthma.

XX Example; Fig 29; 266pp; English.

XX The invention relates to novel conjugates comprising antibody fragments
 CC covalently attached to nonproteinaceous polymer molecules. The invention
 CC is useful for treating interleukin (IL)-8 mediated diseases or disorders
 CC such as inflammatory diseases, acute lung injury e.g. adult respiratory
 CC distress syndrome (ARDS), ischemic reperfusion injury e.g. myocardial
 CC infarction, hypovolemic shock, inflammatory bowel disease e.g. ulcerative
 CC colitis, bacterial pneumonia and asthma. The invention is also useful as
 CC a reagent in an animal model system for in vivo study of the biological
 CC functions of the antigen recognised by the conjugate. The present
 CC sequence is human IgG1 subgroup III VH (heavy chain variable domain)
 CC protein. This sequence is used in the exemplification of the invention

XX Sequence 116 AA;

Query Match 100.0%; Score 72; DB 7; Length 116;

Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GIFYGTYFPDY 12
 |||||
 Db 100 GIFYGTYFPDY 111

RESULT 10
 AAW62013

ID AAW62013 standard; peptide; 121 AA.

XX AAW62013;

XX 01-OCT-1998 (first entry)

XX Heavy chain variable region of humanised anti-CD11a antibody.

XX Complementarity determining region; heavy chain variable region;

XX humanised antibody; MHM24(ab)-8; anti-CD11a antibody;

XX human CD11a I domain; MHM24 epitope; alpha subunit;

XX lymphocyte function-associated antigen 1; LFA-1; immunoassay;
 KW in vivo imaging; diagnosis; CD11a-associated disease.

XX Mus sp.

XX Homo sapiens.

XX MO9823761-A1.

XX 04-JUN-1998.

XX 20-OCT-1997; 97WO-US019041.

XX 27-NOV-1996; 96US-00757205.

XX (GETH) GENENTECH INC.

XX Jardiou PM, Presta LG;

XX WPI; 1998-32237/28.

XX New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
 PT also to treat conditions such as immunological or inflammatory disease.
 PS Claim 7; Page 50; 66pp; English.

XX The present sequence represents the heavy chain variable region of a
 CC humanised anti-CD11a antibody that binds specifically to the human CD11a
 CC I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte
 CC function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-
 CC -CD11a antibodies are used to determine presence of CD11a in usual
 CC immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-
 CC associated diseases (typically immune responses and inflammation such as
 CC psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
 CC leukaemia, etc

XX Sequence 121 AA;

Query Match 100.0%; Score 72; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GIFYGTYFPDY 12
 |||||
 Db 99 GIFYGTYFPDY 110

RESULT 11
 AAW62019

ID AAW62019 standard; peptide; 121 AA.

XX AAW62019;

XX

```

DT 01-OCT-1998 (first entry)
XX Rheusused heavy chain of humanised anti-CD11a antibody.
XX
XX Complementarity determining region; heavy chain variable region;
XX humanised antibody; MM24F(ab)-8; anti-CD11a antibody;
XX human CD11a I domain; MM24 epitope; alpha subunit;
XX lymphocyte function-associated antigen 1; LFA-1; immunoassay;
XX in vivo imaging; diagnosis; CD11a-associated disease.
XX
XX Unidentified.
XX
XX WO9823761-A1.
XX
XX 04-JUN-1998.
XX
XX 20-OCT-1997; 97WO-US019041.
XX
XX 27-NOV-1996; 96US-00757205.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Jardieu PM, Presta LG;
XX
XX WPI; 1998-322737/28.
XX
XX New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
XX also to treat conditions such as immunological or inflammatory disease.
XX
XX Disclosure; Page 56; 66pp; English.
XX
XX The present sequence represents the heavy chain of a "rheusused" (sic)
XX humanised anti-CD11a antibody that binds specifically to the human CD11a
XX I domain (MM24 epitope). CD11a refers to the alpha subunit of lymphocyte
XX function-associated antigen 1 (LFA-1) from any mammal. The humanised anti
XX -CD11a antibodies are used to determine presence of CD11a in usual
XX immunoassays or by in vivo imaging, particularly for diagnosis of CD11a-
XX associated diseases (typically immune responses and inflammation such as
XX psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
XX leukaemia, etc
XX
XX Sequence 121 AA;
SQ
Query Match 100.0%; Score 72; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTTYFDY 12
DB 99 GIFYGTTYFDY 110

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PD 04-JUN-1998.
XX
XX 29-OCT-1997; 97WO-US020169.
XX
XX 27-NOV-1996; 96US-00756150.
XX
XX (GERTH ) GENENTECH INC.
XX
XX Jardieu PM, Presta LG;
XX
XX WPI; 1998-322726/28.
XX
XX Mutants of species-dependent antibodies with affinity for non-human
XX mammalian antigen - greater than for parent antibody, particularly used
XX for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
XX directed against CD11a.
XX
XX Claim 13; Page 59-60; 71pp; English.
XX
XX This sequence represents the heavy chain variable domain of a mutant
XX murine antibody MM24 of the invention. The mutants are of a species-
XX dependent antibody (Ab), and have an amino acid substitution in a
XX variable region of the Ab, and binding affinity for an antigen (Ag) from
XX a non-human mammal at least 10 times stronger than for the wild type Ab
XX against the Ag. The mutant antibodies are particularly intended for
XX administration to a non-human mammal in preclinical studies (e.g. of
XX infection, immunity, haematopoiesis or transplantation). They can also be
XX used diagnostically (to identify specific proteins) or therapeutically,
XX e.g. where directed against CD11a (lymphocyte function-associated antigen
XX -1) or intercellular adhesion molecule-1 against a wide variety of
XX inflammatory or autoimmune diseases, malignancies, transplant rejection,
XX human immune deficiency virus infection and tumour cell invasion.
XX Conversion to the mutant form allows useful antibodies to be produced
XX from antibodies which normally have affinity for non-human analogues of
XX the Ag too low to be of any use
XX
XX Sequence 121 AA;
SQ
Query Match 100.0%; Score 72; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTTYFDY 12
DB 99 GIFYGTTYFDY 110

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```

RESULT 12
AAW63542
ID AAW63542 standard; protein; 121 AA.
XX
XX AAW63542;
XX
XX 06-OCT-1998 (first entry)
XX
XX Murine MM24 heavy chain variable domain mutant.
XX
XX Antibody mutant production; species-dependent antibody; malignancy;
XX infection; haematopoiesis; lymphocyte function-associated antigen-1;
XX intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
XX autoimmune disease; transplant rejection; tumour cell invasion;
XX human immune deficiency virus infection; heavy chain.
XX
XX Synthetic.
XX
XX Mus sp.
XX
XX MO9823746-A1.
XX

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RESULT 13
AAW63531
ID AAW63531 standard; protein; 121 AA.
XX
XX AAW63531;
XX
XX 06-OCT-1998 (first entry)
XX
XX Murine MM24 heavy chain.
XX
XX Antibody mutant production; species-dependent antibody; malignancy;
XX infection; haematopoiesis; lymphocyte function-associated antigen-1;
XX intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
XX autoimmune disease; transplant rejection; tumour cell invasion;
XX human immune deficiency virus infection; heavy chain.
XX
XX Mus sp.
XX
XX WO9823746-A1.
XX
XX 04-JUN-1998.
XX
XX 29-OCT-1997; 97WO-US020169.
XX
XX 27-NOV-1996; 96US-00756150.
XX

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PA (GETH) GENENTECH INC.
 XX Jardieu PM, Presta LG;
 XX WPI: 1998-322726/28.
 DR
 XX Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD11a.
 XX
 XX Disclosure: Page 54; 71pp; English.
 PS
 XX This sequence represents the heavy chain of the murine antibody MEM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 CC
 XX SQ Sequence 121 AA;
 XX
 XX Query Match 100.0%; Score 72; DB 2; Length 121;
 XX Best Local Similarity 100.0%; Pred. No. 0.0017;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 1 GIFYGYTTYFDY 12
 XX |||||
 Db 99 GIFYGYTTYFDY 110
 XX
 RESULT 14
 AA63532
 ID AAW63532 standard; protein; 121 AA.
 XX
 AC AAW63532;
 XX
 DT 06-OCT-1998 (first entry)
 XX
 DE Humanised MEM24 heavy chain.
 XX
 KW Antibody mutant production; species-dependent antibody; malignancy;
 KW infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KW intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 KW autoimmune disease; transplant rejection; tumour cell invasion;
 KW human immune deficiency virus infection; heavy chain.
 XX
 OS Synthetic.
 XX
 FN WO9823746-A1.
 XX
 PD 04-JUN-1998.
 XX
 PF 29-OCT-1997; 97WO-US020169.
 XX
 PR 27-NOV-1996; 96US-00756150.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI: 1998-322726/28.
 XX

PT Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD11a.
 XX
 XX Disclosure: Page 55; 71pp; English.
 PS
 XX This sequence represents the heavy chain of the humanised antibody MEM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 CC
 XX SQ Sequence 121 AA;
 XX
 XX Query Match 100.0%; Score 72; DB 2; Length 121;
 XX Best Local Similarity 100.0%; Pred. No. 0.0017;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 1 GIFYGYTTYFDY 12
 XX |||||
 Db 99 GIFYGYTTYFDY 110
 XX
 RESULT 15
 AA82348
 ID AAY82348 standard; protein; 121 AA.
 XX
 AC AAY82348;
 XX
 DT 22-JUN-2000 (first entry)
 XX
 DE Rhesusised antibody mutant heavy chain SEQ ID NO:24.
 XX
 KW Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 KW antitumour; antiviral; inflammation; immunological response; LFA-1;
 KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KW viral infection; transplant rejection; graft rejection.
 XX
 OS Macaca mulatta.
 XX
 FN Mus sp.
 XX
 PD US6037454-A.
 XX
 PF 14-MAR-2000.
 XX
 PR 20-NOV-1997; 97US-00974899.
 XX
 PA 27-NOV-1996; 96US-0031971P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI: 2000-282241/24.
 XX
 PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 PT inflammation and transplant rejection, contains human heavy variable
 PT region complementarily determining regions.
 XX
 PS Example; Fig 1; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that
CC binds specifically to the human CD11a I-domain. The Ab has anti-
CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
CC involved in leucocyte adhesion associated with inflammatory and
CC immunological responses. The Ab are used: (i) optionally when coupled to
CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
CC rhinitis, leukaemia, viral infections and many others, also for
CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
CC to active anticancer agent; and (v) for affinity chromatography. The Ab
CC retain about the same activity in adhesion and mixed lymphocyte response
CC assays as the murine antibodies from which they are derived. The murine
CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
CC between Jurkat cells (expressing LFA-1) and normal epidermal
CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
CC sequence represents the amino acid sequence of a rhensised antibody
CC mutant heavy chain, which is used in the exemplification of the present
CC invention
CC
SQ Sequence 121 AA;
Query Match 100.0%; Score 72; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTTYFDY 12
Db 99 GIFYGTTYFDY 110
RESULT 16
AA82336
ID AAY82336 standard; protein; 121 AA.
AC AAY82336;
DT 22-JUN-2000 (first entry)
XX
DE Humanised anti-CD11a antibody heavy chain variable region SEQ ID NO:5.
XX
KW Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
KW antitumour; antiviral; inflammation; immunological response; LFA-1;
KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
KW viral infection; transplant rejection; graft rejection.
XX
OS Homo sapiens.
OS Mus sp.
XX
XX US6037454-A,
XX 14-MAR-2000.
XX PD
XX PF 20-NOV-1997; 97US-00974899.
XX PR 27-NOV-1996; 96US-0031971P.
XX PA (GETH) GENENTECH INC.
XX PI Jardieu PM, Presta LG;
XX DR WPI; 2000-282241/24.
XX PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.
XX PT inflammation and transplant rejection, contains human heavy variable
XX PT region complementarity determining regions.
XX PS Claim 1, Fig 1; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that
CC binds specifically to the human CD11a I-domain. The Ab has anti-
CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
CC involved in leucocyte adhesion associated with inflammatory and
CC immunological responses. The Ab are used: (i) optionally when coupled to
CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
CC rhinitis, leukaemia, viral infections and many others, also for
CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
CC to active anticancer agent; and (v) for affinity chromatography. The Ab
CC retain about the same activity in adhesion and mixed lymphocyte response
CC assays as the murine antibodies from which they are derived. The murine
CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
CC between Jurkat cells (expressing LFA-1) and normal epidermal
CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
CC sequence represents the heavy chain variable region of the humanised anti
CC -CD11a Ab
CC
SQ Sequence 121 AA;
Query Match 100.0%; Score 72; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTTYFDY 12
Db 99 GIFYGTTYFDY 110
RESULT 17
AA82346
ID AAY82346 standard; protein; 121 AA.
AC AAY82346;
DT 22-JUN-2000 (first entry)
XX
DE Murine MHM24 heavy chain amino acid sequence SEQ ID NO:4.
XX
KW Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
KW antitumour; antiviral; inflammation; immunological response; LFA-1;
KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
KW viral infection; transplant rejection; graft rejection.
XX
OS Mus sp.
XX
XX US6037454-A.
XX PN
XX PD 14-MAR-2000.
XX PF 20-NOV-1997; 97US-00974899.
XX PR 27-NOV-1996; 96US-0031971P.
XX PA (GETH) GENENTECH INC.
XX PI Jardieu PM, Presta LG;
XX DR WPI; 2000-282241/24.
XX PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.
XX PT inflammation and transplant rejection, contains human heavy variable
XX PT region complementarity determining regions.
XX PS Example; Fig 1; 38pp; English.
XX CC The present invention describes a humanised anti-CD11a antibody (Ab) that

binds specifically to the human CD11a I-domain. The Ab has anti-inflammatory, immunosuppressant, antitumour and antiviral activities. The Ab blocks lymphocyte adhesion associated with inflammatory and CC involved in leucocyte adhesion associated with inflammatory and CC immunological responses. The Ab are used: (i) optionally when coupled to a cytoxin, to treat or prevent disorders mediated by lymphocyte CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis, CC inflammatory bowel disease, eczema, systemic lupus erythematosus, CC rhinitis, leukaemia, viral infections and many others, also for CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs to active anticancer agent; and (v) for affinity chromatography. The Ab CC retain about the same activity in adhesion and mixed lymphocyte response assays as the murine antibodies from which they are derived. The murine CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion CC between Jurkat cells (expressing LFA-1) and normal epidermal CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1). CC The fully humanized version of MHM24 had IC50 0.13 nM. The present CC sequence represents the amino acid sequence of murine MHM24 heavy chain, CC which is used in the exemplification of the present invention

SO Sequence 121 AA;

Query Match 100.0%; Score 72; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYFGTYTDPY 12
|||
Db 99 GIFYFGTYTDPY 110

RESULT 18

ADG38012 standard; protein; 121 AA.

ADG39012;

26-FEB-2004 (first entry)

Rheusused mouse anti-CD11a I-domain antibody VL.

Mouse; CD11a; I-domain; monoclonal antibody;
Cluster of differentiation 11a; mixed lymphocyte response assay;
Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
diabetes mellitus; prodrug activating enzyme.

Synthetic.

Mus sp.

US2003207336-A1.

06-NOV-2003.

28-FEB-2001; 2001US-00795798.

27-NOV-1996; 96US-0031971P.
20-NOV-1997; 97US-00974899.
20-OCT-1999; 99US-00420745.

(GETH) GENENTECH INC.

Jardieu PM, Presta LG;

WPI; 2004-051511/05.

Humanized anti-CD11a antibody useful for treating lymphocyte function-associated antigen mediated disorder e.g. psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

PS Example; SEQ ID NO 24; 43pp; English.

The invention relates to a Humanised anti-cluster of differentiation (CD) 11a antibody having specificity to human CD11a I-domain or CD11a with a Kd value of not more than 1x10⁻⁸ M, or concentration for 50 % inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte response assay or for preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)-1. Also included are a kit comprising the antibody and instructions for use to detect the CD11a protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising the vector and producing the antibody by culturing the cell so that the antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The antibody is useful for determining the presence of CD11a protein and for treating lymphocyte function-associated antigen 1 mediated disorder such as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a prodrug activating enzyme, or as an affinity purification agent. The present sequence is the light chain of a rheusused anti-CD11a antibody of the invention.

SO Sequence 121 AA;

Query Match 100.0%; Score 72; DB 8; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYFGTYTDPY 12
|||
Db 99 GIFYFGTYTDPY 110

RESULT 19

ADG38992 standard; protein; 121 AA.

ADG38992;

26-FEB-2004 (first entry)

Mouse anti-CD11a antibody heavy chain variable region.

Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
VH; cluster of differentiation 11a; mixed lymphocyte response assay;
Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
diabetes mellitus; prodrug activating enzyme.

Mus sp.

US2003207336-A1.

06-NOV-2003.

28-FEB-2001; 2001US-00795798.

27-NOV-1996; 96US-0031971P.
20-NOV-1997; 97US-00974899.
20-OCT-1999; 99US-00420745.

(GETH) GENENTECH INC.

Jardieu PM, Presta LG;

WPI; 2004-051511/05.

Humanized anti-CD11a antibody useful for treating lymphocyte function-associated antigen mediated disorder e.g. psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

PS Example; SEQ ID NO 4; 43pp; English.

XX The invention relates to a Humanised anti-cluster of differentiation
 CC (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 CC a Kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MEM24 on CD11a. The
 CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is the heavy chain variable region (VH) of the wild-type
 CC mouse anti-CD11a I domain monoclonal antibody MEM24.

XX Sequence 121 AA;

Query Match 100.0%; Score 72; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GIFYGTYFDY 12
 |||||
 DB 99 GIFYGTYFDY 110

RESULT 20

ADG38993
 ID ADG38993 standard; protein; 121 AA.

AC ADG38993;

DT 26-FEB-2004 (first entry)

DE Humanised Mouse anti-CD11a antibody heavy chain variable region.

XX Mouse; CD11a; I-domain; monoclonal antibody; heavy chain variable region;
 KW VH; cluster of differentiation 11a; mixed lymphocyte response assay;
 KW Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 KW ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 KW psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; prodrug activating enzyme; humanised.

OS Synthetic.
 OS Mus sp.

PN US2003207336-A1.

PD 06-NOV-2003.

PF 28-FEB-2001; 2001US-00795798.

PR 27-NOV-1996; 96US-0031971P.

PR 20-NOV-1997; 97US-00974899.

PR 20-OCT-1999; 99US-00420745.

PA (GETH) GENENTECH INC.

PI Jardieu PM, Presta LG;

XX WPI, 2004-051511/05.

PT Humanized anti-CD11a antibody useful for treating lymphocyte function-
 PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

XX Claim 7; SEQ ID NO 5; 43pp; English.

XX The invention relates to a Humanised anti-cluster of differentiation
 CC (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 CC a Kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MEM24 on CD11a. The
 CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is the heavy chain variable region (VH) of the humanised
 CC mouse anti-CD11a I domain monoclonal antibody MEM24.

XX Sequence 121 AA;

Query Match 100.0%; Score 72; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GIFYGTYFDY 12
 |||||
 DB 99 GIFYGTYFDY 110

RESULT 21

ADRO3368
 ID ADRO3368 standard; protein; 121 AA.

AC ADRO3368;

DT 21-OCT-2004 (first entry)

DE Humanised MEM24 F(ab)-8 antibody variable heavy chain protein.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain;
 KW VH; murine; human; fusion protein.

OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.

PN US2004146507-A1.

PD 29-JUL-2004.

PF 03-DEC-2003; 2003US-00727737.

PR 27-NOV-1996; 96US-0031945P.

PR 20-NOV-1997; 97US-00975329.

PA (GETH) GENENTECH INC.

PI Jardiou PM, Presta LG;
 XX WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 5; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MHM24) Flab-8 variable heavy chain protein. This sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 121 AA;
 XX
 Query Match 100.0%; Score 72; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GIFYGTYFPDY 12
 Db 99 GIFYGTYFPDY 110
 XX
 RESULT 22
 ADR03380
 ID ADR03380 standard; protein; 121 AA.
 XX
 AC ADR03380;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Rheusised MHM24 antibody variable heavy chain mutant protein.
 XX
 KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 KW VH; murine; rhesus macaque; fusion protein; mutant; mutein.
 XX
 OS Mus sp.
 OS Macaca mulatta.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX
 PF 03-DEC-2003; 2003US-0072737.
 XX

PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Jardiou PM, Presta LG;
 XX WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 17; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is rheusised murine anti-human CD11a monoclonal
 CC antibody (MHM24) variable heavy chain protein. This sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 121 AA;
 XX
 Query Match 100.0%; Score 72; DB 8; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GIFYGTYFPDY 12
 Db 99 GIFYGTYFPDY 110
 XX
 RESULT 23
 ADR03367
 ID ADR03367 standard; protein; 121 AA.
 XX
 AC ADR03367;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Murine MHM24 antibody variable heavy chain protein.
 XX
 KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 KW VH; murine.
 XX
 OS Mus sp.
 OS US2004146507-A1.
 XX
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX

CC purifying a protein, which comprises a CH2/CH3 region by protein A
 CC affinity chromatography and for reducing leaching of protein A during
 CC protein A affinity chromatography. The current sequence represents the
 CC variable heavy chain amino acid sequence of CD11a.
 XX
 SQ Sequence 121 AA;

Query Match 100.0%; Score 72; DB 9; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTTYFDY 12
 |||||
 DB 99 GIFYGTTYFDY 110

RESULT 26
 ADP11670
 ID ADP11670 standard; protein; 451 AA.

XX ADP11670;
 XX
 DT 26-FEB-2004 (first entry)
 DE anti-CD11a rhumAb heavy chain amino acid sequence #SEQ ID 4.

XX Purifying target protein; non-affinity purification;
 KM high-performance tangential flow filtration; HPRFP; pharmaceutical;
 KM diagnostic; therapeutic; antibody.

XX Synthetic.
 OS
 PM WO2003102132-A2.

XX 11-DEC-2003.

XX 25-APR-2003; 2003WO-US013054.

XX 26-APR-2002; 2002US-0375953P.

XX (GETH) GENENTECH INC.

XX Fahnner RL, Follman D, Lebreton B, Van Reis R;

XX WPI; 2004-043096/04.

XX Purifying target protein from mixture containing host cell protein
 PT involves subjecting mixture to non-affinity purification, high-
 PT performance tangential flow filtration and isolating purified protein.

XX Disclosure; SEQ ID NO 4; 77pp; English.

XX The invention relates to a method for purifying a target protein from a
 CC mixture containing a host cell protein. This method comprises subjecting
 CC the mixture to a non-affinity purification followed by high-performance
 CC tangential flow filtration (HPRFP) and isolating the protein in a purify
 CC containing less than 100 parts/million (ppm) of the host cell protein,
 CC where the method of the invention includes no affinity purification
 CC process. The method of the invention is useful for purifying a target
 CC protein from a mixture containing a host cell protein, and is useful for
 CC incorporating the isolated protein into a pharmaceutical formulation.
 CC Proteins purified using the method of the invention are useful in a
 CC pharmaceutical respect, and are also useful in various diagnostic and
 CC therapeutic purposes. The method of the invention is efficient in
 CC purifying a target protein from a mixture containing a host cell protein,
 CC and may also be effectively performed at low cost. The current sequence
 CC represents the anti-CD11a rhumAb heavy chain amino acid sequence. This
 CC particular protein was used to demonstrate the method of the invention.

XX Sequence 451 AA;

Query Match 100.0%; Score 72; DB 8; Length 451;
 Best Local Similarity 100.0%; Pred. No. 0.0069;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GIFYGTTYFDY 12
 |||||
 DB 99 GIFYGTTYFDY 110

RESULT 27
 ADR03408
 ID ADR03408 standard; peptide; 11 AA.

XX ADR03408;
 XX
 DT 21-OCT-2004 (first entry)
 DE

XX Humanised MHM24 CDR-H3 peptide.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KM rhinovirus infection; inflammatory skin disease; psoriasis;
 KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculosis; sarcoidosis; polymyositis;
 KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KM skin hypersensitivity disorder; poison ivy; poison oak;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
 KM VH; murine; human; fusion protein; complementarity determining region;
 KM CDR.

XX Mus sp.
 OS Homo sapiens.
 OS Chimeric.

XX US2004146507-A1.

XX 29-JUL-2004.

XX 03-DEC-2003; 2003US-00727737.

XX 27-NOV-1996; 96US-0031945P.

XX 20-NOV-1997; 97US-00975329.

XX (GETH) GENENTECH INC.

XX Jardieu PM, Preesta LG;

XX WPI; 2004-552640/53.

XX New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.

XX Example; SEQ ID NO 45; 54pp; English.

XX The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MHM24) CDR-H3 peptide. This sequence is used in the exemplification of

CC the invention.
XX
SQ Sequence 11 AA;
Query Match 90.3%; Score 65; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYFGTYFPD 11
Db 1 GIFYFGTYFPD 11
RESULT 28
ADR03414
ID ADR03414 standard; peptide; 11 AA.
XX
AC ADR03414;
XX
DT 21-OCT-2004 (first entry)
XX
DE Humanised MEM24 CDR-H2 mutant peptide, ThrH100aAa.
XX
KM CD11a antibody; human immunodeficiency virus infection; HIV infection;
KM rhinovirus infection; inflammatory skin disease; psoriasis;
KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
KM tuberculosis; sarcoidosis; polymyositis;
KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KM skin hypersensitivity disorder; poison ivy; poison oak;
KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
KM graft versus host disease; cancer; gene therapy;
KM murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain;
KM VH; murine; human; fusion protein; complementarity determining region;
KM CDR; mutant; mutein.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN US2004146507-A1.
XX
PD 29-JUL-2004.
XX
PF 03-DEC-2003; 2003US-00727737.
XX
PR 27-NOV-1996; 96US-0031945P.
PR 20-NOV-1997; 97US-00975329.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 2004-552640/53.
XX
PT New antibody mutant of a species-dependent antibody, useful for treating
PT and preventing infectious diseases, psoriasis, inflammatory bowel
PT disease, allergic conditions, autoimmune diseases, or cancer.
XX
PS Example; SEQ ID NO 51; 54pp; English.
XX
CC The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as
CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary

CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC disorders such as poison ivy and poison oak, B-cell malignancies such as
CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is humanised murine anti-human CD11a monoclonal antibody
CC (MEM24) CDR-H3 mutant peptide. This sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 11 AA;
Query Match 83.3%; Score 60; DB 8; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.01; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GIFYFGTYFPD 11
Db 1 GIFYFGTYFPD 11
RESULT 29
ADR03413
ID ADR03413 standard; peptide; 11 AA.
XX
AC ADR03413;
XX
DT 21-OCT-2004 (first entry)
XX
DE Humanised MEM24 CDR-H2 mutant peptide, ThrH100aAa.
XX
KM CD11a antibody; human immunodeficiency virus infection; HIV infection;
KM rhinovirus infection; inflammatory skin disease; psoriasis;
KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
KM tuberculosis; sarcoidosis; polymyositis;
KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KM skin hypersensitivity disorder; poison ivy; poison oak;
KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
KM graft versus host disease; cancer; gene therapy;
KM murine anti-human CD11a monoclonal antibody; MEM24; variable heavy chain;
KM VH; murine; human; fusion protein; complementarity determining region;
KM CDR; mutant; mutein.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
PN US2004146507-A1.
XX
PD 29-JUL-2004.
XX
PF 03-DEC-2003; 2003US-00727737.
XX
PR 27-NOV-1996; 96US-0031945P.
PR 20-NOV-1997; 97US-00975329.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 2004-552640/53.
XX
PT New antibody mutant of a species-dependent antibody, useful for treating
PT and preventing infectious diseases, psoriasis, inflammatory bowel
PT disease, allergic conditions, autoimmune diseases, or cancer.
XX
PS Example; SEQ ID NO 50; 54pp; English.
XX
CC The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin

CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD1a monoclonal antibody
 CC (MHM24) CDR-H3 mutant peptide. This sequence is used in the
 CC exemplification of the invention.

CC Sequence 11 AA;

Query Match 83.3%; Score 60; DB 8; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.01;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GIFYFGTTYFD 11
 |||||
 Db 1 GIFYFGATYFD 11

RESULT 30

ADRO3412 standard; peptide; 11 AA.

ADRO3412;

21-OCT-2004 (first entry)

Humanised MHM24 CDR-H2 mutant peptide, TyrH99A1a.

CD1a antibody; human immunodeficiency virus infection; HIV infection;
 rhinovirus infection; inflammatory skin disease; psoriasis;
 inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 adult respiratory distress syndrome; allergic disease; eczema; asthma;
 autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 tuberculosis; sarcoidosis; polymyositis;
 chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 skin hypersensitivity disorder; poison ivy; poison oak;
 B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 graft versus host disease; cancer; gene therapy;
 murine anti-human CD1a monoclonal antibody; MHM24; variable heavy chain;
 VH; murine; human; fusion protein; complementarity determining region;
 CDR; mutant; mutein.

Mus sp.
 Homo sapiens.
 Chimeric.

US2004146507-A1.

29-JUL-2004.

03-DEC-2003; 2003US-00727737.

27-NOV-1996; 96US-0031945P.

20-NOV-1997; 97US-00975329.

(GETH) GENENTECH INC.

Jardieu PM, Presta LG;

WPI; 2004-552640/53.

New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.

PS Example; SEQ ID NO 49; 54pp; English.

XX The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD1a monoclonal antibody
 CC (MHM24) CDR-H3 mutant peptide. This sequence is used in the
 CC exemplification of the invention.

CC Sequence 11 AA;

Query Match 77.8%; Score 56; DB 8; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.043;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GIFYFGTTYFD 11
 |||||
 Db 1 GIFYFGATYFD 11

RESULT 31

ADRO3411 standard; peptide; 11 AA.

ADRO3411;

21-OCT-2004 (first entry)

Humanised MHM24 CDR-H2 mutant peptide, TyrH97A1a.

CD1a antibody; human immunodeficiency virus infection; HIV infection;
 rhinovirus infection; inflammatory skin disease; psoriasis;
 inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 adult respiratory distress syndrome; allergic disease; eczema; asthma;
 autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 tuberculosis; sarcoidosis; polymyositis;
 chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 skin hypersensitivity disorder; poison ivy; poison oak;
 B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 graft versus host disease; cancer; gene therapy;
 murine anti-human CD1a monoclonal antibody; MHM24; variable heavy chain;
 VH; murine; human; fusion protein; complementarity determining region;
 CDR; mutant; mutein.

Mus sp.
 Homo sapiens.
 Chimeric.

US2004146507-A1.

29-JUL-2004.

03-DEC-2003; 2003US-00727737.

27-NOV-1996; 96US-0031945P.

20-NOV-1997; 97US-00975329.

(GETH) GENENTECH INC.

Jardieu PM, Presta LG;

DR WPI; 2004-552640/53.
XX
PT New antibody mutant of a species-dependent antibody, useful for treating
PT and preventing infectious diseases, psoriasis, inflammatory bowel
PT disease, allergic conditions, autoimmune diseases, or cancer.
XX
PS Example; SEQ ID NO 48; 54pp; English.
XX
CC The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such as
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as
CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC disorders such as poison ivy and poison oak, B-cell malignancies such as
CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is humanised murine anti-human CD11a monoclonal antibody
CC (MHM24) CDR-H3 mutant peptide. This sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 11 AA:
XX
Query Match 77.8%; Score 56; DB 8; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GIFYGTYTFFD 11
DB 1 GIFYGTYTFFD 11
RESULT 32
ADW38415
ID ADW38415 standard; peptide; 11 AA.
XX
AC ADW38415;
XX
DT 21-OCT-2004 (first entry)
XX
DE Humanised MHM24 CDR-H2 mutant peptide, TyrHI00CALA.
XX
KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
KW rhinovirus infection; inflammatory skin disease; psoriasis;
KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
KW tuberculosis; sarcoidosis; polymyositis;
KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KW skin hypersensitivity disorder; poison ivy; poison oak;
KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
KW graft versus host disease; cancer; gene therapy;
KW murine anti-human CD11a monoclonal antibody; MHM24; variable heavy chain;
KW VH; murine; human; fusion protein; complementarily determining region;
KW CDR; mutant; mutlein.
XX
XX
XX Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
XX US2004146507-A1.
PN
XX
XX 29-JUL-2004.
PD
XX
XX 03-DEC-2003; 2003US-0027737.
PF
XX
XX 27-NOV-1996; 96US-0031945P.
PR

PR 20-NOV-1997; 97US-00975329.
XX
XX (GETH) GENENTECH INC.
PA
XX Jardiou PM, Presta LG;
PI
XX
XX WPI; 2004-552640/53.
XX
XX
PT New antibody mutant of a species-dependent antibody, useful for treating
PT and preventing infectious diseases, psoriasis, inflammatory bowel
PT disease, allergic conditions, autoimmune diseases, or cancer.
XX
PS Example; SEQ ID NO 52; 54pp; English.
XX
CC The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such as
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as
CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC disorders such as poison ivy and poison oak, B-cell malignancies such as
CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is humanised murine anti-human CD11a monoclonal antibody
CC (MHM24) CDR-H3 mutant peptide. This sequence is used in the
CC exemplification of the invention.
XX
SQ Sequence 11 AA:
XX
Query Match 77.8%; Score 56; DB 8; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GIFYGTYTFFD 11
DB 1 GIFYGTYTFFD 11
RESULT 33
ADW38454
ID ADW38454 standard; protein; 122 AA.
XX
AC ADW38454;
XX
DT 24-MAR-2005 (first entry)
XX
DE CD11a heavy chain variable region #1.
XX
KW CD11a heavy chain variable region #1.
KW monoclonal antibody; CD11a; light-chain variable region;
KW heavy-chain variable region.
XX
XX
XX Homo sapiens.
OS
XX
XX CN1439651-A.
PN
XX
XX 03-SEP-2003.
PD
XX
XX 20-FEB-2002; 2002CN-00110866.
PF
XX
XX 20-FEB-2002; 2002CN-00110866.
PR
XX
XX (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
PA
XX
XX Wang H, Wang J;
PI
XX
XX WPI; 2004-169719/17.
DR
XX
XX N-PSDB; ADW38456.
XX

PT Recombinant human CD11a monoclonal antibody and its preparation and
PT medicinal composition.
XX
PS Claim 1; Page 12-13; 16pp; Chinese.
XX
CC The present invention relates to a recombinant monoclonal antibody for
CC human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
CC No.5 in light-chain variable region and the amino acid sequence shown by
CC SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
CC biactivity and the expression in host cell are greatly increased. The
CC DNA molecule for coding the antibody, its preparation process and the
CC medicinal composition containing it are also disclosed. The present
CC sequence represents a heavy chain variable region of human CD11a.
XX
SQ Sequence 122 AA;
XX
Query Match 76.4%; Score 55; DB 8; Length 122;
Best Local Similarity 83.3%; Pred. No. 0.77;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GIVEFGTYFDY 12
Db 100 GIVEFGTYFDY 111

RESULT 34
AAR93002
ID AAR93002 standard; protein; 120 AA.
XX
AC AAR93002;
XX
DT 25-MAR-2003 (revised)
DT 18-MAY-1996 (first entry)
XX
DE Monoclonal antibody IOR-CEA-1 variable region heavy chain.
XX
XX IOR-CEA-1; monoclonal antibody; mouse; heavy chain; variable region;
XX framework; cloning; computer; algorithm; human; immunogenicity;
XX site-directed mutagenesis; T-lymphocyte epitope;
XX complementarity determining region; tertiary structure; point mutation;
XX antibody engineering; protein engineering; humanised antibody;
XX antitumour; cancer; therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 1..16
FT /note= "Predicted T-lymphocyte antigen"
FT 26..30
FT /note= "Amino acids involved in tertiary structure"
FT 31..35
FT /note= "Complementarity determining region"
FT 34
FT /note= "Amino acid involved in tertiary structure"
FT 50..66
FT /note= "Complementarity determining region"
FT 53..56
FT /note= "Amino acid involved in tertiary structure"
FT 72
FT /note= "Amino acid involved in tertiary structure"
FT 98
FT /note= "Amino acid involved in tertiary structure"
FT 99..109
FT /note= "Complementarity determining region"
FT 100..117
FT /note= "Predicted T-lymphocyte antigen"
XX
XX EP699755-A2.
XX
XX 06-MAR-1996.
XX
XX 27-JUN-1995; 95BP-00201752.
XX

PR 30-JUN-1994; 94CU-00000080.
XX
XX (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
XX Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;
XX
XX WPI; 1996-130770/14.
XX
XX Identifying interspecies differences in amino acid sequence of Ig T-cell
XX epitopes - by sequence comparison, also humanised antibodies contg.
XX altered T-cell epitopes, retaining antigen specificity but not
XX immunogenicity, esp. for tumour treatment.
XX
PS Claim 22; Fig 9; 33pp; English.
XX
CC The sequence represents the heavy chain variable region from mouse
CC monoclonal antibody IOR-CEA-1. The framework sequence is analysed for T-
CC cell antigenic sequences using a computer algorithm, and compared with
CC human Ig sequences. The human Ig with highest homology (AAR93003) is
CC isolated, and residues not within a complementarity determining region,
CC canonical structure or Vennier zone are modified to reduce immunogenicity
CC in humans (e.g. in sequence AAR93004). This method, which involves the
CC introduction of only a few point mutations into T-cell epitope coding
CC regions, is generally applicable in humanisation of mouse antibodies. The
CC resulting humanised antibodies may be used e.g. as antitumour agents.
CC They retain the antigen recognition of the original antibody, but are not
CC immunogenic in humans. (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 120 AA;
XX
Query Match 75.0%; Score 54; DB 2; Length 120;
Best Local Similarity 63.6%; Pred. No. 1.1;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 2 IYFGTYFDY 12
Db 99 VYVYGSSTYFDY 109

RESULT 35
AAR93004
ID AAR93004 standard; protein; 120 AA.
XX
AC AAR93004;
XX
DT 25-MAR-2003 (revised)
DT 18-MAY-1996 (first entry)
XX
DE Humanised antibody IOR-CEA-1 variable region heavy chain.
XX
XX Humanised antibody; IOR-CEA-1; monoclonal antibody; mouse; heavy chain;
XX variable region; framework; cloning; computer; algorithm; human;
XX immunogenicity; site-directed mutagenesis; T-lymphocyte epitope;
XX complementarity determining region; tertiary structure; point mutation;
XX antibody engineering; protein engineering; antitumour; cancer; therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT 2..3
FT /note= "Mutated residues"
FT 5..6
FT /note= "Mutated residues"
FT 9..10
FT /note= "Mutated residues"
FT 15
FT /note= "Mutated residue"
FT 26..30
FT /note= "Amino acids involved in tertiary structure"
FT 31..35
FT /note= "Complementarity determining region"
FT 34
FT /note= "Amino acid involved in tertiary structure"
FT

FT	Region	50..66	/note= "Complementarity determining region"
FT	Region	53..56	/note= "Amino acid involved in tertiary structure"
FT	Region	72	/note= "Amino acid involved in tertiary structure"
FT	Region	98	/note= "Amino acid involved in tertiary structure"
FT	Region	99..109	/note= "Complementarity determining region"
FT	Misc-difference	115..116	/note= "Mutated residues"
XX	EP69755-A2.		
PD	06-MAR-1996.		
XX	27-JUN-1995;	95EP-00201752.	
XX	30-JUN-1994;	94CU-00000080.	
XX	(IMMU-) CENT IMMUNOLOGIA MOLECULAR.		
PI	Rodriguez RP, Valladares JL, Mateo De Acosta Del Rio CM;		
XX	WPI; 1996-130770/14.		
XX	Identifying interspecies differences in amino acid sequence of Ig T-cell		
PT	epitopes - by sequence comparison, also humanised antibodies contg.		
PT	altered T-cell epitopes, retaining antigen specificity but not		
FT	immunogenicity, esp. for tumour treatment.		
XX	Claim 22; Fig 9; 33pp; English.		
CC	The sequence represents a humanised mutant form of a heavy chain variable		
CC	region from mouse monoclonal antibody IOR-CEA-1. The native antibody		
CC	framework sequence (AAR93002) is analysed for T-cell antigenic sequences		
CC	using a computer algorithm, and compared with human Ig sequences. The		
CC	human Ig with highest homology (e.g. AAR93003) is isolated, and residues		
CC	not within a complementarity determining region, canonical structure or		
CC	Vernier zone are modified to reduce immunogenicity in humans to produce a		
CC	humanised antibody. This method, which involves the introduction of only		
CC	a few point mutations into T-cell epitope coding regions, is generally		
CC	applicable in humanisation of mouse antibodies. The resulting humanised		
CC	antibodies may be used e.g. as antitumour agents. They retain the antigen		
CC	recognition of the original antibody, but are not immunogenic in humans.		
XX	(Updated on 25-MAR-2003 to correct PI field.)		
SQ	Sequence 120 AA;		
Query Match	75.0%;	Score 54;	DB 2; Length 120;
Best Local Similarity	63.6%;	Pred. No. 1.1;	
Matches	7; Conservative	4; Mismatches	0; Indels 0; Gaps 0
QY	2 IYFGTYTYPDY 12		
	: :		
Db	99 VYVYGSSTYDPY 109		
RESULT 36			
ADF72730			
ID	ADF72730 standard; protein; 232 AA.		
XX	ADF72730;		
AC			
XX	26-FEB-2004 (first entry)		
DE	Divalent CEA-specific single chain antibody (diabody), SEQ 17.		
XX	Single chain antibody; scFv; human carcinoembryonic antigen;		
XX	CEA-specific; monoclonal antibody; CB-CEA.1; IOR-CEA.1; CB/IOR-CEA.1;		
KW	tumour cell identification; tumour imaging; drug targeting;		
KW	immunotherapy; cancer; breast; lung; colon; cytostatic; mouse; murine;		

XX divalent; diabody.
 OS Synthetic.
 OS Mus sp.
 PN WO2003093315-A2.
 XX 13-NOV-2003.
 PD 28-APR-2003; 2003WO-CU000005.
 XX 29-APR-2002; 2002CU-00000086.
 XX (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
 PA Gavilondo Cowley JV, Ayala Avila M, Freyre Almeida FDLM;
 PI Acevedo Castro BE, Bell Garcia H, Roque Navarro LT, Gonzalez Lopez LJ;
 PI Cremata Alvarez JA, Montesino Segui R;
 XX WPI; 2003-854481/79.
 DR New antibody fragments, useful for treatment and diagnosis of tumors,
 PT that recognize glycosylated carcino-embryonal antigens.
 XX
 PS Claim 4; SEQ ID NO 17; 49pp; Spanish.
 XX
 CC The invention relates to monovalent and divalent (dibody) single chain
 CC antibodies (scFv; ADF72729-ADF72730) specific for human carcinoembryonic
 CC antigen (CEA). The single chain antibodies are derived from the murine
 CC monoclonal antibody known as CB-CEA.1 or 1or-CEA.1 (referred to in the
 CC specification as CB/1or-CEA.1). The invention also relates to synthetic
 CC antibody fragments containing the heavy and light chain variable regions
 CC of the single chain antibodies of the invention, artificially joined
 CC together as Fab fragments, as other scFv fragments, as bispecific
 CC antibodies, or fused to biologically active domains; vectors that encode
 CC the single chain antibodies or their fragments; and host cells comprising
 CC the vectors. The CEA-specific single chain antibodies can be used to
 CC identify tumour cells that express CEA, but do not cross-react with
 CC normal human tissues or cells (except normal colonic mucosa, where CEA is
 CC occasionally present). The antibodies and antibody fragments can also be
 CC used for imaging or treatment of CEA-expressing tumours such as those of
 CC the colon, lung or breast, and can additionally be used to target
 CC therapeutic agents to such tumours. The single chain antibodies retain
 CC high affinity for CEA, but since they are 2.5-5 times smaller than the
 CC complete monoclonal antibody, they have better tissue penetration and are
 CC less immunogenic in humans. The present sequence is related to the
 CC invention.
 CC
 SQ Sequence 232 AA:
 Query Match 75.0%; Score 54; DB 7; Length 232;
 Best Local Similarity 63.6%; Pred. No. 2.2;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0.
 QY 2 IYFGTTYEDY 12
 :.:|:|:|
 Db 98 VYGGSSYFDY 108
 RESULT 37
 ADF72729
 ID ADF72729 standard; protein, 241 AA.
 XX
 AC ADF72729;
 XX
 DT 26-FEB-2004 (first entry)
 DE Monovalent CEA-specific single chain antibody (scFv), SEQ 16.
 XX
 KW Single chain antibody; scFv; human carcinoembryonic antigen;
 KW CEA-specific; monoclonal antibody; CB-CEA.1; 1or-CEA.1; CB/1or-CEA.1;
 KW tumour cell identification; tumour imaging; drug targeting;
 KW immunotherapy; cancer; breast; lung; colon; cytostatic; mouse; murine;

KW monovalent.
 XX Synthetic.
 OS Mus sp.
 XX WO2003093315-A2.
 PN 13-NOV-2003.
 PD 28-APR-2003; 2003WO-CU000005.
 XX 29-APR-2002; 2002CU-00000086.
 PR (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
 XX
 PA Gaviñondo Cowley JV, Ayala Avila M, Freyre Almeida FDLM;
 PI Acevedo Castro BE, Bell Garcia H, Roque Navarro LT, Gonzalez Lopez LJ;
 P1 Cremata Alvarez JA, Montesino Segui R;
 XX WPI; 2003-854481/79.
 DR
 XX New antibody fragments, useful for treatment and diagnosis of tumors,
 PT that recognize glycosylated carcino-embryonal antigens.
 PS
 XX Claim 2; SEQ ID NO 16; 49pp; Spanish.
 XX
 CC The invention relates to monovalent and divalent (diabody) single chain
 CC antibodies (scFv; ADF72732-ADF72730) specific for human carcinoembryonic
 CC antigen (CEA). The single chain antibodies are derived from the murine
 CC monoclonal antibody known as CB-CEA.1 or ior-CEA.1 (referred to in the
 CC specification as CB/ior-CEA.1). The invention also relates to synthetic
 CC antibody fragments containing the heavy and light chain variable regions
 CC of the single chain antibodies of the invention, artificially joined
 CC together as Fab fragments, as other scFv fragments, as bispecific
 CC antibodies, or fused to biologically active domains; vectors that encode
 CC the single chain antibodies or their fragments; and host cells comprising
 CC the vectors. The CEA-specific single chain antibodies can be used to
 CC identify tumor cells that express CEA, but do not cross-react with
 CC normal human tissues or cells (except normal colonic mucosa, where CEA is
 CC occasionally present). The antibodies and antibody fragments can also be
 CC used for imaging or treatment of CEA-expressing tumors such as those of
 CC the colon, lung or breast, and can additionally be used to target
 CC therapeutic agents to such tumors. The single chain antibodies retain
 CC high affinity for CEA, but since they are 2.5-5 times smaller than the
 CC complete monoclonal antibody, they have better tissue penetration and are
 CC less immunogenic in humans. The present sequence is related to the
 CC invention.
 CC
 XX
 SQ Sequence 241 AA;
 Query Match 75.0%; Score 54; DB 7; Length 241;
 Best Local Similarity 63.6%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IYFGTYFDY 12
 :|||:||||
 Db 98 VYVYGSYFDY 108
 RESULT 38
 ADF72734 ID ADF72734 standard; protein; 255 AA.
 XX
 AC ADF72734;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE His-tagged divalent CEA-specific single chain diabody MS, SEQ 21.
 XX
 KW Single chain antibody; scFv; human carcinoembryonic antigen;
 KW CEA-specific; monoclonal antibody; CB-CEA.1, ior-CEA.1; CB/ior-CEA.1;
 KW tumour cell identification; tumour imaging; drug targeting;
 KW immunotherapy; cancer; breast; lung; colon; cytosstatic; mouse; murine;

KW divalent; diabody; hexahistidine tag.
 XX Synthetic.
 OS Mus sp.
 XX WO2003093315-A2.
 PN 13-NOV-2003.
 PD 28-APR-2003; 2003WO-CU000005.
 XX 29-APR-2002; 2002CU-00000086.
 PR (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
 XX
 PA Gaviñondo Cowley JV, Ayala Avila M, Freyre Almeida FDLM;
 PI Acevedo Castro BE, Bell Garcia H, Roque Navarro LT, Gonzalez Lopez LJ;
 P1 Cremata Alvarez JA, Montesino Segui R;
 XX WPI; 2003-854481/79.
 DR
 XX New antibody fragments, useful for treatment and diagnosis of tumors,
 PT that recognize glycosylated carcino-embryonal antigens.
 PS
 XX Example 5; SEQ ID NO 21; 49pp; Spanish.
 XX
 CC The invention relates to monovalent and divalent (diabody) single chain
 CC antibodies (scFv; ADF72729-ADF72730) specific for human carcinoembryonic
 CC antigen (CEA). The single chain antibodies are derived from the murine
 CC monoclonal antibody known as CB-CEA.1 or ior-CEA.1 (referred to in the
 CC specification as CB/ior-CEA.1). The invention also relates to synthetic
 CC antibody fragments containing the heavy and light chain variable regions
 CC of the single chain antibodies of the invention, artificially joined
 CC together as Fab fragments, as other scFv fragments, as bispecific
 CC antibodies, or fused to biologically active domains; vectors that encode
 CC the single chain antibodies or their fragments; and host cells comprising
 CC the vectors. The CEA-specific single chain antibodies can be used to
 CC identify tumor cells that express CEA, but do not cross-react with
 CC normal human tissues or cells (except normal colonic mucosa, where CEA is
 CC occasionally present). The antibodies and antibody fragments can also be
 CC used for imaging or treatment of CEA-expressing tumors such as those of
 CC the colon, lung or breast, and can additionally be used to target
 CC therapeutic agents to such tumors. The single chain antibodies retain
 CC high affinity for CEA, but since they are 2.5-5 times smaller than the
 CC complete monoclonal antibody, they have better tissue penetration and are
 CC less immunogenic in humans. The present sequence is related to the
 CC invention.
 CC
 XX
 SQ Sequence 255 AA;
 Query Match 75.0%; Score 54; DB 7; Length 255;
 Best Local Similarity 63.6%; Pred. No. 2.4; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IYFGTYFDY 12
 :|||:||||
 Db 98 VYVYGSYFDY 108
 RESULT 39
 ADK34542 ID ADK34542 standard; protein; 206 AA.
 XX
 AC ADK34542;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Novel human polypeptide SegID6624.
 XX
 KW antiarthritic; antiparkinsonian; neuroprotective; nootropic;
 KW immunosuppressive; cytostatic; antiproliferative; antiinflammatory;
 KW antibacterial; antiviral; antifungal; antiparasitic; gene therapy;
 KW arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer;

KW		pneumonia; inflammatory bowel disease; infection; bacteria; virus;
KM		fungal; parasite: human.
XX	Homo sapiens.	
OS		
XX		
XX	Key	Location/Qualifiers
XX	Misc-difference	1..206
FT	/label= OTHER	
FT	/note= "OTHER= All Xaa's in this sequence are unknown amino acids or the site of a stop codon within the DNA sequence"	
FT		
XX		
PN	MO200216439-A2.	
XX		
PD	28-FEB-2002.	
XX		
PF	05-MAR-2001; 2001WO-US004941.	
XX		
PR	07-MAR-2000; 2000US-00519705.	
PR	19-MAY-2000; 2000US-00574454.	
XX		
PA	(HYSEQ-) HYSEQ INC.	
XX		
PI	Tang YT, Liu C, Drmanac RT;	
DR	WPI; 2002-280918/32.	
XX		
PT	Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's disease, and inflammatory bowel disease.	
PT		
XX		
PS	Claim 20; SEQ ID NO 6624; 504bp; English.	
CC	This invention relates to a novel isolated polynucleotide comprising a nucleotide sequence selected from one of 1680 sequences, a mature protein coding portion of them, an active domain of them and their complementary sequences. The invention may be useful for the production of compounds with an antiarthritic, antiparkinsonian, neuroprotective, nootropic, immunosuppressive, cytostatic, antipsoriatic, antiinflammatory, antibacterial, antiviral, antifungal or antiparasitic activity. In addition, the disclosed sequences may be useful for gene therapy. The polypeptides or their antibodies are useful for treating many diseases such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer, psoriasis, inflammatory bowel disease and infections caused by bacteria, viruses, fungi or parasites. The present sequence is that of a human polypeptide of the invention.	
CC		
CC		
XX	Sequence 206 AA:	
SO		
	Query Match	72.2%; Score 52; DB 5; Length 206;
	Best Local Similarity	80.0%; Pred. No. 3.9;
	Matches	8; Conservative 1; Mismatches 1; Indels 0; Gaps 0
OY	1 GIYYGTTYF 10 : :	
DB	58 GYFYGYTRYF 67	
RESULT 40		
ID	ADQI7153 standard; peptide; 13 AA.	
XX	ADQI7153;	
AC		
DT	07-OCT-2004 (first entry)	
DE	Murine anti-NGF Mab 911 heavy chain extended CDR3 mutant peptide 3.	
XX		
XX	nerv growth factor; anti-NGF antibody; E13.5 trigeminal neurone; analgesic; immunomodulator; post-surgical pain; rheumatoid arthritis; osteoarthritis; inflammatory cachexia; gene therapy;	
KM	monoclonal antibody 911; heavy chain extended CDR3;	
KW	complementarily determining region; murine; mouse; mutant; mutein.	

XX	Mus sp.
OS	Synthetic.
XX	
FH	Key
FT	Misc-difference 8
FT	/note= "Wild-type Ser substituted by Thr"
XX	
XX	WO2004058184-A2.
XX	
PD	15-JUL-2004.
XX	
XX	24-DEC-2003; 2003WO-US041252.
PP	
XX	24-DEC-2002; 2002US-0436905P.
PR	28-JAN-2003; 2003US-0443522P.
PR	08-OCT-2003; 2003US-0510006P.
XX	
PA	(RINA-) RINAT NEUROSCIENCE CORP.
PI	
PI	Shelton DL, Pons J, Rosenthal A;
DR	WPI; 2004-525786/50.
XX	
PT	New anti-nerve growth factor antibodies for preventing or treating pain,
PT	including post-surgical pain, rheumatoid arthritis pain or osteoarthritis
PT	pain, or for treating inflammatory cachexia associated with rheumatoid
PT	arthritis.
XX	
PS	Example 1; SEQ ID NO 48; 186pp; English.
XX	
CC	The invention relates to a novel anti-nerve growth factor (NGF) antibody
CC	which binds NGF with a KD of less than about 2 nM and inhibits human NGF-
CC	dependent survival of mouse E13.5 trigeminal neurones with an IC50 of
CC	about 100 or 10 pm or less, where the IC50 is measured in the presence of
CC	about 15 or 1.5 pM of human NGF. The antibody of the invention
CC	demonstrates analgesic and immunomodulator activities and may be useful
CC	for preventing and/or treating pain, including post-surgical pain and
CC	pain associated with rheumatoid arthritis or osteoarthritis. The antibody
CC	may be further utilised for treating inflammatory cachexia associated
CC	with rheumatoid arthritis, as well as during gene therapy procedures. The
CC	current sequence is that of a murine anti-NGF Mab (monoclonal antibody)
CC	911 heavy chain extended CDR3 (complementarity determining region) mutant
CC	peptide of the invention which was used during construction of the
CC	humanised anti-NGF E3 antibody.
XX	
XX	Sequence 13 AA;
XX	SEQ
Query Match	70.1%; Score 50.5; DB 8; Length 13;
Best Local Similarity	76.9%; Pred.No. 0.37;
Matches 10; Conservative	1; Mismatches 1; Indels 1; Gaps 1,
Oy	1 GIYFGTTFYPDY 12
	:
	:
Dd	1 GGYYTGTTYFPDY 13
RESULT 41	
ID	ADR03409
AC	ADR03409 standard; peptide; 11 AA.
XX	
AD	ADR03409;
DT	
XX	21-OCT-2004 (first entry)
DE	
XX	Humanised MHM24 CDR-H2 mutant peptide, H3.
KM	
KM	CD14 antibody; human immunodeficiency virus infection; HIV infection;
KM	rhinovirus infection; inflammatory skin disease; psoriasis;
KM	inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KM	adult respiratory distress syndrome; allergic disease; eczema; asthma;
KM	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KM	SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;

KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukemia; hairy cell leukemia;
 KW graft versus host disease; cancer; gene therapy; MM24; variable heavy chain;
 KW murine anti-human CD11a monoclonal antibody; MM24; variable heavy chain;
 KW VH; murine; human; fusion protein; complementarity determining region;
 KW CDR; mutant; mutein.
 XX
 XX Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 XX US2004146507-A1.
 XX
 XX 29-JUL-2004.
 XX
 XX 03-DEC-2003; 2003US-00727737.
 XX
 XX 27-NOV-1996; 96US-0031945P.
 XX 20-NOV-1997; 97US-00975329.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 XX Jardieu PM, Presta LG;
 XX WPI; 2004-552640/53.
 XX
 XX New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 XX Example; SEQ ID NO 46; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukemia and hairy cell leukemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MM24) CDR-H3 mutant peptide. This sequence is used in the
 CC exemplification of the invention.
 CC
 XX Sequence 11 AA;
 SQ
 Query Match 65.3%; Score 47; DB 8; Length 11;
 Best Local Similarity 81.8%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GIFYGTYFPD 11
 DB 1 GIFAFTYFPD 11
 RESULT 42
 ID ADO17117 standard; peptide; 13 AA.
 XX
 XX ADO17117;
 XX
 XX 07-OCT-2004 (first entry)
 XX
 DE Murine anti-NGF Mab 911 heavy chain extended CDR3 wild-type peptide.
 XX

KW nerve growth factor; anti-NGF antibody; E13.5 trigeminal neurone;
 KW analgesic; immunomodulator; post-surgical pain; rheumatoid arthritis;
 KW osteoarthritis; inflammatory cachexia; gene therapy;
 KW monoclonal antibody 911; heavy chain extended CDR3;
 KW complementarity determining region; murine; mouse; wild-type.
 XX
 OS Mus sp.
 XX
 XX WO2004058184-A2.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-US041252.
 XX
 XX 24-DEC-2002; 2002US-0436905P.
 XX 28-JAN-2003; 2003US-0443522P.
 XX 08-OCT-2003; 2003US-0510006P.
 XX
 XX (RINA-) RINAT NEUROSCIENCE CORP.
 XX
 XX Shelton DL, Pons J, Rosenthal A;
 XX WPI; 2004-525786/50.
 XX
 XX New anti-nerve growth factor antibodies for preventing or treating pain,
 PT including post-surgical pain, rheumatoid arthritis pain or osteoarthritis
 PT pain, or for treating inflammatory cachexia associated with rheumatoid
 PT arthritis.
 XX
 XX Claim 6; SEQ ID NO 11; 186pp; English.
 XX
 CC The invention relates to a novel anti-nerve growth factor (NGF) antibody
 CC which binds NGF with a KD of less than about 2 nM and inhibits human NGF-
 CC dependent survival of mouse E13.5 trigeminal neurons with an IC50 of
 CC about 100 or 10 pM or less, where the IC50 is measured in the presence of
 CC about 15 or 1.5 pM of human NGF. The antibody of the invention
 CC demonstrates analgesic and immunomodulator activities and may be useful
 CC for preventing and/or treating pain, including post-surgical pain and
 CC pain associated with rheumatoid arthritis or osteoarthritis. The antibody
 CC may be further utilised for treating inflammatory cachexia associated
 CC with rheumatoid arthritis, as well as during gene therapy procedures. The
 CC current sequence is that of the murine anti-NGF Mab (monoclonal antibody)
 CC 911 heavy chain extended CDR3 (complementarity determining region) wild-
 CC type peptide of the invention.
 CC
 XX Sequence 13 AA;
 SQ
 Query Match 64.6%; Score 46.5; DB 8; Length 13;
 Best Local Similarity 69.2%; Pred. No. 1.5;
 Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 GIFYGTYFPD 12
 DB 1 GGYIGTSYFPD 13
 RESULT 43
 ID ADR03410 standard; peptide; 11 AA.
 XX
 XX ADR03410;
 XX
 XX 21-OCT-2004 (first entry)
 XX
 DE Humanised MM24 CDR-H2 mutant peptide, H3B.
 XX
 XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;

FT	Misc-difference 8
FT	/note= "Wild-type Ser substituted by Ala"
PV	
PN	WO2004058184-A2.
PD	15-JUL-2004.
XX	
XX	24-DEC-2003; 2003WO-US041252.
PF	
PR	24-DEC-2002; 2002US-0436905P.
XX	28-JAN-2003; 2003US-0443522P.
PR	08-OCT-2003; 2003US-051006P.
XX	
PA	(RINA-) RINAT NEUROSCIENCE CORP.
PI	Shelton DL, Pons J, Rosenthal A;
DR	WPI; 2004-525786/50.
XX	
XX	New anti-nerve growth factor antibodies for preventing or treating pain,
PT	including post-surgical pain, rheumatoid arthritis pain or osteoarthritis
PT	pain, or for treating inflammatory cachexia associated with rheumatoid
PT	arthritis.
PS	
Example 1; SEQ ID NO 47, 186pp; English.	
XX	
CC	The invention relates to a novel anti-nerve growth factor (NGF) antibody
CC	which binds NGF with a KD of less than about 2 nM and inhibits human NGF-
CC	dependent survival of mouse E13.5 trigeminal neurones with an IC50 of
CC	about 100 or 10 pM or less, where the IC50 is measured in the presence of
CC	about 15 or 1.5 pM of human NGF. The antibody of the invention
CC	demonstrates analgesic and immunomodulator activities and may be useful
CC	for preventing and/or treating pain, including post-surgical pain and
CC	pain associated with rheumatoid arthritis or osteoarthritis. The antibody
CC	may be further utilised for treating inflammatory cachexia associated
CC	with rheumatoid arthritis, as well as during gene therapy procedures. The
CC	current sequence is that of a murine anti-NGF Mab (monoclonal antibody)
CC	911 heavy chain extended CDR3 (complementarily determining region) mutant
CC	peptide of the invention which was used during construction of the
CC	humanised anti-NGF E3 antibody.
XX	
SQ	Sequence 13 AA;
Query Match	63.2%; Score 45.5; DB 8; Length 13;
Best Local Similarity	69.2%; Pred. No. 2.2;
Matches	9; Conservative 1; Mismatches 2; Indels 1; Gaps 1.
OY	1 GIIFYGTT-YFPDY 12 : Db 1 GGYYGTAYTFDY 13
RESULT 46	
ADQI7151	standard; peptide; 13 AA.
ID ADQI7151	
AC ADQI7151;	
DT 07-OCT-2004	(first entry)
DE Murine anti-NGF Mab 911 heavy chain extended CDR3 mutant peptide 1.	
KX nerve growth factor; anti-NGF antibody; E13.5 trigeminal neurone;	
KX analgesic; immunomodulator; post-surgical pain; rheumatoid arthritis;	
KX osteoarthritis; inflammatory cachexia; gene therapy;	
KX monoclonal antibody 911; heavy chain extended CDR3;	
KX complementarity determining region; murine; mouse; mutant; mutain.	
OS Mus sp.	
OS Synthetic.	
Key Location/Qualifiers	
FT Misc-difference 4	

```

FF      /note= "Wild-type Tyr substituted by Trp"
FN      WO2004058184-A2.
PN      XX
PD      15-JUL-2004.
PP      XX
PE      24-DEC-2003; 2003WO-US041252.
PX      XX
PR      24-DEC-2002; 2002US-0436905P.
PR      28-JAN-2003; 2003US-0443522P.
PR      08-OCT-2003; 2003US-0510006P.
PX      XX
PA      (RINA-) RINAT NEUROSCIENCE CORP.
PI      Shelton DL, Pons J, Rosenthal A;
DR      WPI, 2004-525786/50.
PX      XX
PT      New anti-nerve growth factor antibodies for preventing or treating pain,
PT      including post-surgical pain, rheumatoid arthritis pain or osteoarthritis
PT      pain, or for treating inflammatory cachexia associated with rheumatoid
PT      arthritis.
PX      XX
PS      Example 1; SEQ ID NO 46; 186pp; English.
XX      XX
XX      The invention relates to a novel anti-nerve growth factor (NGF) antibody
XX      CC which binds NGF with a KD of less than about 2 nM and inhibits human NGF-
XX      CC dependent survival of mouse E13.5 trigeminal neurons with an IC50 of
XX      CC about 100 or 10 pM or less, where the IC50 is measured in the presence of
XX      CC about 15 or 1.5 pM of human NGF. The antibody of the invention
XX      CC demonstrates analgesic and immunomodulator activities and may be useful
XX      CC for preventing and/or treating pain, including post-surgical pain and
XX      CC pain associated with rheumatoid arthritis or osteoarthritis. The antibody
XX      CC may be further utilised for treating inflammatory cachexia associated
XX      CC with rheumatoid arthritis, as well as during gene therapy procedures. The
XX      CC current sequence is that of a murine anti-NGF Mab (monoclonal antibody)
XX      CC 911 heavy chain extended CDR3 (complementarity determining region) mutant
XX      CC peptide of the invention which was used during construction of the
XX      CC humanised anti-NGF E3 antibody.
XX      XX
SQ      Sequence 13 AA;

Query Match          61.8%; Score 44.5; DB 8; Length 13;
Best Local Similarity 69.2%; Pred. No. 3.2;
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY      1 GIVFGTT-YEPDY 12
      1 |::|||::|||
      1 GGIVTGTSTYFPDY 13
DB      1 GGIVTGTSTYFPDY 13

RESULT 47
ADO32163
ID      ADO32163 standard; Protein; 118 AA.
XX      XX
XX      ADO32163;
XX      XX
DT      12-AUG-2004 (first entry)
XX      XX
DE      Mouse anti-CD33 antibody heavy chain homologous protein SEQ ID NO:79.
XX      XX
XX      anti-CD33 antibody; epitope-binding fragment;
XX      KM complementarity-determining region; CDR; immunconjugate; cytostatic;
XX      KM antibody; myelodysplastic syndrome; acute myeloid leukaemia;
XX      KM chronic myeloid leukaemia; pro-myelocytic leukaemia; mouse; heavy chain.
XX      XX
OS      Mus musculus.
XX      OS
PN      WO2004043344-A2.
PD      27-MAY-2004.
XX      XX
PF      05-NOV-2003; 2003WO-US032737.
XX      XX

```


XX 07-NOV-2002; 2002US-0424332P.
 PR (IMMU-) IMMUNOGEN INC.
 PA Hoffee MG, Tavares D, Lutz RJ;
 PI WPI; 2004-411619/38.
 DR
 XX
 PT New antibodies that bind to CD33, useful for treating a disease
 PT associated with CD33 expression, such as myelodysplastic syndrome, acute
 PT or chronic myeloid leukemia.
 PS Example 3; SEQ ID NO 79; 124bp; English.
 XX
 CC The present invention describes an isolated anti-CD33 antibody or its
 CC epitope-binding fragment comprising: (a) at least one complementarily-
 CC determining region (CDR); or (b) at least heavy chain variable region
 CC comprising 3 CDRs, and at least one light chain variable region, where
 CC the CDR has the ability to bind CD33. Also described: (1) an
 CC immunocongate comprising the antibody or its epitope-binding fragment
 CC linked to a drug or prodrug; (2) a composition comprising the antibody or
 CC epitope-binding fragment and a drug or prodrug; (3) a pharmaceutical
 CC composition comprising the immunocongate, composition or the antibody
 CC defined above, or its epitope-binding fragment, and a pharmaceutical
 CC agent; (4) a diagnostic reagent comprising the antibody defined above,
 CC where the antibody or antibody fragment is labelled; (5) inhibiting the
 CC growth of a cell expressing CD33 by contacting the cell with the above
 CC defined antibody or its epitope-binding fragment, immunocongate, or
 CC (pharmaceutical) composition; (6) determining whether a biological sample
 CC contains a myelogenous cancer cell; (7) an improved antibody or its
 CC epitope-binding fragment that specifically binds to CD33; (8) an isolated
 CC polynucleotide encoding the antibody or its epitope-binding fragment
 CC defined above; (9) an isolated polynucleotide encoding a light or heavy
 CC chain of the antibody defined above or its epitope-binding fragment; (10)
 CC a recombinant vector comprising the polynucleotide; (11) a host cell
 CC transformed with the recombinant vector; (12) producing an antibody or
 CC its epitope-binding fragment having the ability to bind CD33; and (13)
 CC obtaining CD33 from a biological material. The anti-CD33 antibody has
 CC cytostatic activity. The antibody or its epitope-binding fragment,
 CC immunocongate, composition can be used for treating a subject having a
 CC disease where CD33 is expressed, such as myelodysplastic syndrome, acute
 CC myeloid leukaemia, chronic myeloid leukaemia or pro-myelocytic leukaemia.
 CC It can also be used for inhibiting the growth of cells expressing CD33,
 CC and for in vivo imaging or as affinity purification agents. The present
 CC sequence represents a mouse anti-CD33 antibody heavy chain homologous
 CC amino acid sequence, which is used in an example from the present
 CC invention.
 CC
 SQ Sequence 118 AA;
 XX
 XX
 Query Match 61.1%; Score 44; DB 8; Length 118;
 Best Local Similarity 66.7%; Pred. No. 39;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FYGTTYFDY 12
 :|||:||||
 Db 100 YYGSSYFDY 108
 XX
 XX
 RESULT 48
 ADH17831
 ID ADH17831 standard; protein; 120 AA.
 XX
 AC ADH17831;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Murine antibody lngp heavy chain variable region protein.
 XX
 XX antibody EMI64; insulin-like growth factor-I receptor; IGF-IR antagonist;
 KW breast cancer; colon; ovarian carcinoma; osteosarcoma; cervical;
 KW prostate; lung; synovial carcinoma; pancreatic; murine; mouse;

KW heavy chain variable region; lngp.
 XX
 OS Mus sp.
 XX
 PN WO2003106621-A2.
 XX
 PD 24-DEC-2003.
 XX
 PF 12-JUN-2003; 2003WO-US016211.
 XX
 PR 14-JUN-2002; 2002US-00170390.
 XX
 PA (IMMU-) IMMUNOGEN INC.
 XX
 PI Singh R, Tavares DJ, Dagdigian NB;
 XX
 DR WPI; 2004-082172/08.
 XX
 PT Novel murine antibody EMI64 or antibody fragment that specifically binds
 PT to insulin-like growth factor-I-receptor useful for treating breast
 PT cancer, colon cancer, lung cancer, prostate cancer.
 PS Example 2; SEQ ID NO 71; 155bp; English.
 XX
 CC The invention relates to a novel murine antibody EMI64 or antibody
 CC fragment that specifically binds to insulin-like growth factor-I receptor
 CC (IGF-IR) where the antibody is an antagonist of the receptor, is
 CC substantially devoid of agonist activity toward the receptor and is
 CC capable of inhibiting the growth of a cancer cell by greater than 80% in
 CC the presence of a growth stimulant chosen from serum, IGF-I and IGF-II.
 CC The antibody of the invention may be useful for diagnosing or treating a
 CC patient having a cancer selected from breast cancer, colon cancer,
 CC ovarian carcinoma, osteosarcoma, cervical cancer, prostate cancer, lung
 CC cancer, synovial carcinoma and pancreatic cancer. The current sequence is
 CC that of the murine anti-IGF-IR antibody EMI64-related protein of the
 CC invention.
 CC
 SQ Sequence 120 AA;
 XX
 XX
 Query Match 61.1%; Score 44; DB 8; Length 120;
 Best Local Similarity 66.7%; Pred. No. 39;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FYGTTYFDY 12
 :|||:||||
 Db 101 YYGSSYFDY 109
 XX
 XX
 RESULT 49
 ADH17832
 ID ADH17832 standard; protein; 120 AA.
 XX
 AC ADH17832;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Murine antibody lngp heavy chain variable region protein.
 XX
 XX antibody EMI64; insulin-like growth factor-I receptor; IGF-IR antagonist;
 KW breast cancer; colon; ovarian carcinoma; osteosarcoma; cervical;
 KW prostate; lung; synovial carcinoma; pancreatic; murine; mouse;
 KW heavy chain variable region; lngp.
 XX
 OS Mus sp.
 XX
 PN WO2003106621-A2.
 XX
 PD 24-DEC-2003.
 XX
 PF 12-JUN-2003; 2003WO-US016211.
 XX
 PR 14-JUN-2002; 2002US-00170390.
 XX

PA (IMMU-) IMMUNOGEN INC.
XX
PI Singh R, Tavares DJ, Dagdigian NE;
XX
DR WPI; 2004-082172/08.
XX
PT Novel murine antibody EM164 or antibody fragment that specifically binds
PT to insulin-like growth factor-I-receptor useful for treating breast
PT cancer, colon cancer, lung cancer, prostate cancer.
XX
XX Example 2; SEQ ID NO 72; 155bp; English.
XX
CC The invention relates to a novel murine antibody EM164 or antibody
CC fragment that specifically binds to insulin-like growth factor-I receptor
CC (IGF-IR) where the antibody is an antagonist of the receptor, is
CC substantially devoid of agonist activity toward the receptor and is
CC capable of inhibiting the growth of a cancer cell by greater than 80% in
CC the presence of a growth stimulant chosen from serum, IGF-I and IGF-II.
CC The antibody of the invention may be useful for diagnosing or treating a
CC patient having a cancer selected from breast cancer, colon cancer, a
CC ovarian carcinoma, osteosarcoma, cervical cancer, prostate cancer, lung
CC cancer, synovial carcinoma and pancreatic cancer. The current sequence is
CC that of the murine anti-IGF-IR antibody EM164-related protein of the
CC invention.
XX
SQ Sequence 120 AA;
XX
Query Match 61.1%; Score 44; DB 8; Length 120;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 4 FYGTTYPDY 12
:|::|||
DB 101 YYGSSYFDY 109
XX
RESULT 50
ADM11463
ID ADM11463 standard; protein; 120 AA.
XX
AC ADM11463;
XX
DT 24-MAR-2005 (first entry)
XX
DE Murine anti-IGF 1 receptor antibody EM164 VH-homologous lngp protein.
XX
KW antibody; cytostatic; cancer; neoplasm; breast tumor; colon tumor;
KW uterine cervix tumor; prostatic cancer; lung tumor; pancreas tumor;
KW ovary tumor; carcinoma; osteosarcoma; melanoma; nervous system tumor;
KW gene therapy; heavy chain variable region.
XX
OS Unidentified.
XX
PN US2004265307-A1.
XX
PD 30-DEC-2004.
XX
PF 08-DEC-2003; 2003US-00729441.
XX
PR 14-JUN-2002; 2002US-00170390.
XX
PA (IMMU-) IMMUNOGEN INC.
XX
PI Singh R, Tavares DJ, Dagdigian NE;
XX
DR WPI; 2005-074033/08.
XX
PT New composition comprising anti-insulin-like growth-factor-I receptor and
PT an agent, useful for treating cancer, e.g. ovarian carcinoma,
PT osteosarcoma, melanoma, multiple myeloma, neuroblastoma, or
PT rhabdomyosarcoma.
XX
PS Example 2; SEQ ID NO 72; 84bp; English.

XX
CC The invention relates to a novel composition comprising a first
CC therapeutic agent which is an antibody, or its epitope binding fragment,
CC and a second therapeutic agent. The antibody specifically binds to
CC insulin-like growth factor I (IGF 1) receptor. The IGF 1 receptor has
CC been implicated in promoting growth, transformation and survival of tumor
CC cells and several types of tumor are known to express higher than normal
CC levels of IGF 1 receptor. The composition of the invention demonstrates
CC cytostatic activity and may be useful for treating cancer, particularly
CC breast, colon, cervical, prostate, lung, or pancreatic cancer, ovarian
CC carcinoma, osteosarcoma, synovial carcinoma, melanoma, multiple myeloma,
CC neuroblastoma or rhabdomyosarcoma. Such treatment may be achieved with
CC the use of gene therapy techniques. The current sequence is that of an
CC antibody light chain variable region protein which shows homology to the
CC murine anti-IGF 1 receptor antibody EM164 heavy chain variable region
CC protein of the invention.
XX
SQ Sequence 120 AA;
XX
Query Match 61.1%; Score 44; DB 9; Length 120;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 4 FYGTTYPDY 12
:|::|||
DB 101 YYGSSYFDY 109

Search completed: January 17, 2006, 11:58:36
Job time : 102.091 secs

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:48:18 ; Search time 11.2727 Seconds
(without alignments)
102.424 Million cell updates/sec

Title: US-10-665-658-12
Perfect score: 72
Sequence: 1 GIFYGTYFDY 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	75.0	120	2 A44371	Ig heavy chain V r
2	51	70.8	24	2 PH1698	Ig heavy chain V r
3	51	70.8	24	2 PH1713	Ig heavy chain V r
4	51	70.8	24	2 PH1685	Ig heavy chain V r
5	51	70.8	24	2 PH1712	Ig heavy chain V r
6	51	70.8	26	2 PH1718	Ig heavy chain V r
7	51	70.8	26	2 PH1702	Ig heavy chain V r
8	51	70.8	34	2 PH1747	Ig heavy chain V r
9	50	69.4	24	2 PH1683	Ig heavy chain V r
10	49	68.1	24	2 PH1710	Ig heavy chain V r
11	47	65.3	26	2 PH1703	Ig heavy chain V r
12	46	63.9	34	2 PH1748	Ig heavy chain V r
13	46	63.9	341	2 H83162	probable amino aci
14	45	62.5	2	2 D69426	surface layer prot
15	44.5	61.1	25	2 PH1686	Ig heavy chain V r
16	44	61.1	23	2 PH1694	Ig heavy chain V r
17	44	61.1	25	2 PH1701	Ig heavy chain V r
18	44	61.1	113	2 S25041	Ig heavy chain V r
19	44	61.1	120	2 B22769	Ig heavy chain V r
20	44	61.1	139	1 MMS18	Ig heavy chain pre
21	44	61.1	287	4 PC4402	general l-amino ac
22	44	61.1	331	2 AD3553	Ig heavy chain V r
23	43.5	60.4	111	2 S25033	Ig heavy chain V r
24	43.5	60.4	111	2 S25034	Ig heavy chain V r
25	43	59.7	24	2 PH1696	Ig heavy chain V r
26	43	59.7	25	2 A49038	Ig lambda chain V
27	43	59.7	227	2 A95238	hypothetical prote
28	43	59.7	234	2 B98102	L-ribulose-phospha
29	43	59.7	459	2 A71849	hypothetical prote
30	42.5	59.0	109	2 S25038	Ig heavy chain V r
31	42.5	59.0	111	2 S25032	Ig heavy chain V r
32	42	58.3	24	2 PH1711	Ig heavy chain V r
33	42	58.3	25	2 PH1715	Ig heavy chain V r
34	42	58.3	645	1 ODPI	Cytochrome-c oxida
35	42	58.3	645	1 S07751	Cytochrome-c oxida
36	41	56.9	102	2 PH1490	Ig heavy chain V r
37	41	56.9	114	2 PH1523	Ig heavy chain V r
38	41	56.9	114	2 PH1522	Ig heavy chain V r
39	41	56.9	119	2 PH1510	Ig heavy chain V r
40	41	56.9	119	2 PH1505	Ig heavy chain V r
41	41	56.9	119	2 PH1518	Ig heavy chain V r
42	41	56.9	119	2 PH1517	Ig heavy chain V r
43	41	56.9	119	2 PH1502	Ig heavy chain V r
44	41	56.9	119	2 PH1521	Ig heavy chain V r
45	41	56.9	119	2 PH1500	Ig heavy chain V r
46	41	56.9	119	2 PH1516	Ig heavy chain V r
47	41	56.9	119	2 PH1503	Ig heavy chain V r
48	41	56.9	119	2 PH1504	Ig heavy chain V r
49	41	56.9	119	2 PH1520	Ig heavy chain V r
50	41	56.9	119	2 PH1519	Ig heavy chain V r
51	41	56.9	119	2 PH1512	Ig heavy chain V r
52	41	56.9	135	2 PH1494	Ig heavy chain V r
53	41	56.9	135	2 PH1493	Ig heavy chain V r
54	41	56.9	140	2 PH1498	Ig heavy chain V r
55	41	56.9	140	2 PH1483	Ig heavy chain V r
56	41	56.9	140	2 PH1482	Ig heavy chain V r
57	41	56.9	140	2 PH1484	Ig heavy chain V r
58	41	56.9	140	2 PH1489	Ig heavy chain V r
59	41	56.9	174	2 B90354	hypothetical prote
60	41	56.9	176	2 F90369	hypothetical prote
61	41	56.9	483	2 T03909	hypothetical prote
62	40.5	56.2	25	2 PH1700	Ig heavy chain V-D
63	40	55.6	117	2 S01822	Ig heavy chain V r
64	40	55.6	122	2 S24287	Ig heavy chain V r
65	40	55.6	220	2 G90290	hypothetical prote
66	40	55.6	334	2 D22735	hypothetical prote
67	40	55.6	339	2 T27931	Ig heavy chain V r
68	40	55.6	542	2 B81662	apolipoprotein N-a
69	40	55.6	591	2 JC7657	mannan endo-1,4-de
70	39.5	54.9	23	2 PH1725	Ig heavy chain V r
71	39.5	54.9	25	2 PH1716	Ig heavy chain V r
72	39.5	54.9	33	2 PH1741	Ig heavy chain V r
73	39.5	54.9	80	2 S25050	Ig heavy chain V r
74	39.5	54.9	102	2 S25025	Ig heavy chain V r
75	39.5	54.9	106	2 S25036	Ig heavy chain V r
76	39.5	54.9	111	2 S25024	Ig heavy chain V r
77	39.5	54.9	111	2 S25055	Ig heavy chain V r
78	39.5	54.9	111	2 S25054	Ig heavy chain V r
79	39.5	54.9	111	2 S25052	Ig heavy chain V r
80	39.5	54.9	111	2 S25030	Ig heavy chain V r
81	39.5	54.9	111	2 S25031	Ig heavy chain V r
82	39.5	54.9	111	2 S25051	Ig heavy chain V r
83	39.5	54.9	258	2 A88986	Ig heavy chain V r
84	39.5	54.2	34	2 PH1746	Ig heavy chain V r
85	39	54.2	309	2 T12991	hypothetical prote
86	39	54.2	352	2 H64172	hypothetical prote
87	39	54.2	362	2 S16303	polygalacturonase
88	39	54.2	362	2 UC7374	polygalacturonase
89	39	54.2	362	2 S61924	conserved hypothet
90	39	54.2	459	2 H64667	conserved hypothet
91	39	54.2	548	2 C75466	phytoene dehydroge
92	39	54.2	871	2 T40845	dna ligase - ftsH1
93	39	54.2	1059	1 A35210	ferroxidase (EC 1.
94	39	54.2	1069	1 KUH1	ferroxidase (EC 1.
95	38.5	53.5	144	2 B41287	Ig heavy chain pre
96	38.5	53.5	432	2 AE1285	glutamate-1-semial
97	38.5	53.5	432	2 AH1656	Ig heavy chain - m
98	38	52.8	11	2 S25056	Ig heavy chain V
99	38	52.8	32	2 B49038	Ig heavy chain V r
100	38	52.8	32	2 PH1735	Ig heavy chain V r
101	38	52.8	35	2 PH1750	Ig heavy chain V r
102	38	52.8	36	2 PH1752	Ig heavy chain V r

103	38	52.8	38	2	C49038	Ig lambda chain V	176	36	50.0	276	2	D84021	hypothetical prote
104	38	52.8	56	2	E49038	Ig lambda chain V	177	36	50.0	294	2	AC2915	acyl-CoA thioester
105	38	52.8	58	2	D49038	Ig lambda chain V	178	36	50.0	305	2	E91146	probable periplasm
106	38	52.8	70	2	B59230	androgen-binding p	179	36	50.0	305	2	A85992	probable periplasm
107	38	52.8	76	2	F51592	Ig heavy chain V r	180	36	50.0	305	2	F65119	hypothetical amino
108	38	52.8	88	2	F51515	Ig heavy chain V r	181	36	50.0	310	2	D70139	conserved hypotet
109	38	52.8	128	2	S31514	Ig heavy chain - h	182	36	50.0	316	2	G64238	hypothetical prote
110	38	52.8	140	2	S70442	Ig heavy chain pre	183	36	50.0	316	2	F97689	acyl-CoA thioester
111	38	52.8	184	2	P96925	biLy protein precu	184	36	50.0	317	2	T20302	hypothetical prote
112	38	52.8	202	2	G64625	hypothetical prote	185	36	50.0	318	2	G90193	ABctransporter SSO
113	38	52.8	243	2	A71886	hypothetical prote	186	36	50.0	326	2	T15194	hypothetical prote
114	38	52.8	280	2	T34905	probable hydrolase	187	36	50.0	334	2	F69495	conserved hypotet
115	38	52.8	280	2	T28684	hypothetical prote	188	36	50.0	336	2	F86319	Hypothetical prote
116	38	52.8	411	2	T22095	hypothetical prote	189	36	50.0	347	2	S71178	photosystem I prot
117	38	52.8	423	2	AF1335	transcription regu	190	36	50.0	361	2	T12571	cinamyl-alcohol d
118	38	52.8	430	2	B64129	adenosylmethionine	191	36	50.0	374	2	B97258	glycosyltransferas
119	38	52.8	467	2	B75322	probable oligendo	192	36	50.0	377	2	AD0315	conserved hypotet
120	38	52.8	489	2	T47747	cysteine-tRNA lliga	193	36	50.0	385	2	T45966	hypothetical prote
121	38	52.8	576	2	T12005	NADH2 dehydrogenas	194	36	50.0	387	2	B90436	hypothetical prote
122	38	52.8	576	2	C85047	probable transposo	195	36	50.0	411	1	OXMSL	protein-lysine 6-o
123	38	52.8	874	2	A10281	probable insectici	196	36	50.0	411	1	OXRTL	protein-lysine 6-o
124	38	52.8	952	2	AC0447	probable insectici	197	36	50.0	417	1	OXHUL	protein-lysine 6-o
125	38	52.8	984	2	AE0290	insecticial toxin	198	36	50.0	420	2	A45166	chitinase (EC 3.2.
126	38	52.8	1011	2	AD0447	probable insectici	199	36	50.0	423	2	UQ1975	glucosase-I-phosphat
127	37.5	52.1	33	2	PH1740	Ig heavy chain V r	200	36	50.0	423	2	H90507	amino acid transpo
128	37.5	52.1	341	2	D64565	ribonucleoside-dip	201	36	50.0	446	2	T07404	probable glucosylt
129	37.5	52.1	444	2	C71858	aminotransferase l	202	36	50.0	466	2	T35670	hypothetical prote
130	37.5	52.1	444	2	G90446	Ig heavy chain V r	203	36	50.0	469	2	C72538	probable cysteinyl
131	37	51.4	109	2	PH1016	Ig heavy chain V r	204	36	50.0	475	2	C72538	arginine/ornithine
132	37	51.4	109	2	PH1023	Ig heavy chain V r	205	36	50.0	475	2	T46745	hypothetical prote
133	37	51.4	113	2	S25044	Ig heavy chain V r	206	36	50.0	475	2	T47778	methionine transpo
134	37	51.4	118	2	T03756	hypothetical prote	207	36	50.0	574	2	S61943	hypothetical prote
135	37	51.4	119	2	S03077	Ig heavy chain V r	208	36	50.0	649	2	T24505	UDP-sugar hydrolas
136	37	51.4	121	1	GWMS11	Ig heavy chain V r	209	36	50.0	682	2	C84295	photosystem I prot
137	37	51.4	131	2	S65197	probable membrane	210	36	50.0	739	2	S06337	photosystem I prot
138	37	51.4	135	2	S78051	Ig heavy chain pre	211	36	50.0	750	1	AL1V67	photosystem I P700
139	37	51.4	145	2	F90320	conserved hypotet	212	36	50.0	750	1	AL1NTP7	photosystem I P700
140	37	51.4	265	2	G37271	metalloproteinas	213	36	50.0	750	1	A1R2P7	photosystem I P700
141	37	51.4	265	2	F37271	metalloproteinas	214	36	50.0	750	1	S00444	photosystem I prot
142	37	51.4	290	2	E37271	metalloproteinas	215	36	50.0	751	2	A28341	photosystem I P700
143	37	51.4	365	2	F71437	probable resistanc	216	36	50.0	751	2	S58552	photosystem I prot
144	37	51.4	475	2	D88451	protein K10D2.2 [1	217	36	50.0	751	2	S18242	photosystem I prot
145	37	51.4	478	2	T33985	hypothetical prote	218	36	50.0	751	2	T07278	photosystem I P700
146	37	51.4	505	2	C64502	hypothetical prote	219	36	50.0	752	2	S73205	photosystem I prot
147	37	51.4	525	2	A93601	periplasmic oligop	220	36	50.0	755	1	S20922	photosystem I prot
148	37	51.4	526	2	G82981	probable binding p	221	36	50.0	761	2	S00703	photosystem I prot
149	37	51.4	564	2	S63405	hexose transport p	222	36	50.0	812	2	AC3138	fimbrial usher pro
150	37	51.4	564	2	S50520	hexose transport p	223	36	50.0	812	2	D98149	hypothetical prote
151	37	51.4	567	2	S57187	sugar transport pr	224	36	50.0	854	2	AC2309	hypothetical prote
152	37	51.4	567	2	S67809	hexose transport p	225	36	50.0	877	2	UX0256	DNA-directed DNA p
153	37	51.4	581	2	T12095	beta-fructofuranos	226	36	50.0	955	2	T18435	hypothetical prote
154	37	51.4	614	2	B96656	unknown protein, 4	227	36	50.0	972	2	E97421	NADH dehydrogenase
155	37	51.4	651	2	A26581	beta-glucuronidase	228	36	50.0	994	2	AD2639	pH adaptation potass
156	37	51.4	726	2	S52141	ATPase - Brwnia a	229	36	50.0	1119	2	T15842	hypothetical prote
157	37	51.4	903	2	S60257	meltirin alpha - mo	230	36	50.0	2817	2	B97033	uncharacterized pr
158	36.5	50.7	23	2	PH1724	Ig heavy chain V r	231	36	49.3	26	2	PH1704	Ig heavy chain V r
159	36.5	50.7	23	2	PH1681	Ig heavy chain V r	232	36	49.3	27	2	PH1719	Ig heavy chain V r
160	36	50.0	98	2	A81219	hypothetical prote	233	36	49.3	33	2	PH1743	Ig heavy chain V r
161	36	50.0	107	2	D71122	hypothetical prote	234	36	49.3	398	2	AF0049	probable membrane
162	36	50.0	108	2	B30352	protein-lysine 6-o	235	36	49.3	403	2	T44836	glycosyltransferas
163	36	50.0	111	2	PH1007	Ig heavy chain V r	236	36	49.3	815	2	T40524	hypothetical prote
164	36	50.0	122	2	A49049	Ig heavy chain V r	237	36	48.6	24	2	PH1697	Ig heavy chain V r
165	36	50.0	124	2	S57715	chitinase (EC 3.2.	238	36	48.6	94	2	S26461	Ig heavy chain V r
166	36	50.0	140	2	PH1488	Ig heavy chain V r	239	36	48.6	98	2	S12414	Ig heavy chain V r
167	36	50.0	141	2	S31697	Ig heavy chain V r	240	36	48.6	98	2	S26903	Ig heavy chain V r
168	36	50.0	146	2	B95205	conserved domain p	241	36	48.6	99	2	S26801	Ig heavy chain V r
169	36	50.0	158	2	S58016	probable olfactory	242	36	48.6	99	2	S26807	Ig heavy chain V r
170	36	50.0	161	2	D70040	hypothetical prote	243	36	48.6	99	2	S26800	Ig heavy chain V r
171	36	50.0	168	2	S54337	protein-lysine 6-o	244	36	48.6	99	2	S26802	Ig heavy chain V r
172	36	50.0	226	2	C29504	hypothetical 24K p	245	36	48.6	99	2	S26803	Ig heavy chain V r
173	36	50.0	231	2	G83883	L-tibulose-5-phosp	246	36	48.6	99	2	S12418	Ig heavy chain V r
174	36	50.0	231	2	S28703	hypothetical prote	247	36	48.6	100	2	S78056	Ig heavy chain V r
175	36	50.0	232	2	T11072	cytochrome-c oxida	248	36	48.6	104	2	S24255	Ig heavy chain V r

249	35	48.6	110	2	S44110	Ig heavy chain V-D	322	35	48.6	1776	1	RRMP1M	genome polypeptide
250	35	48.6	116	2	S37456	Ig mu chain - huma	323	35	48.6	3010	1	S18030	genome polypeptide
251	35	48.6	117	2	S34964	Ig heavy chain pre	324	35	48.6	4488	1	RRIHM2	genome polypeptide
252	35	48.6	120	2	S36273	Ig heavy chain V r	325	34.5	47.9	86	2	D33989	Ig heavy chain V-4
253	35	48.6	120	2	PT0370	Ig mu chain precu	326	34.5	47.9	261	2	T11306	cytochrome-c oxida
254	35	48.6	121	2	S44113	Ig heavy chain V r	327	34.5	47.9	579	2	AB2177	hypothetical prote
255	35	48.6	124	2	S31684	Ig heavy chain V r	328	34.5	47.9	662	2	G89909	transketolase [imp
256	35	48.6	128	2	A37267	Ig heavy chain V r	329	34	47.2	39	2	S26939	Ig heavy chain V r
257	35	48.6	135	2	S31604	Ig heavy chain V r	330	34	47.2	39	2	S26937	Ig heavy chain V r
258	35	48.6	143	2	S03747	small membrane pro	331	34	47.2	90	2	PH1485	Ig heavy chain V r
259	35	48.6	147	2	S13519	Ig heavy chain V r	332	34	47.2	118	2	P00266	Ig V-D-J region (N
260	35	48.6	156	2	AB0079	hypothetical prote	333	34	47.2	122	2	S69912	Ig heavy chain V-I
261	35	48.6	182	2	P97201	hypothetical prote	334	34	47.2	129	1	DZHUMA	Ig heavy chain V r
262	35	48.6	200	2	B86700	transposon-related	335	34	47.2	132	2	A38911	Ig heavy chain V r
263	35	48.6	209	2	T48225	hypothetical prote	336	34	47.2	137	2	S31585	Ig heavy chain V r
264	35	48.6	231	2	P64642	hypothetical prote	337	34	47.2	140	2	PH1486	Ig heavy chain V r
265	35	48.6	240	2	B64461	spore coat polysac	338	34	47.2	140	2	PH1499	Ig heavy chain pre
266	35	48.6	247	2	C84070	hypothetical prote	339	34	47.2	142	2	C34903	Ig heavy chain pre
267	35	48.6	253	2	E90070	hypothetical prote	340	34	47.2	157	2	S58024	probable 1,2-dioxy
268	35	48.6	255	2	C90078	hypothetical prote	341	34	47.2	162	2	D83332	probable membrane
269	35	48.6	255	2	T20806	hypothetical prote	342	34	47.2	166	2	P97128	hypothetical prote
270	35	48.6	266	2	T24430	hypothetical prote	343	34	47.2	167	2	AE2342	cystic fibrosis tr
271	35	48.6	278	2	E95128	conserved hypotet	344	34	47.2	174	2	B39323	hypothetical prote
272	35	48.6	282	2	B97999	conserved hypotet	345	34	47.2	175	2	D83767	hypothetical prote
273	35	48.6	282	2	C97357	uncharacterized co	346	34	47.2	180	2	T49198	transcription regu
274	35	48.6	295	2	JM0079	heterogeneous nucl	347	34	47.2	181	2	ERAD75	early E3 20.6k gly
275	35	48.6	301	2	T12890	hypothetical prote	348	34	47.2	189	1	ERAD75	ABC transporter Am
276	35	48.6	308	2	AB0547	Arac-family trans	349	34	47.2	206	2	JC5491	olfactory receptor
277	35	48.6	334	2	T27658	hypothetical prote	350	34	47.2	206	2	T38472	olfactory receptor
278	35	48.6	334	2	T27658	hypothetical prote	351	34	47.2	216	2	T38480	hypothetical prote
279	35	48.6	337	2	JC5023	CMF-sialic acid tr	352	34	47.2	219	2	B81534	l-ribulose-phospha
280	35	48.6	344	2	G97302	ribonucleotide red	353	34	47.2	220	2	G90047	hypothetical prote
281	35	48.6	351	2	G71372	probable ribonucle	354	34	47.2	243	2	H64108	hypothetical prote
282	35	48.6	374	2	B96737	hypothetical prote	355	34	47.2	244	2	G86617	hypothetical prote
283	35	48.6	381	2	T29626	hypothetical prote	356	34	47.2	244	2	H72006	spore coat polysac
284	35	48.6	381	2	G72352	hypothetical prote	357	34	47.2	246	2	S33726	hypothetical prote
285	35	48.6	393	2	S27881	beta-alanine synth	358	34	47.2	250	2	T33551	hypothetical prote
286	35	48.6	399	2	B71140	hypothetical prote	359	34	47.2	255	2	G84181	H+-transporting tw
287	35	48.6	402	2	G75011	hypothetical prote	360	34	47.2	256	2	S58743	conserved hypotet
288	35	48.6	404	2	T19922	hypothetical prote	361	34	47.2	259	2	D81083	conserved hypotet
289	35	48.6	404	2	H97055	membrane bound tra	362	34	47.2	259	2	D81859	serine/threonine p
290	35	48.6	413	2	D71112	hypothetical prote	363	34	47.2	269	2	G90261	hypothetical prote
291	35	48.6	417	2	F75303	aminopeptidase - D	364	34	47.2	284	2	H97991	hypothetical prote
292	35	48.6	468	2	P82012	hypothetical prote	365	34	47.2	286	2	T22354	glucose-1-phosphat
293	35	48.6	483	2	A71958	outer membrane pro	366	34	47.2	293	2	AG0921	glucose-1-phosphat
294	35	48.6	508	2	AF0314	probable aldehyde	367	34	47.2	293	2	D86065	glucose-1-phosphat
295	35	48.6	514	2	T48987	hypothetical prote	368	34	47.2	293	2	B91219	oxoaldehyde, pr
296	35	48.6	546	2	MMBYH2	glucose transport	369	34	47.2	293	2	D90456	glucose-1-phosphat
297	35	48.6	546	2	F71951	periplasmic dipept	370	34	47.2	293	2	H65182	glucose-1-phosphat
298	35	48.6	546	2	S48313	hexose transport p	371	34	47.2	325	1	ERADP7	fiber protein - hu
299	35	48.6	549	1	B64557	dipeptide ABC tran	372	34	47.2	325	2	D37476	translation initia
300	35	48.6	556	2	TS1081	glucose transport	373	34	47.2	328	2	T46558	suppressor of unco
301	35	48.6	566	2	TS3042	hypothetical prote	374	34	47.2	328	2	T46558	conserved hypotet
302	35	48.6	567	2	S31294	hexose transport p	375	34	47.2	332	2	F87319	hypothetical prote
303	35	48.6	585	2	AC0506	probable sulfatase	376	34	47.2	335	2	T42745	ribosomal protein
304	35	48.6	585	2	AB8436	subtilisin homolog	377	34	47.2	339	2	S53844	probable transport
305	35	48.6	589	2	T33785	hypothetical prote	378	34	47.2	364	2	H85856	probable transport
306	35	48.6	607	2	AB3511	oligomendopitidase	379	34	47.2	364	2	F91012	hypothetical ABC t
307	35	48.6	608	2	T28301	ORF MSV140 hypot	380	34	47.2	364	2	A64987	conserved hypotet
308	35	48.6	631	2	D69750	phosphotransferase	381	34	47.2	366	2	D69951	hypothetical prote
309	35	48.6	660	2	H85227	membrane-associate	382	34	47.2	371	2	T46421	lipopolysaccharide
310	35	48.6	660	2	AC0016	hypothetical prote	383	34	47.2	374	2	F72355	probable nucleotid
311	35	48.6	698	2	AC0016	4-alpha-glucanotra	384	34	47.2	383	2	H81097	probable glucose-1
312	35	48.6	747	2	S37694	gene PC326 protein	385	34	47.2	419	2	E71207	probable outer mem
313	35	48.6	751	2	E86834	maltosephosphoryla	386	34	47.2	428	2	E90793	fibritogen gamma-A
314	35	48.6	762	2	T38081	probable mitochond	387	34	47.2	437	1	FGRTGA	fibritogen gamma-A
315	35	48.6	885	1	S26723	DNA-directed RNA p	388	34	47.2	437	1	FGRTGA	fibritogen gamma-A
316	35	48.6	1016	1	H71460	ATP-dependent perm	389	34	47.2	437	1	FGRTGA	fibritogen gamma-A
317	35	48.6	1049	1	S19421	transcription - rep	390	34	47.2	438	2	F97234	ethanolamin perme
318	35	48.6	1171	2	E97295	hypothetical prote	391	34	47.2	442	2	C71687	proline/betain tra
319	35	48.6	1249	2	T26294	serine proteinase,	392	34	47.2	442	2	UCS911	lysine - lactobacil
320	35	48.6	1308	2	A90428	putative US snRNP-	393	34	47.2	444	2	S05313	fibritogen gamma-B
321	35	48.6	1436	2	A99115	cystic fibrosis tr	394	34	47.2	445	1	FGRTGB	fibritogen gamma-B

395	34	47.2	453	1	FGHUGB	fibrinogen gamma-B
396	34	47.2	457	2	SS0357	sugar transport pr
397	34	47.2	459	2	T24934	hypothetical prote
398	34	47.2	463	1	P2ML13	I2 protein - human
399	34	47.2	474	2	D83810	amino acid carrier
400	34	47.2	487	2	E96782	hypothetical prote
401	34	47.2	522	2	S01031	alpha-amylase (EC
402	34	47.2	522	2	A31556	glucose transport
403	34	47.2	523	2	S06920	glucose transport
404	34	47.2	524	2	A31318	glucose transport
405	34	47.2	539	2	A85603	hypothetical protei
406	34	47.2	544	2	S75109	cytochrome-c oxida
407	34	47.2	545	2	AB0290	probable membrane
408	34	47.2	550	2	B93446	oligopeptidase ABC t
409	34	47.2	556	2	G93052	thermopsin precurs
410	34	47.2	560	2	S46724	hexose transport p
411	34	47.2	566	2	S59382	hypothetical prote
412	34	47.2	567	2	S11295	glucose transport
413	34	47.2	567	2	S50708	hexose transport p
414	34	47.2	567	2	S49600	hexose transport p
415	34	47.2	569	2	S50771	hexose transport p
416	34	47.2	570	2	S43185	hexose transport p
417	34	47.2	570	2	S43186	hexose transport p
418	34	47.2	570	2	H90370	thermopsin precurs
419	34	47.2	591	1	N020F	glucose-6-phosphat
420	34	47.2	592	2	S43742	hexose transport p
421	34	47.2	598	2	SS1456	probable membrane
422	34	47.2	598	2	S66954	probable membrane
423	34	47.2	599	2	S67084	probable membrane
424	34	47.2	622	2	D90373	hypothetical prote
425	34	47.2	650	2	S23217	beta-fructofuranos
426	34	47.2	693	2	A12584	hypothetical prote
427	34	47.2	728	2	H97366	ribonucleotide red
428	34	47.2	736	2	C82151	sensor histidine k
429	34	47.2	750	2	SS5586	phosphatidylglycer
430	34	47.2	750	2	B86135	phosphoglycerol tr
431	34	47.2	750	2	G91293	probable phosphat
432	34	47.2	752	2	T06838	probable maltose p
433	34	47.2	752	2	C81781	phosphatidylglycer
434	34	47.2	763	2	AD1070	hypothetical prote
435	34	47.2	801	2	S50660	hypothetical prote
436	34	47.2	816	2	S70368	DNA polymerase I -
437	34	47.2	879	2	JC4286	DNA-directed DNA p
438	34	47.2	916	2	I55441	vp165 - rat
439	34	47.2	984	2	T50309	hypothetical WD-re
440	34	47.2	1028	2	B86473	113.9k hypothetical
441	34	47.2	1092	2	T20117	hypothetical prote
442	34	47.2	1382	1	INHUR	insulin receptor p
443	34	47.2	1382	1	INHUR	insulin receptor p
444	34	47.2	1383	2	A36080	insulin receptor p
445	34	47.2	1630	2	T40217	hypothetical prote
446	34	47.2	1659	2	G95057	endo-beta-N-acetyl
447	34	47.2	1659	2	H97926	hypothetical prote
448	34	47.2	1880	2	T18531	tractin - medicina
449	34	47.2	2152	2	T45583	hypothetical prote
450	34	47.2	3343	2	S44887	ZK112.7 protein -
451	33.5	46.5	25	2	PH1733	Ig heavy chain V r
452	33.5	46.5	33	2	PH1742	Ig heavy chain V r
453	33.5	46.5	33	2	PH1738	Ig heavy chain V r
454	33.5	46.5	33	2	PH1739	Ig heavy chain V r
455	33.5	46.5	261	2	T11460	cytochrome-c oxida
456	33.5	46.5	302	2	D86449	FSD14.20 protein -
457	33.5	46.5	323	2	E75459	probable phosphor
458	33.5	46.5	355	2	S76940	hypothetical prote
459	33.5	46.5	356	2	T18015	glutamate-1-semial
460	33.5	46.5	392	2	G69637	glutamate-1-semial
461	33.5	46.5	437	1	G83767	ornithine-oxo-acid
462	33.5	46.5	439	1	XNHUO	ornithine-oxo-acid
463	33.5	46.5	439	1	XNMSO	ornithine-oxo-acid
464	33.5	46.5	439	1	XNRTO	ornithine-oxo-acid
465	33.5	46.5	831	2	A99304	penicillin acylase
466	33.5	46.5	1403	2	H97131	uncharacterized, p
467	33	45.8	36	2	PH1753	Ig heavy chain V r
468	33	45.8	40	2	S05686	hypothetical prote
469	33	45.8	40	2	A05047	hypothetical prote
470	33	45.8	89	2	T18817	hypothetical prote
471	33	45.8	92	2	D96947	hypothetical prote
472	33	45.8	102	2	I57691	ubiquinol-cytochro
473	33	45.8	111	2	C69158	conserved hypotbet
474	33	45.8	119	2	F27888	Ig heavy chain V r
475	33	45.8	123	1	AVMSH6	Ig heavy chain V r
476	33	45.8	128	2	C37267	Ig heavy chain V r
477	33	45.8	141	2	I47209	Ig heavy chain var
478	33	45.8	144	1	AVMS67	Ig heavy chain pre
479	33	45.8	151	2	AF0014	conserved hypotbet
480	33	45.8	153	2	AB0214	probable membrane
481	33	45.8	163	2	S58028	probable olfactory
482	33	45.8	164	2	H95889	phosphoesterase-re
483	33	45.8	164	2	AG0539	probable lipoprote
484	33	45.8	166	2	C43748	hypothetical prote
485	33	45.8	167	2	T36290	probable integral
486	33	45.8	168	2	C81923	probable membrane
487	33	45.8	173	2	AA8300	lens membrane prot
488	33	45.8	173	1	S07734	MDH2 dehydrogenas
489	33	45.8	197	2	A44363	voltage-gated dily
490	33	45.8	224	2	B71228	hypothetical prote
491	33	45.8	225	2	B75196	hypothetical prote
492	33	45.8	237	2	T26600	hypothetical prote
493	33	45.8	242	2	F84788	hypothetical prote
494	33	45.8	243	2	T16605	hypothetical prote
495	33	45.8	250	2	T29866	hypothetical prote
496	33	45.8	251	2	S74482	UDP-N-acetyl-D-man
497	33	45.8	260	2	S70589	cytochrome-c oxida
498	33	45.8	264	2	AG3354	hypothetical prote
499	33	45.8	283	2	C23660	calcium channel pr
500	33	45.8	283	2	T20734	hypothetical prote
501	33	45.8	287	2	D69536	hypothetical prote
502	33	45.8	290	2	T00103	glucose-1-phosphat
503	33	45.8	293	2	AB0470	glucose-1-phosphat
504	33	45.8	294	2	A23660	calcium channel pr
505	33	45.8	294	2	B23660	calcium channel pr
506	33	45.8	295	2	AA9906	glucose-1-phosphat
507	33	45.8	299	2	F69108	phytoene synthase
508	33	45.8	316	2	B69315	acetylornithine de
509	33	45.8	317	2	T73887	hypothetical prote
510	33	45.8	327	2	T77483	hypothetical prote
511	33	45.8	334	2	D82793	hypothetical prote
512	33	45.8	336	2	AG0307	conserved hypotbet
513	33	45.8	337	2	SS4402	Spix protein - Syn
514	33	45.8	340	2	T26923	hypothetical prote
515	33	45.8	341	2	T32715	hypothetical prote
516	33	45.8	342	2	B82208	amino acid ABC tra
517	33	45.8	347	2	S12955	calcium channel pr
518	33	45.8	350	2	AH1604	B. subtilis Yqgu p
519	33	45.8	355	2	H72150	B8L protein - Vari
520	33	45.8	360	2	T45649	hypothetical prote
521	33	45.8	362	2	S12895	polysialacturonase
522	33	45.8	363	2	H82178	conserved hypotbet
523	33	45.8	362	2	S57763	branched-chain ami
524	33	45.8	365	2	C83512	conserved hypotbet
525	33	45.8	368	2	C90487	oxidoreductase (im
526	33	45.8	371	2	E70464	conserved hypotbet
527	33	45.8	373	2	A66797	hypothetical prote
528	33	45.8	379	2	AS3077	ubiquinol-cytochro
529	33	45.8	386	2	H86870	hypothetical prote
530	33	45.8	388	2	E64707	outer membrane pro
531	33	45.8	388	2	C71813	probable outer mem
532	33	45.8	407	2	AD0706	O-antigen polymera
533	33	45.8	407	2	A43672	O-antigen polymera
534	33	45.8	409	2	T25935	hypothetical prote
535	33	45.8	413	2	T39168	probable agmatinas
536	33	45.8	416	2	T80846	probable isocitrat
537	33	45.8	419	2	F72866	alkaline exonuclea
538	33	45.8	420	2	T41870	AtK-EXO orf13 - B
539	33	45.8	423	2	C95085	sodium-dependent t
540	33	45.8	423	2	AC0775	probable nucleosid

541	33	45.8	430	2	T42430	probable ornithine
542	33	45.8	431	2	T76773	ATP binding compon
543	33	45.8	432	2	A97120	proton/sodium-glut
544	33	45.8	443	2	G75038	probable sodium/pr
545	33	45.8	444	2	T26229	hypothetical prote
546	33	45.8	451	2	F69825	sodium-dependent t
547	33	45.8	452	2	F36837	D6L protein - vari
548	33	45.8	452	2	T28443	probable host rang
549	33	45.8	459	2	AC1543	protoporphyrinogen
550	33	45.8	465	2	SS1613	cyclin homolog Cln
551	33	45.8	465	2	A69585	amino acid carrier
552	33	45.8	467	2	T21341	hypothetical prote
553	33	45.8	469	2	F69403	hypothetical prote
554	33	45.8	470	2	B83989	amino acid carrier
555	33	45.8	472	2	T47436	protein kinase-lik
556	33	45.8	474	2	B86607	cyteineyl tRNA syn
557	33	45.8	474	2	F72016	cyteine-CRNA ligase
558	33	45.8	475	2	F84140	amino acid transpo
559	33	45.8	478	2	D82622	coenzyme F390 synt
560	33	45.8	484	2	E64432	spore coat polysac
561	33	45.8	485	2	H83938	methylmalonate-sem
562	33	45.8	485	2	G97324	probable membrane
563	33	45.8	487	2	A69645	methylmalonate-sem
564	33	45.8	492	2	S53322	fructose transport
565	33	45.8	492	2	B90276	methylmalonate-sem
566	33	45.8	502	2	I53268	glut 5 protein - r
567	33	45.8	507	2	B83988	proline transpore
568	33	45.8	510	2	D70825	probable methylmal
569	33	45.8	519	2	T43756	ATPase subunit 1 l
570	33	45.8	538	2	H86605	acylglycerophospho
571	33	45.8	538	2	A72018	Aas bifunctional p
572	33	45.8	539	1	A42467	alkaline phosphata
573	33	45.8	542	2	S63222	MPA3 protein - ye
574	33	45.8	573	2	T27869	sphingomyelin phos
575	33	45.8	573	2	S78197	probable maturase
576	33	45.8	589	2	G84777	probable beta-fruc
577	33	45.8	598	2	D70104	DNA topoisomerase
578	33	45.8	608	2	E64610	outer membrane pro
579	33	45.8	629	2	B64610	outer membrane pro
580	33	45.8	634	2	A64521	outer membrane pro
581	33	45.8	638	2	B71904	probable outer mem
582	33	45.8	639	2	C95342	nitroux-oxide redu
583	33	45.8	640	2	AG1269	threonyl-CRNA synt
584	33	45.8	640	2	A11631	threonyl-CRNA synt
585	33	45.8	641	2	A64667	outer membrane pro
586	33	45.8	643	2	B71848	probable outer mem
587	33	45.8	645	2	H89951	threonyl-CRNA synt
588	33	45.8	646	2	H89843	hypothetical prote
589	33	45.8	650	2	G70169	heat shock protein
590	33	45.8	651	2	E71904	probable outer mem
591	33	45.8	652	2	T41162	hypothetical prote
592	33	45.8	654	2	F83260	hypothetical prote
593	33	45.8	658	2	G90389	conserved hypothet
594	33	45.8	668	2	A71986	probable outer mem
595	33	45.8	674	2	B84381	acylaminoacyl-pept
596	33	45.8	690	2	AB0124	outer membrane pro
597	33	45.8	691	2	C64548	outer membrane pro
598	33	45.8	694	1	C65137	4-alpha-glucanotra
599	33	45.8	694	2	A86007	4-alpha-glucanotra
600	33	45.8	694	2	B91161	4-alpha-glucanotra
601	33	45.8	696	2	G71829	probable outer mem
602	33	45.8	726	2	B29828	ferric anguibactin
603	33	45.8	753	2	T07543	photosystem I prot
604	33	45.8	761	1	SS2769	subtilisin-like pr
605	33	45.8	763	2	S67684	probable membrane
606	33	45.8	825	2	S75173	hypothetical prote
607	33	45.8	879	2	T19919	hypothetical prote
608	33	45.8	884	2	A31928	glucose transport
609	33	45.8	933	2	D64490	hypothetical prote
610	33	45.8	976	2	G87389	Tomb-dependent rec
611	33	45.8	1204	2	C75015	probable pyrolysin
612	33	45.8	1228	2	AE2397	protoporphyrin IX
613	33	45.8	1300	2	T03166	probable immediate
614	33	45.8	1331	2	S05011	calcium channel al
615	33	45.8	1421	2	T49500	hypothetical prote
616	33	45.8	1513	2	S45768	mitotic spindle pr
617	33	45.8	1661	2	T13330	head-activator bin
618	33	45.8	2091	2	A97077	hypothetical prote
619	33	45.8	2139	2	A44467	voltage-dependent
620	33	45.8	2143	2	U04427	calcium channel pr
621	33	45.8	2166	2	S11339	calcium channel pr
622	33	45.8	2171	2	S05054	calcium channel pr
623	33	45.8	2220	2	A45290	cytochrome b - Clo
624	33	45.8	2364	2	T40884	cytochrome b - Clo
625	33	45.8	2366	2	S10317	toxin B - Clostrid
626	33	45.8	2367	2	S70172	toxin B - Clostrid
627	33	45.8	2367	2	S15102	alpha-2-macroglobu
628	33	45.8	4543	1	S02392	alpha-2-macroglobu
629	33	45.8	4544	1	S25111	alpha-2-macroglobu
630	33	45.8	4545	1	S25111	Ig heavy chain V r
631	32.5	45.1	34	2	AH0423	probable membrane
632	32.5	45.1	37	2	S38565	Ig heavy chain V r
633	32.5	45.1	118	2	S38565	Ig heavy chain V r
634	32.5	45.1	121	2	PL0281	Ig heavy chain V r
635	32.5	45.1	125	2	PT0353	Ig heavy chain pre
636	32.5	45.1	140	1	HYMSG7	early E3 20.5K gly
637	32.5	45.1	189	1	BRAD35	hypothetical prote
638	32.5	45.1	189	2	S52803	hypothetical prote
639	32.5	45.1	303	2	T15835	probable exported
640	32.5	45.1	316	2	AD0101	hypothetical prote
641	32.5	45.1	426	2	AD0527	glutamate-1-semial
642	32.5	45.1	426	2	P90648	glutamate-1-semial
643	32.5	45.1	426	2	F85499	glutamate-1-semial
644	32.5	45.1	426	2	B64739	glutamate-1-semial
645	32.5	45.1	426	2	A37848	prophage p13 prote
646	32.5	45.1	511	2	C86798	transketolase homo
647	32.5	45.1	664	2	A11237	transketolase homo
648	32.5	45.1	664	2	AP1600	nitrate reductase
649	32.5	45.1	729	2	S36605	probable membrane
650	32.5	45.1	825	2	S64783	hypothetical prote
651	32.5	45.1	825	2	T29165	Ig heavy chain V r
652	32.5	45.1	3766	2	PH1678	Ig heavy chain V r
653	32.5	45.1	22	2	PH1695	Ig heavy chain V r
654	32.5	45.1	23	2	PH1695	monocytic chemotact
655	32.5	45.1	25	2	I67552	photosystem II 4K
656	32.5	45.1	40	1	F2W74U	photosystem II pro
657	32.5	45.1	40	1	F2W74U	photosystem II pro
658	32.5	45.1	40	1	S04065	hypothetical prote
659	32.5	45.1	40	2	S03194	probable photosyst
660	32.5	45.1	40	2	T07478	photosystem II pro
661	32.5	45.1	40	2	A12286	photosystem II cen
662	32.5	45.1	40	2	T06869	nuclear pore prote
663	32.5	45.1	53	2	A56512	keratin, scale (cl
664	32.5	45.1	73	2	A60136	Ig heavy chain V r
665	32.5	45.1	84	2	PH1487	Ig heavy chain V r
666	32.5	45.1	98	2	B24754	Ig heavy chain V r
667	32.5	45.1	102	2	S14593	hypothetical prote
668	32.5	45.1	102	2	S03228	hypothetical prote
669	32.5	45.1	105	2	F72452	15U ribosomal prot
670	32.5	45.1	110	2	B90416	Ig kappa chain V r
671	32.5	45.1	112	2	D28195	spemadhesin PSP-I
672	32.5	45.1	112	2	S65875	Ig heavy chain - h
673	32.5	45.1	117	2	S31109	Ig heavy chain V-I
674	32.5	45.1	119	1	GIHWDW	Ig heavy chain V-I
675	32.5	45.1	120	2	GIHWDW	Ig heavy chain V-I
676	32.5	45.1	122	2	S11740	Ig heavy chain pre
677	32.5	45.1	122	2	C82926	hypothetical prote
678	32.5	45.1	155	1	KRCHS	keratin, scale - c
679	32.5	45.1	157	2	S57996	probable olfactory
680	32.5	45.1	161	2	D87481	conserved hypothet
681	32.5	45.1	188	2	AC1305	methylphosphotriis
682	32.5	45.1	191	2	AC1305	probable purine/py
683	32.5	45.1	193	2	S28747	cytochrome-c oxida
684	32.5	45.1	199	2	S38867	eggshell protein -
685	32.5	45.1	202	2	B86811	hypothetical prote
686	32.5	45.1	205	2	D95200	conserved hypothet
687	32.5	45.1	205	2	C98067	hypothetical prote

687	32	44.4	211	2	T25237	hypothetical prote	760	32	44.4	386	2	F95911	probable hydrocarb
688	32	44.4	213	2	T49938	hypothetical prote	761	32	44.4	386	2	T38150	aminoalcoholphosph
689	32	44.4	219	2	S74483	hypothetical prote	762	32	44.4	387	2	T07687	omega-6 desaturase
690	32	44.4	226	2	AC0634	conserved hypotnet	763	32	44.4	407	2	D83460	cytochrome c-type
691	32	44.4	232	2	C70180	conserved hypotnet	764	32	44.4	413	2	S77371	hypothetical prote
692	32	44.4	233	2	T19432	hypothetical prote	765	32	44.4	415	2	A86539	rod shape protein
693	32	44.4	236	2	E89976	conserved hypotnet	766	32	44.4	416	2	C72026	hypothetical prote
694	32	44.4	233	2	E86935	hypothetical prote	767	32	44.4	416	2	AE2527	hypothetical prote
695	32	44.4	243	2	AC0665	ABC transporter AT	768	32	44.4	417	2	C44038	tryptophan permeas
696	32	44.4	248	2	E64703	outer membrane pro	769	32	44.4	419	2	T39920	probable glucanase
697	32	44.4	248	2	E71816	probable outer mem	770	32	44.4	421	2	T44511	hypothetical prote
698	32	44.4	250	2	A10258	probable phage pro	771	32	44.4	422	2	G72234	hypothetical prote
699	32	44.4	251	2	T13104	minor tail protein	772	32	44.4	424	2	S17571	carboxypeptidase T
700	32	44.4	254	2	D97031	TPR-repeat-contain	773	32	44.4	425	2	C83903	hypothetical prote
701	32	44.4	259	2	S58988	cytochrome-c oxida	774	32	44.4	426	2	T44522	hypothetical prote
702	32	44.4	261	2	T11293	cytochrome-c oxida	775	32	44.4	426	2	AH3117	hypothetical prote
703	32	44.4	262	2	T11355	cytochrome-c oxida	776	32	44.4	427	2	AC1394	human N-acetylgluc
704	32	44.4	264	2	AB3547	transcription regu	777	32	44.4	427	2	AE1769	weakly human N-ace
705	32	44.4	268	1	WEBR11	NAD ADP-ribosyltra	778	32	44.4	428	2	F98169	hypothetical prote
706	32	44.4	269	1	A25973	pertussis toxin ch	779	32	44.4	431	2	G75108	pyridoxal-phosphat
707	32	44.4	269	1	B25973	pertussis toxin ch	780	32	44.4	432	1	I39877	diaminopimelate de
708	32	44.4	269	1	WEBR1P	NAD ADP-ribosyltra	781	32	44.4	438	2	AE3231	conjugal transfer
709	32	44.4	270	2	B85648	probable transcrip	782	32	44.4	438	2	A71026	probable aminotran
710	32	44.4	270	2	B90788	probable transcrip	783	32	44.4	442	2	D72498	probable serine hy
711	32	44.4	292	2	T31325	menaquinone biosyn	784	32	44.4	442	2	F82488	Ca-dicarboxylate t
712	32	44.4	293	2	T29326	hypothetical prote	785	32	44.4	442	2	T39284	hypothetical prote
713	32	44.4	301	2	C72359	conserved hypotnet	786	32	44.4	443	2	S65963	flavastatin (EC 3.
714	32	44.4	301	2	T17885	major capsid-like	787	32	44.4	445	2	S06992	wall-associated pr
715	32	44.4	302	1	F70021	proline dehydrogen	788	32	44.4	445	2	H97091	chitinase family p
716	32	44.4	302	2	T21843	hypothetical prote	789	32	44.4	447	2	S52437	CBP-diacylglycerol
717	32	44.4	306	2	B88555	protein F54C8.6 [i	790	32	44.4	447	2	AE2295	hypothetical prote
718	32	44.4	307	2	T23302	hypothetical prote	791	32	44.4	449	2	S16748	proline-rich prote
719	32	44.4	309	2	S40748	hypothetical prote	792	32	44.4	450	2	D90047	hypothetical prote
720	32	44.4	315	2	C64381	proteinase IV (EC	793	32	44.4	453	2	G89045	protein B0238.2 [i
721	32	44.4	316	2	T22197	hypothetical prote	794	32	44.4	453	2	S51453	probable membrane
722	32	44.4	319	2	T38533	su1 protein homol	795	32	44.4	457	2	AE0507	probable transport
723	32	44.4	324	2	S62543	hypothetical prote	796	32	44.4	459	2	I64224	aromatic amino aci
724	32	44.4	325	2	F86321	F614.12 protein -	797	32	44.4	459	2	T16632	hypothetical prote
725	32	44.4	329	2	I40881	choloyleglycine hyd	798	32	44.4	460	2	UC5137	beta-glucosidase (
726	32	44.4	329	2	T20546	hypothetical prote	799	32	44.4	461	2	T27651	hypothetical prote
727	32	44.4	330	2	A10491	probable membrane	800	32	44.4	462	2	AH1053	probable exported
728	32	44.4	330	2	AE2870	hypothetical prote	801	32	44.4	464	2	T33249	hypothetical prote
729	32	44.4	330	2	G97646	thiamin biosynthes	802	32	44.4	470	2	T05258	glycine hydroxymet
730	32	44.4	332	2	B89004	protein T24A6.9 [i	803	32	44.4	470	2	S74896	hypothetical prote
731	32	44.4	334	2	B83785	ferrichrome ABC tr	804	32	44.4	474	2	A64691	type III restructic
732	32	44.4	337	2	A89047	protein C10G8.1 [i	805	32	44.4	476	1	UC6505	streptomycin 2 (EC
733	32	44.4	345	2	T41355	Su1 homolog - fis	806	32	44.4	476	1	KCRTS2	glucosyltransferas
734	32	44.4	345	2	A64370	adenylosuccinate s	807	32	44.4	476	2	T03747	glucosyltransferas
735	32	44.4	347	2	D83605	probable binding p	808	32	44.4	476	2	T03745	hypothetical prote
736	32	44.4	351	1	D84430	probable acid phos	809	32	44.4	483	2	B82722	hypothetical prote
737	32	44.4	351	2	T21855	hypothetical prote	810	32	44.4	485	2	F81001	peptide transport
738	32	44.4	356	2	D97057	stage II aporinati	811	32	44.4	485	2	G82016	probable peptide t
739	32	44.4	357	2	F82982	carabolic alanine	812	32	44.4	486	2	D70932	probable monooxygen
740	32	44.4	359	2	AC0040	alanine racemase (813	32	44.4	489	2	H86711	4-alpha-glucanotra
741	32	44.4	360	2	H83094	phospho-N-acetylmu	814	32	44.4	490	2	T14545	probable sugar tra
742	32	44.4	360	2	JC2443	chemokine (C-C) re	815	32	44.4	493	2	S78384	acetyl-CoA carboxy
743	32	44.4	360	2	AB0172	probable outer mem	816	32	44.4	494	2	AG3103	mannitol 2-dehydro
744	32	44.4	360	2	T20340	hypothetical prote	817	32	44.4	498	1	S48058	cytochrome P450 Cy
745	32	44.4	361	2	S57182	probable polygalac	818	32	44.4	499	2	S26454	hypothetical prote
746	32	44.4	364	2	S28771	polygalacturonase	819	32	44.4	500	2	G71633	hypothetical prote
747	32	44.4	368	2	S17980	pgal protein - Asp	820	32	44.4	510	2	G71365	Adp,ATP carrier pr
748	32	44.4	369	2	S70847	outer membrane por	821	32	44.4	515	2	UC7533	probable carnitine
749	32	44.4	373	2	T13024	probable protein k	822	32	44.4	515	2	UC5458	inulinase (EC 3.2.
750	32	44.4	373	2	T39179	chemokine (C-C) re	823	32	44.4	517	2	S77255	hypothetical prote
751	32	44.4	374	2	I38450	mitogen-activated	824	32	44.4	519	2	H97724	multidrug resistan
752	32	44.4	376	2	S40471	cell shape-determi	825	32	44.4	520	2	A85025	hypothetical prote
753	32	44.4	379	2	D81515	endopolygalacturon	826	32	44.4	525	2	S26022	cytochrome-c oxida
754	32	44.4	380	2	S62742	endopolygalacturon	827	32	44.4	525	2	C98183	mannitol 2-dehydro
755	32	44.4	380	2	S62743	hypothetical prote	828	32	44.4	526	2	T21811	hypothetical prote
756	32	44.4	382	2	S74947	outer membrane uah	829	32	44.4	528	2	H70140	oligopeptide ABC t
757	32	44.4	382	2	D64904	probable iprn prot	830	32	44.4	529	2	C75577	extracellular solu
758	32	44.4	384	2	A70805	proline-rich prote	831	32	44.4	530	2	C66154	hypothetical prote
759	32	44.4	385	2	T16180		832	32	44.4	532	2	H83083	probable binding p

833	32	44.4	533	2	C83084	probable binding p	906	32	44.4	1288	2	E71884	vacuolating cyto
834	32	44.4	534	2	S21961	proline-rich prote	907	32	44.4	1290	2	G64630	vacuolating cyto
835	32	44.4	535	2	T52048	probable beta-gluc	908	32	44.4	1291	2	S44983	vacuolating cyto
836	32	44.4	537	2	G83083	probable binding p	909	32	44.4	1298	2	A48999	protein-tyrosine k
837	32	44.4	542	2	B87373	ABC transporter, A	910	32	44.4	1363	2	T58375	protein-tyrosine k
838	32	44.4	546	1	COBYC1	cyclin I - yeast	911	32	44.4	1379	2	UC4954	vacuolar endothei
839	32	44.4	551	1	VHNZ4A	nucleocapsid prote	912	32	44.4	1417	2	AG2137	hypothetical prote
840	32	44.4	551	1	VHNZ4B	nucleocapsid prote	913	32	44.4	1447	2	S50918	DNA helicase TP51
841	32	44.4	555	2	AC0998	mannosyl transfera	914	32	44.4	1526	2	A4406	DNA topoisomerase
842	32	44.4	559	2	AC0998	probable membrane	915	32	44.4	1530	2	A40493	DNA topoisomerase
843	32	44.4	583	2	S19476	hypothetical prote	916	32	44.4	1553	2	T30227	pipercolate-incorpo
844	32	44.4	585	2	T48513	hypothetical prote	917	32	44.4	1553	2	S67483	3-dehydroquinatase
845	32	44.4	608	2	S76192	hypothetical prote	918	32	44.4	1573	2	T50113	hypothetical prote
846	32	44.4	619	2	B90141	hypothetical prote	919	32	44.4	1581	2	T32963	hypothetical prote
847	32	44.4	633	2	T02673	heterogeneous nucl	920	32	44.4	1715	2	G84429	hypothetical prote
848	32	44.4	647	2	P95189	thionyl-L-cRNA synt	921	32	44.4	1852	2	A37860	calcium channel pr
849	32	44.4	650	2	T00617	endostyle-specific	922	32	44.4	2175	2	A59255	myosin VIIa, long
850	32	44.4	660	2	G98055	threonine-L-cRNA lig	923	32	44.4	2215	2	T30870	myosin VIIa - mous
851	32	44.4	664	2	T14132	NADH2 dehydrogenas	924	32	44.4	3591	1	S21010	filamentous hemag
852	32	44.4	664	2	A69138	NADH2 dehydrogenas	925	31.5	43.8	23	2	PH1727	Ig heavy chain V r
853	32	44.4	665	2	T51198	DNA-dependent RNA	926	31.5	43.8	23	2	PH0276	Ig heavy chain CDR
854	32	44.4	672	2	T25876	related to myo-ino	927	31.5	43.8	24	2	PH0276	Ig heavy chain pre
855	32	44.4	683	2	JH0810	guanylate cyclase	928	31.5	43.8	136	1	HYMS81	Ig heavy chain pre
856	32	44.4	690	2	H75126	wingless receptor	929	31.5	43.8	141	2	A39276	Ig heavy chain pre
857	32	44.4	694	2	S71786	hypothetical prote	930	31.5	43.8	165	2	A83930	Ig heavy chain pre
858	32	44.4	695	2	E70923	hypothetical prote	931	31.5	43.8	183	1	G44057	early E3 20.6k gly
859	32	44.4	700	2	T38028	hypothetical prote	932	31.5	43.8	184	2	B72168	A37R protein - var
860	32	44.4	702	2	T13505	NADH2 dehydrogenas	933	31.5	43.8	184	2	T28578	BR protein - vario
861	32	44.4	703	2	T13393	NADH2 dehydrogenas	934	31.5	43.8	184	2	A36852	A36R protein - var
862	32	44.4	706	2	T13391	NADH2 dehydrogenas	935	31.5	43.8	185	2	H42520	A33R protein - vac
863	32	44.4	713	1	ALBSG7	cyclomaltopecterin	936	31.5	43.8	187	1	C44057	EBV glycoprotein -
864	32	44.4	716	2	E82620	peptidyl-dipeptida	937	31.5	43.8	187	1	ERAD86	early E3 20.6k gly
865	32	44.4	726	2	A90771	hypothetical prote	938	31.5	43.8	201	2	B81892	hypothetical prote
866	32	44.4	726	2	E85633	hypothetical prote	939	31.5	43.8	201	2	B81892	conserved hypotet
867	32	44.4	726	2	C64839	probable ATPase yc	940	31.5	43.8	201	2	H81131	conserved hypotet
868	32	44.4	750	2	JC1067	psaa protein - Sor	941	31.5	43.8	220	2	A83962	L-serine dehydrata
869	32	44.4	751	1	S26071	photosystem I prot	942	31.5	43.8	226	2	E70001	hypothetical prote
870	32	44.4	760	2	T25756	beta-glucosidase (943	31.5	43.8	258	2	C68846	lipase [imported]
871	32	44.4	763	2	JC4376	beta-glucosidase (944	31.5	43.8	260	2	H34284	cytochrome-c oxida
872	32	44.4	764	2	H83879	3-oxoacyl-L-acyl-ca	945	31.5	43.8	260	2	T11798	cytochrome-c oxida
873	32	44.4	768	2	S52684	probable membrane	946	31.5	43.8	261	2	T11434	cytochrome-c oxida
874	32	44.4	778	2	C70412	outer membrane pro	947	31.5	43.8	261	2	T11839	cytochrome-c oxida
875	32	44.4	790	2	G82756	conserved hypotet	948	31.5	43.8	261	2	S26157	cytochrome-c oxida
876	32	44.4	812	2	A81621	conserved hypotet	949	31.5	43.8	261	2	T11253	cytochrome-c oxida
877	32	44.4	820	2	AE2130	ferrichrome-iron r	950	31.5	43.8	261	2	T11486	cytochrome-c oxida
878	32	44.4	831	2	F72044	CT620 hypothetical	951	31.5	43.8	261	2	T11770	cytochrome-c oxida
879	32	44.4	831	2	C86581	CT620 hypothetical	952	31.5	43.8	262	1	OTFR3	hypothetical prote
880	32	44.4	841	2	D95960	probable cytochrom	953	31.5	43.8	264	2	B46314	hypothetical prote
881	32	44.4	852	2	A75253	glutaminyL-cRNA sy	954	31.5	43.8	274	2	D97653	conserved hypotet
882	32	44.4	858	1	E72419	flagellar hook-aas	955	31.5	43.8	274	2	AB2877	hypothetical prote
883	32	44.4	865	1	S02196	DNA-directed RNA p	956	31.5	43.8	275	2	AD2333	hypothetical prote
884	32	44.4	870	2	G69006	DNA-directed RNA p	957	31.5	43.8	364	2	S36403	catechol O-methyl
885	32	44.4	882	2	B96788	protein T4012.15 (958	31.5	43.8	364	2	S36404	catechol O-methyl
886	32	44.4	882	2	AG1209	B. subtilis YfhO p	959	31.5	43.8	364	2	S28612	catechol O-methyl
887	32	44.4	964	2	S13329	hypothetical prote	960	31.5	43.8	365	2	T09780	probable caffeate
888	32	44.4	1010	2	T33372	hypothetical prote	961	31.5	43.8	365	2	S18568	lignin-bispecific
889	32	44.4	1013	2	G71460	probable outer mem	962	31.5	43.8	365	2	T09673	caffeate O-methyl
890	32	44.4	1018	1	S73720	cytochrome accese	963	31.5	43.8	366	2	S40146	catechol O-methyl
891	32	44.4	1048	1	A70592	hypothetical prote	964	31.5	43.8	371	2	T04756	chitinase homolog
892	32	44.4	1062	2	S51969	FUN43 protein - ye	965	31.5	43.8	375	2	T34166	N-acetylornithine
893	32	44.4	1084	2	C82931	hypothetical prote	966	31.5	43.8	376	2	G70301	hypothetical prote
894	32	44.4	1086	2	T05407	hypothetical prote	967	31.5	43.8	400	2	S75147	probable periplasm
895	32	44.4	1127	2	T03105	major single-stran	968	31.5	43.8	426	2	B81835	hypothetical prote
896	32	44.4	1129	2	T19779	hypothetical prote	969	31.5	43.8	426	2	C81129	hypothetical prote
897	32	44.4	1132	2	C75259	probable iron-sulf	970	31.5	43.8	434	2	H97028	xre family DNA-bin
898	32	44.4	1132	2	A86335	T20H2.9 protein -	971	31.5	43.8	445	2	S27492	hypothetical prote
899	32	44.4	1139	1	E64234	cytochrome accese	972	31.5	43.8	514	2	C70446	conserved hypotet
900	32	44.4	1144	2	A75132	hypothetical prote	973	31.5	43.8	558	2	D70449	probable beta-gluc
901	32	44.4	1203	2	A59257	myosin VIIa, short	974	31.5	43.8	636	1	T37843	transketolase [EC
902	32	44.4	1207	2	T16011	hypothetical prote	975	31.5	43.8	656	1	P95237	transketolase [EC
903	32	44.4	1231	2	AC2863	sensory transducti	976	31.5	43.8	658	2	G98101	transketolase [EC
904	32	44.4	1243	2	B97640	vacuolating cyto	977	31.5	43.8	776	2	C69072	anaerobic ribonuci
905	32	44.4	1287	2	B53739	vacuolating cyto	978	31.5	43.8	776	2	C69072	anaerobic ribonuci

ALIGNMENTS

979	31.5	43.8	1394	2	S66876	ATP-dependent tran
980	31.5	43.8	1577	2	T30858	glucosyltransferas
981	31.5	43.8	3078	2	T28432	variant-specific s
982	31	43.1	40	2	D48310	photosystem II pro
983	31	43.1	43	2	S11111	Ig heavy chain V r
984	31	43.1	63	2	A69035	hypothetical prote
985	31	43.1	85	2	D70488	cytochrome-c oxida
986	31	43.1	88	2	E25155	Ig heavy chain V r
987	31	43.1	90	2	JC7395	salmon-type gonado
988	31	43.1	91	2	PI0242	Ig heavy chain V r
989	31	43.1	91	2	S44791	P0968.9 protein -
990	31	43.1	95	1	WSWL42	E5 protein - human
991	31	43.1	97	2	PI0118	Ig heavy chain V-I
992	31	43.1	98	2	S26902	Ig heavy chain V r
993	31	43.1	98	2	S12421	Ig heavy chain V r
994	31	43.1	99	2	S26899	Ig heavy chain V r
995	31	43.1	106	1	NRA5TP	ribonuclease TL (B
996	31	43.1	107	2	PI0240	Ig heavy chain V r
997	31	43.1	107	2	PI0243	Ig heavy chain V r
998	31	43.1	107	2	PI0241	Ig heavy chain V r
999	31	43.1	108	1	KVRB2K	Ig kappa chain V r
1000	31	43.1	108	2	PH1010	Ig heavy chain V r

RESULT 1

A44371
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Apr-1993 #sequence_revision 30-Apr-1993 #text_change 21-Jan-2000
C:Accession: A44371
R:Ayala, M.; Duenas, M.; Santos, A.; Vazquez, J.; Menendez, A.; Silva, A.; Gavilondo, J.; Bortolniquies 13, 790-799, 1992
A:Title: Bacterial single-chain antibody fragments, specific for carcinoembryonic antigen
A:Reference number: A44371; MUID:93040204; PMID:1418981
A:Accession: A44371
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <AYA>
A:Cross-references: UNIPARC:UPI000014758D; GB:S49453; NID:9259511; PIDN:AAB24086.1; PID:
A:Note: This sequence is inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIP:119635)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 54; DB 2; Length 120;
Best Local Similarity 63.6%; Pred. No. 0.1;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYFGTTYFDY 12
:|:|:|:|:|:|
DB 99 VYVGSYFDY 109

RESULT 2

PH1698
Ig heavy chain V region (clone NP-7-11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1698
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1698
A:Molecule type: mRNA
A:Residues: 1-24 <MCH>
A:Cross-references: UNIPARC:UPI0000176A69
A:Experimental source: B cell
A:Note: the authors translated the codon AGT for residue 14 as Thr
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 70.8%; Score 51; DB 2; Length 24;
Best Local Similarity 70.0%; Pred. No. 0.063;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTTFYDY 12
:|:|:|:|:|:|
DB 15 VYVGSYFDY 24

RESULT 3

PH1713
Ig heavy chain V region (clone ASC-11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1713
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1713
A:Molecule type: mRNA
A:Residues: 1-24 <MCH>
A:Cross-references: UNIPARC:UPI0000176A76
A:Experimental source: B cell
A:Note: the authors translated GTA for residue 11 as Thr and ACA for residue 13 as Ala
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.8%; Score 51; DB 2; Length 24;
Best Local Similarity 70.0%; Pred. No. 0.063;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTTFYDY 12
:|:|:|:|:|:|
DB 15 VYVGSYFDY 24

RESULT 4

PH1685
Ig heavy chain V region (clone NP-6-16) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1685
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1685
A:Molecule type: mRNA
A:Residues: 1-24 <MCH>
A:Cross-references: UNIPARC:UPI0000176A5D
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.8%; Score 51; DB 2; Length 24;
Best Local Similarity 70.0%; Pred. No. 0.063;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTTFYDY 12
:|:|:|:|:|:|
DB 15 VYVGSYFDY 24

RESULT 5

PH1712
Ig heavy chain V region (clone ASC-10) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1712
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993
A>Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1712

A:Molecule type: mRNA
A:Residues: 1-24 <MCH>

A:Cross-references: UNIPARC:UPI0000176A75

A:Experimental source: B cell

A>Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.8%; Score 51; DB 2; Length 24;
Best Local Similarity 70.0%; Pred. No. 0.063;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTYFDY 12
|:|:|:|:|
DB 15 YYYGSSYFDY 24

RESULT 6

PH1718

Ig heavy chain V region (clone ASC-16) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1718

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A>Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH1718

A:Molecule type: mRNA

A:Residues: 1-26 <MCH>

A:Cross-references: UNIPARC:UPI0000176A7B

A:Experimental source: B cell

A>Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.8%; Score 51; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 0.069;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTYFDY 12
|:|:|:|:|
DB 17 YYYGSSYFDY 26

RESULT 7

PH1702

Ig heavy chain V region (clone NP-7-15) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1702

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A>Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH1702

A:Molecule type: mRNA

A:Residues: 1-26 <MCH>

A:Cross-references: UNIPARC:UPI0000176A6C

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.8%; Score 51; DB 2; Length 26;
Best Local Similarity 70.0%; Pred. No. 0.069;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTYFDY 12
|:|:|:|:|

DB 17 YYYGSSYFDY 26

RESULT 8

PH1747

Ig heavy chain V region (clone NP-12-13) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1747

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A>Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH1747

A:Molecule type: mRNA

A:Residues: 1-34 <MCH>

A:Cross-references: UNIPARC:UPI0000176A95

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.8%; Score 51; DB 2; Length 34;
Best Local Similarity 70.0%; Pred. No. 0.089;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTYFDY 12
|:|:|:|:|
DB 25 YYYGSSYFDY 34

RESULT 9

PH1683

Ig heavy chain V region (clone NP-6-14) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1683

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A>Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH1683

A:Molecule type: mRNA

A:Residues: 1-24 <MCH>

A:Cross-references: UNIPARC:UPI0000176A5B

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 69.4%; Score 50; DB 2; Length 24;
Best Local Similarity 70.0%; Pred. No. 0.092;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFYGTYFDY 12
|:|:|:|:|
DB 15 YYYGSSYFDY 24

RESULT 10

PH1710

Ig heavy chain V region (clone ASC-8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1710

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A>Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH1710

A:Molecule type: mRNA

A:Residues: 1-24 <MCH>

A:Cross-references: UNIPARC:UPI0000176A73

A:Experimental source: B cell

A>Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 1

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 68.1%; Score 49; DB 2; Length 24;
Best Local Similarity 70.0%; Pred. No. 0.13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFYGTYFPDY 12
|||:||||
DB 15 YYGSSYFPDY 24

RESULT 11

PH1703
Ig heavy chain V region (clone NP-7-16) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1703

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A:Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH1703

A:Molecule type: mRNA

A:Residues: 1-26 <MCH>

A:Cross-references: UNIPARC:UPI0000176A6D

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 60.3%; Score 47; DB 2; Length 26;
Best Local Similarity 60.0%; Pred. No. 0.3;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTYFPDY 12
|||:||||
DB 17 YYGSSYFPDY 26

RESULT 12

PH1748
Ig heavy chain V region (clone NP-12-14) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1748

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A:Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH1748

A:Molecule type: mRNA

A:Residues: 1-34 <MCH>

A:Cross-references: UNIPARC:UPI0000176A96

A:Experimental source: B cell

A>Note: the authors translated the codon GGA for residue 21 as Ala

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 63.9%; Score 46; DB 2; Length 34;
Best Local Similarity 60.0%; Pred. No. 0.57;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTYFPDY 12
|||:||||
DB 25 YYGSSYFPDY 34

RESULT 13

H83162
probable amino acid-binding protein PA3858 [imported] - Pseudomonas aeruginosa (strain F

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: H83162

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
Lory, S.; Olson, M.V

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: H83162

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <STO>

A:Cross-references: UNIPROT:Q9HXE8, UNIPARC:UPI000000C5B46; GB:AE004803; GB:AE004091; NID

A:Experimental source: strain PA01

C:Genetics:

Query Match 63.9%; Score 46; DB 2; Length 341;
Best Local Similarity 72.7%; Pred. No. 5.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTYFPD 11
|||:||||
DB 116 GIFYGTYFPD 126

RESULT 14

D69426
surface layer protein B (slpB-2) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: D69426

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirsness, E.F.

Glodok, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo-

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: D69426

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-2425 <KLE>

A:Cross-references: UNIPROT:O28859; UNIPARC:UPI000056D2C; GB:AE001006; GB:AE000782; NID

Query Match 62.5%; Score 45; DB 2; Length 2425;
Best Local Similarity 54.5%; Pred. No. 52;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIFYGTYFPD 11
|||:||||
DB 179 GIFYGTYFPD 189

RESULT 15

PH1686
Ig heavy chain V region (clone NP-6-17) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1686

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A:Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH1686

A:Molecule type: mRNA

A:Residues: 1-25 <MCH>

A:Cross-references: UNIPARC:UPI0000176A5E

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 61.8%; Score 44.5; DB 2; Length 25;
Best Local Similarity 72.7%; Pred. No. 0.73;

Matches 8; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
QY 3 YFYGTT-YFDY 12
|:|:|:|:|
DB 15 YYGSSYFDY 25

RESULT 16

ig heavy chain V region (clone NP-7-7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1694
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1694
A:Molecule type: mRNA
A:Residues: 1-23 <MCH>
A:Cross-references: UNIPARC:UPI0000176A66
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 61.1%; Score 44; DB 2; Length 23;
Best Local Similarity 66.7%; Pred. No. 0.81;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YFYGTTYPD 11
|:|:|:|
DB 15 YYGSSYFDY 23

RESULT 17

PH1701
ig heavy chain V region (clone NP-7-14) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1701
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1701
A:Molecule type: mRNA
A:Residues: 1-25 <MCH>
A:Cross-references: UNIPARC:UPI0000176A6B
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 61.1%; Score 44; DB 2; Length 25;
Best Local Similarity 66.7%; Pred. No. 0.88;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
|:|:|:|
DB 17 YYGSSYFDY 25

RESULT 18

S25041
ig heavy chain V region (focus 1012 DNA Nr.10 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C:Accession: S25041; S25043
R:Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
A:Reference number: S25024
A:Accession: S25041
A:Molecule type: nucleic acid

A:Residues: 1-113 <JAC>
A:Cross-references: UNIPARC:UPI000011609B; EMBL:X67351; NID:950884; PIDN:CAA47766.1; PIC
A:Experimental source: focus 1012 DNA Nr.10
A:Accession: S25043
A:Molecule type: nucleic acid

A:Residues: 1-113 <JAM>
A:Cross-references: UNIPARC:UPI000011609B; EMBL:X67343; NID:950888; PIDN:CAA47758.1; PID
A:Experimental source: focus 1012 DNA Nr.3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 61.1%; Score 44; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 3.8;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
|:|:|:|
DB 97 YYGSSYFDY 105

RESULT 19

B22769
ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996
C:Accession: B22769
R:Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982
A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026; PMID:7188353
A:Accession: B22769
A:Molecule type: protein
A:Residues: 1-120 <DIL>
A:Cross-references: UNIPARC:UPI0000176B76
A:Note: the sequences of two spontaneously arising somatic variants, B1-8.V1 and B1-8.V2;
A:Note: peptides and unsequenced residues were positioned by homology with the B1-8 seq
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 61.1%; Score 44; DB 2; Length 120;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
|:|:|:|
DB 101 YYGSSYFDY 109

RESULT 20

MHS18
ig heavy chain precursor V region (B1-8) - mouse
N:Contains: ig heavy chain precursor V region 186-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A90809; B90809; A22769; A02034; A02036
R:Botwell, A.L.M.; Paekind, M.; Reh, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, L
Cell 24, 625-637, 1981
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som
A:Reference number: A90809; MUID:81234548; PMID:6788376
A:Accession: A90809
A:Molecule type: DNA
A:Residues: 1-139 <B18>
A:Cross-references: UNIPROT:P01751; UNIPARC:UPI000002708B; GB:J00529; NID:g195114; PIDN
A:Accession: B90809
A:Molecule type: DNA
A:Residues: 1-117 <1862>
A:Cross-references: UNIPARC:UPI000017372E
A:Note: the B1-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapt
A:Note: the 186-2 germline gene was cloned from a library of C57BL/6 DNA
R:Dildrop, R.; Bruggemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.
EMBO J. 1, 635-640, 1982

A:Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between
A:Reference number: A90971; MUID:84236026; PMID:7188353
A:Accession: A22769
A:Molecule type: protein
A:Residues: 20-139 <DIL>
A:Cross-references: UNIPARC:UPI000002BD97
A:Note: the V region of the B1-8 delta chain, derived as a spontaneous class switch variant of the mu chain
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region, immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Product: Ig kappa chain V region (B1-8) #status experimental <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:118-124/Region: D segment
F:125-139/Region: J segment (JH2)

Query Match 61.1%; Score 44; DB 1; Length 139;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTFYDY 12
:|||||
Db 120 YYGSSYFDY 128

RESULT 21
PC4402
pe1B leader/Ig heavy chain anti-NP/1inker type 205/alkaline phosphatase fusion protein
C:Species: synthetic
C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C:Accession: PC4402
R:Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997.
A:Title: Construction, bacterial expression, and characterization of hapten-specific sin
A:Reference number: PC4402
A:Accession: PC4402
A:Molecule type: DNA
A:Residues: 1-287 <SU>
A:Cross-references: UNIPARC:UPI000017CF08
C:Keywords: fusion protein

Query Match 61.1%; Score 44; DB 4; Length 287;
Best Local Similarity 66.7%; Pred. No. 9.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTFYDY 12
:|||||
Db 260 YYGSSYFDY 268

RESULT 22
AD3553
general 1-amino acid-binding periplasmic protein aapJ precursor BMEI10349 [imported] - B
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AD3553
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.U.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leless
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AD3553
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <KUR>
A:Cross-references: UNIPROT:O8YD28; UNIPARC:UPI000005844C; GB:AE008918; PIDN:AAL53591.1;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI10349
A:Map position: II

Query Match 61.1%; Score 44; DB 2; Length 331;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTTFYD 11
:|||||
Db 107 GIFYGTTFYD 117

RESULT 23
S25033
Ig heavy chain V region (germinal centre B17 DNA Nr.4 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C:Accession: S25033; S25035
R:Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
A:Reference number: S25024
A:Accession: S25033
A:Molecule type: nucleic acid
A:Residues: 1-111 <JAC>
A:Cross-references: UNIPARC:UPI00001160AE; EMBL:X67370; NID:G50079; PIDN:CAA47782.1; PID
A:Experimental source: germinal centre B17 DNA Nr.4
A:Accession: S25035
A:Molecule type: nucleic acid
A:Residues: 1-111 <JAC>
A:Cross-references: UNIPARC:UPI00001160AE; EMBL:X67372; NID:G50083; PIDN:CAA47784.1; PID
A:Experimental source: germinal centre B17 DNA Nr.6
C:Superfamily: immunoglobulin V region, immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 43.5; DB 2; Length 111;
Best Local Similarity 80.0%; Pred. No. 4.5;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 YFYGTTFYDY 12
:|||||
Db 95 YFYGTTFYDY 103

RESULT 24
S25034
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C:Accession: S25034
R:Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
A:Reference number: S25024
A:Accession: S25034
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-111 <JAC>
A:Cross-references: UNIPARC:UPI00001160AF; EMBL:X67371; NID:G50081; PIDN:CAA47783.1; PID
C:Superfamily: immunoglobulin V region, immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 43.5; DB 2; Length 111;
Best Local Similarity 80.0%; Pred. No. 4.5;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 YFYGTTFYDY 12
:|||||
Db 95 YFYGTTFYDY 103

RESULT 25
PHI696
Ig heavy chain V region (clone NP-7-9) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1696
R:McMeyer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Mossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:831585
A:Accession: PH1696
A:Molecule type: mRNA
A:Residues: 1-24 <MCH>
A:Cross-references: UNIPARC:UPI0000176A68
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 59.7%; Score 43; DB 2; Length 24;
Best Local Similarity 60.0%; Pred. No. 1.2;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFYGTTFDY 12
|:|:|:|:|:|
DB 15 YYYGSLFDY 24

RESULT 26
A49038
Ig lambda chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49038
R:Weiss, U.; Zobebelein, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A:Title: Accumulation of somatic mutants in the B cell compartment after primary immuniz
A:Reference number: A49038; MUID:92164733; PMID:1537385
A:Accession: A49038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-25 <WEI>
A:Cross-references: UNIPARC:UPI00001154F5; GB:S85732; NID:G246314; PIDN:AAB21559.1; PID:
A:Experimental source: spleen
A:Note: sequence extracted from NCBI backbone (NCBIN:85732, NCBI:P:85757)
C:Keywords: heterotetramer; immunoglobulin

Query Match 59.7%; Score 43; DB 2; Length 25;
Best Local Similarity 60.0%; Pred. No. 1.3;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFYGTTFDY 12
|:|:|:|:|:|
DB 13 YYYGSLFDY 22

RESULT 27
A95238
hypothetical protein SP2033 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 05-Oct-2004
C:Accession: A95238
R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: A95238
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-227 <KUR>
A:Cross-references: UNIPROT:Q97N4; UNIPARC:UPI0000051AB8; GB:AE005672; PIDN:AAK76098.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2033

C:Superfamily: Claes II aldolase/adducin, N-terminal

Query Match 59.7%; Score 43; DB 2; Length 227;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YFYGTTFDY 12
|:|:|:|:|:|
DB 106 IPFYGTTHADY 116

RESULT 28
B98102
L-ribulose-phosphate 4-epimerase (EC 5.1.3.4) [imported] - Streptococcus pneumoniae (str
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 05-Oct-2004
C:Accession: B98102
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: B98102
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-234 <KUR>
A:Cross-references: UNIPROT:Q8DN99; UNIPARC:UPI00000E3717; GB:AE007317; PIDN:AML0647.1;
C:Genetics:
A:Gene: arad
C:Superfamily: Claes II aldolase/adducin, N-terminal
C:Keywords: isomerase

Query Match 59.7%; Score 43; DB 2; Length 234;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YFYGTTFDY 12
|:|:|:|:|:|
DB 113 IPFYGTTHADY 123

RESULT 29
A71849
hypothetical protein jhp1110 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: A71849
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: A71849
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <ARN>
A:Cross-references: UNIPROT:Q9ZK32; UNIPARC:UPI00000D7220; GB:AE001538; GB:AE001439; NTL
C:Genetics:
A:Gene: jhp110
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MG0709

Query Match 59.7%; Score 43; DB 2; Length 459;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTTF 10
|:|:|:|:|:|
DB 325 GIFYGTTF 334

RESULT 30

S25038
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C/Accession: S25038; S25037
R/Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A/Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
A/Reference number: S25024
A/Accession: S25038
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-109 <JAC>
A/Cross-references: UNIPARC:UPI00001160B2; EMBL:X67375; NID:G50089; PIDN:CAA47787.1; PID
A/Accession: S25037
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 2-109 <JAC>
A/Cross-references: UNIPARC:UPI00001160B1; EMBL:X67374; NID:G50087; PIDN:CAA47786.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:9-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 59.0%; Score 42.5; DB 2; Length 109;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 YFYGTTYFDY 12
|||:||||
Db 93 YFYG-SYFDY 101

RESULT 31

S25032
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C/Accession: S25032
R/Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A/Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
A/Reference number: S25024
A/Accession: S25032
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-111 <JAC>
A/Cross-references: UNIPARC:UPI00001160AD; EMBL:X67369; NID:G50077; PIDN:CAA47781.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 59.0%; Score 42.5; DB 2; Length 111;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 YFYGTTYFDY 12
|||:||||
Db 95 YFYG-SYFDY 103

RESULT 32

PH1711
Ig heavy chain V region (clone ASC-9) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C/Accession: PH1711
R/McLeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A/Title: Antigen-driven B cell differentiation in vivo.
A/Reference number: PH1675; MUID:93301607; PMID:8315385
A/Accession: PH1711

A/Molecule type: mRNA
A/Residues: 1-24 <MCH>
A/Cross-references: UNIPARC:UPI0000176A74
A/Experimental source: B cell
A/Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 58.3%; Score 42; DB 2; Length 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YFYGTTYFDY 12
|||:||||
Db 15 YRYSGGYFDY 24

RESULT 33

PH1715
Ig heavy chain V region (clone ASC-13) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C/Accession: PH1715
R/McLeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A/Title: Antigen-driven B cell differentiation in vivo.
A/Reference number: PH1675; MUID:93301607; PMID:8315385
A/Accession: PH1715
A/Molecule type: mRNA
A/Residues: 1-25 <MCH>
A/Cross-references: UNIPARC:UPI0000176A78
A/Experimental source: B cell
A/Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 58.3%; Score 42; DB 2; Length 25;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFYGTTYFDY 12
|||:||||
Db 16 YYYGSSFDY 25

RESULT 34

ODPp1
cytochrome-c oxidase (EC 1.9.3.1) chain I - Paramesium sp. mitochondrion
N/Alternate names: cytochrome a3 polypeptide I; cytochrome a3 polypeptide I
C/Species: mitochondrion Paramesium sp.
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C/Accession: A24988
R/Pritchard, A.B.; Seilhamer, J.J.; Cummings, D.J.
Gene 44, 243-253, 1986
A/Title: Paramesium mitochondrial DNA sequences and RNA transcripts for cytochrome oxida
A/Reference number: A91555; MUID:87055241; PMID:3023187
A/Accession: A24988
A/Molecule type: DNA
A/Residues: 1-645 <PRI>
A/Cross-references: UNIPROT:P05489; UNIPARC:UPI000017215F; GB:M15281; NID:G342944; PIDN:
A/Note: in Genbank entry ODPp1, release 109.0, PID:91019626 assumes special genetic code
C/Genetics:
A/Gene: COI
A/Genome: mitochondrion
A/Genetic code: SGC6
A/Start codon: ATA
C/Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C/Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-as
transmembrane protein
F:2-559/Domain: cytochrome-c oxidase chain I homology <COI>
F:54,480/Binding site: heme a iron (His) (axial ligands) #status predicted
F:343,392,393/Binding site: copper (His) #status predicted
F:343-347/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted

C.Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #tex change 07-May-1999
C.Accession: PH1510, PH1501, PH1506, PH1508, PH1511, PH1514
R.Giusti, A.M.; Manner, T.
J. Exp. Med. 177, 797-809, 1993
A.Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A.Reference number: PH1482; MUID:93171820; PMID:8436910
A.Accession: PH1510
A.Status: translation not shown
A.Molecule type: DNA
A.Residues: 1-119 <GIU>
A.Cross-references: UNIPARC:UPI0000176C7C
A.Experimental source: hybridoma cells (clonoma X7-5D3-2, X7-5D3-12, X7-5D3-14, X7-5D3-16)
C.Genetics: 3/1
A.Intons: 3/1
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F.21-104/Domain: immunoglobulin homology <IMM>

Query Match	56.9%	Score 41	DB 2	Length 119
Best Local Similarity	54.5%	Pred. No. 12		
Matches	6	Conservative	3	Mismatches 2
				Indels 0
				Gaps 0
QY	2	IYFYGTTFDY	12	
		: :		
Db	106	VYGGSYTFDY	116	

RESULT 40
PH1505
1g heavy chain V region (clone X7-5D3-11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1505
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1505
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-119 <GIU>
A:Cross-references: UNIPARC:UPI0000176BBO
A:Experimental source: hybridoma cell
C:Genetics:
A:Introns: 3/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-104/Domain: immunoglobulin homology <IMM>

```

Query Match      56.9%; Score 41; DB 2; Length 119;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY      2 IYFYGTTFPDY 12
      :|:|:|:|
      :|:|:|:|
Db      106 VYGGSTYFPDY 116

RESULT 41
PH1518
Ig heavy chain V region (clone X41-21) - mouse (fragment)
CISpecies: Mus musculus (house mouse)
CISDate: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
CISAccession: PH1518
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A>Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1518
A>Status: translation not shown

```

A: Molecule-type: DNA
 A: Residues: 1-119 <GI>
 A: Cross-references: UNIPARC:UPI0000176B9D
 A: Experimental source: hybridoma cell
 C: Genetics:
 A: Introns: 3/1
 C: Superfamily: immunoglobulin V region; immunoglobulin
 C: Keywords: heterotrimer; immunoglobulin
 F: 21-104/Domain: immunoglobulin homology <IM>

Query Match	56.9%	Score 41;	DB 2;	Length 119;
Best Local Similarity	54.5%	Pred. No. 12;		
Matches	6;	Conservative	3;	Mismatches 2;
				Indels 0;
				Gaps 0;
QY	2	IYFGTTYFDY	12	
	:	:		
Db	106	VYGGSYFDY	116	

RESULT 42
PH1517
Ig heavy chain V region (clone X41-7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1517
R:Giusti, A.M., Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1517
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-119 <GIU>
A:Cross-references: UNIPARC:UPI0000176B9C
A:Experimental source: hybridoma cell
C:Genetics:
A:Introns: 3/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-104/Domain: immunoglobulin homology <IMM>

Query Match	Score	DB	Length	
Best Local Similarity	56.9%	41	119	
Matches	54.5%	Fred. No. 12		
6; Conservative	3	Mismatches	2	Indels
			0	Gaps
0%				
QY	2	IYFYGTTFDY	12	
		: :		
Db	106	VYGGSGYTFDY	116	

RESULT 43
 PH1502
 Ig heavy chain V region (clone X7-5D3-5) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: PH1502
 R:Giusti, A.M.; Manser, T.
 U. Exp. Med. 177, 797-809, 1993
 A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have
 d for somatic mutation.
 A:Reference number: PH1482; MUID:93171820; PMID:8436910
 A:Accession: PH1502
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-119 <GI>
 A:Cross-references: UNIPARC:UPI0000176BAE
 A:Experimental source: hybridoma cell
 C:Genetics:
 A:Introns: 3/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:21-104/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 41; DB 2; Length 119;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFYFDY 12
:|:|:|
Db 106 VYGGSYFYFDY 116

RESULT 44

PH1521
Ig heavy chain V region (clone X41-32) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C/Accession: PH1521

R/Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A/Title: Hypermutation is observed only in antibody H chain V region transgenes that have for somatic mutation.

A/Reference number: PH1482; MUID:93171820; PMID:8436910

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-119 <GIU>

A/Cross-references: UNIPARC:UPI0000176B9F

A/Experimental source: hybridoma cell

C/Genetics:

A/Introns: 3/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/21-104/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 41; DB 2; Length 119;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFYFDY 12
:|:|:|
Db 106 VYGGSYFYFDY 116

RESULT 45

PH1500
Ig heavy chain V region (clone X7-5D3-1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C/Accession: PH1500

R/Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A/Title: Hypermutation is observed only in antibody H chain V region transgenes that have for somatic mutation.

A/Reference number: PH1482; MUID:93171820; PMID:8436910

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-119 <GIU>

A/Cross-references: UNIPARC:UPI0000176BAD

A/Experimental source: hybridoma cell

C/Genetics:

A/Introns: 3/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/21-104/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 41; DB 2; Length 119;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFYFDY 12
:|:|:|
Db 106 VYGGSYFYFDY 116

RESULT 46
PH1516
Ig heavy chain V region (clone X41-4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C/Accession: PH1516

R/Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A/Title: Hypermutation is observed only in antibody H chain V region transgenes that have for somatic mutation.

A/Reference number: PH1482; MUID:93171820; PMID:8436910

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-119 <GIU>

A/Cross-references: UNIPARC:UPI0000176B9B

A/Experimental source: hybridoma cell

C/Genetics:

A/Introns: 3/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/21-104/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 41; DB 2; Length 119;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFYFDY 12
:|:|:|
Db 106 VYGGSYFYFDY 116

RESULT 47

PH1503
Ig heavy chain V region (clone X7-5D3-9) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C/Accession: PH1503

R/Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A/Title: Hypermutation is observed only in antibody H chain V region transgenes that have for somatic mutation.

A/Reference number: PH1482; MUID:93171820; PMID:8436910

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-119 <GIU>

A/Cross-references: UNIPARC:UPI0000176BAF

A/Experimental source: hybridoma cell

C/Genetics:

A/Introns: 3/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/21-104/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 41; DB 2; Length 119;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFYFDY 12
:|:|:|
Db 106 VYGGSYFYFDY 116

RESULT 48

PH1504

Ig heavy chain V region (clones X7-5D3-10 and X7-5D3-13) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 03-Feb-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999

C/Accession: PH1504; PH1507

R/Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A>Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1504
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-119 <GIU>
A:Cross-references: UNIPARC:UPI0000176BA5
A:Experimental source: hybridoma cell
C:Genetics:
A:introns: 3/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-104/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 41; DB 2; Length 119;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFDY 12
:|:|:||||
Db 106 VYGGSYTFDY 116

RESULT 49

PH1520

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: PH1520; PH1515; PH1509; PH1513

R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A>Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1520

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-119 <GIU>

A:Cross-references: UNIPARC:UPI0000176C7B

A:Experimental source: hybridoma cell, clone X41-30

A:Accession: PH1515

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-119 <GIU2>

A:Cross-references: UNIPARC:UPI0000176C7B

A:Experimental source: hybridoma cell, clone X41-3

A:Accession: PH1509

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-119 <GIU3>

A:Cross-references: UNIPARC:UPI0000176C7B

A:Experimental source: hybridoma cell, clones X7-SD3-15 and X7-SD3-19

C:Genetics:

A:introns: 3/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:21-104/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 41; DB 2; Length 119;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFDY 12

Db 106 VYGGSYTFDY 116

RESULT 50

PH1519

Ig heavy chain V region (clone X41-29) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C:Accession: PH1519
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A>Title: Hypermutation is observed only in antibody H chain V region transgenes that have
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1519
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-119 <GIU>
A:Cross-references: UNIPARC:UPI0000176B9E
A:Experimental source: hybridoma cell
C:Genetics:
A:introns: 3/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:21-104/Domain: immunoglobulin homology <IMM>

Query Match 56.9%; Score 41; DB 2; Length 119;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFDY 12

Db 106 VYGGSYTFDY 116

Search completed: January 17, 2006, 12:05:54
Job time : 23.2727 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:47:28 ; Search time 67.6364 Seconds

(without alignments)
125.174 Million cell updates/sec

Title: US-10-665-658-12

Perfect score: 72

Sequence: 1 GIFYGTYFDY 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	65.3	329	2	09C4Q2_METTL
2	47	65.3	329	2	09C4Q1_METTL
3	47	65.3	329	2	09C4Q1_METTL
4	46	63.9	341	2	09HXE8_PSEAE
5	46	62.5	366	2	05VLJ6_HEVBR
6	45	62.5	366	2	05VLJ6_HEVBR
7	45	62.5	366	2	05VLJ6_HEVBR
8	45	62.5	366	2	05VLJ6_HEVBR
9	45	62.5	366	2	05VLJ6_HEVBR
10	45	62.5	366	2	05VLJ6_HEVBR
11	45	62.5	366	2	05VLJ6_HEVBR
12	45	62.5	366	2	05VLJ6_HEVBR
13	45	62.5	366	2	05VLJ6_HEVBR
14	45	62.5	366	2	05VLJ6_HEVBR
15	45	62.5	366	2	05VLJ6_HEVBR
16	45	62.5	366	2	05VLJ6_HEVBR
17	45	62.5	366	2	05VLJ6_HEVBR
18	45	62.5	366	2	05VLJ6_HEVBR
19	45	62.5	366	2	05VLJ6_HEVBR
20	45	62.5	366	2	05VLJ6_HEVBR
21	45	62.5	366	2	05VLJ6_HEVBR
22	45	62.5	366	2	05VLJ6_HEVBR
23	45	62.5	366	2	05VLJ6_HEVBR
24	45	62.5	366	2	05VLJ6_HEVBR
25	45	62.5	366	2	05VLJ6_HEVBR
26	45	62.5	366	2	05VLJ6_HEVBR
27	45	62.5	366	2	05VLJ6_HEVBR
28	45	62.5	366	2	05VLJ6_HEVBR
29	45	62.5	366	2	05VLJ6_HEVBR
30	45	62.5	366	2	05VLJ6_HEVBR
31	45	62.5	366	2	05VLJ6_HEVBR

32	43	59.7	389	2	09A1G6_STRPY	09A1G6 streptococc
33	43	59.7	389	2	09B2M6_STRP8	09B2M6 streptococc
34	43	59.7	459	2	09ZK32_HELIPJ	09ZK32 helicobacte
35	43	59.7	492	2	061BF5_CABER	061BF5 caenorhabdi
36	43	59.7	799	2	041289_GIBZE	041289 gibberella
37	43	59.7	1126	2	073MB8_TREDE	073MB8 treponema d
38	43	59.7	1140	2	073L45_TREDE	073L45 treponema d
39	43	59.7	1488	2	073L43_TREDE	073L43 treponema d
40	43	59.7	3320	2	073MPO_TREDE	073MPO treponema d
41	42.5	59.0	336	2	06QQT7_CABER	06QQT7 caenorhabdi
42	42	58.3	89	2	0950Y0_TERTTH	0950Y0 tetrathymena
43	42	58.3	89	2	09XMR7_TERTPY	09XMR7 tetrathymena
44	42	58.3	92	2	07P319_FUSNV	07P319 fusobacteri
45	42	58.3	103	2	081SP5_BACAN	081SP5 bacillus an
46	42	58.3	120	2	06Y510_9APYH	06Y510 lentaria sp
47	42	58.3	135	2	08RGV8_FUSNV	08RGV8 fusobacteri
48	42	58.3	274	2	0728W2_DESVH	0728W2 desulfobact
49	42	58.3	341	2	086TW2_HUMAN	086TW2 homo sapien
50	42	58.3	455	2	09UIB6_HUMAN	09UIB6 homo sapien
51	42	58.3	523	2	06PD65_HUMAN	06PD65 homo sapien
52	42	58.3	529	2	05SHX6_CRYNE	05SHX6 cryptococcu
53	42	58.3	529	2	05K7G0_CRYNE	05K7G0 cryptococcu
54	42	58.3	530	2	04X062_ASFPV	04X062 aspergillu
55	42	58.3	535	2	051Z33_MAGGR	051Z33 magnaporthe
56	42	58.3	535	2	05EMZ7_MAGGR	05EMZ7 magnaporthe
57	42	58.3	645	1	COX1_PARTE	P05489 parametium
58	42	58.3	820	1	08ZOR1_STRAM	08ZOR1 streptomyc
59	41.5	57.6	1818	1	ENC_DROME	08mex1 drosophila
60	41.5	57.6	1823	2	07KV61_DROME	07KV61 drosophila
61	41	56.9	119	2	061519_9HOMO	06Y519 xerocomus n
62	41	56.9	120	1	HV03_MOUSE	P01147 mus musculu
63	41	56.9	174	2	097X56_SULISO	097X56 sulfolobus
64	41	56.9	176	2	097WT8_SULISO	097WT8 sulfolobus
65	41	56.9	214	2	09GK33_ORNAN	09GK33 ornithorhyn
66	41	56.9	290	2	07U931_SYNPX	07U931 synechococc
67	41	56.9	330	2	06OER3_ORYSA	06OER3 oryza sativ
68	41	56.9	403	2	08DBS3_VIBVU	08DBS3 vibrio vuln
69	41	56.9	403	2	07MI47_VIBVU	07MI47 vibrio vuln
70	41	56.9	464	2	068YB0_RHOSR	068YB0 rhodococcus
71	41	56.9	464	2	06REL7_9NOCA	06REL7 rhodococcus
72	41	56.9	467	2	016275_CAREL	016275 caenorhabdi
73	41	56.9	493	2	061LQ3_CABER	061LQ3 caenorhabdi
74	41	56.9	586	2	06GMW1_XENLA	06GMW1 xenopus lae
75	41	56.9	673	2	094G15_ORYSA	094G15 oryza sativ
76	41	56.9	715	2	055XK7_CRYNE	055XK7 cryptococcu
77	41	56.9	715	2	05KMC8_CRYNE	05KMC8 cryptococcu
78	41	56.9	736	2	09AY58_ORYSA	09AY58 oryza sativ
79	41	56.9	737	2	08TJ16_PAREI	08TJ16 paracentrot
80	41	56.9	761	2	055VY2_CRYNE	055VY2 cryptococcu
81	41	56.9	761	2	05KKK9_CRYNE	05KKK9 cryptococcu
82	41	56.9	801	2	04MMU9_ASFPV	04MMU9 aspergillu
83	41	56.9	842	2	07NNT3_GLOVI	07NNT3 gloeobacter
84	41	56.9	842	2	0917S4_DROME	0917S4 drosophila
85	40.5	56.2	105	2	06R9E2_MAIZE	06R9E2 ze mays
86	40.5	56.2	199	2	07P4E2_FUSNV	07P4E2 fusobacteri
87	40.5	56.2	199	2	08RE24_FUSNV	08RE24 fusobacteri
88	40.5	56.2	199	2	05WZS9_SULIS	05WZS9 sulfolobus
89	40	55.6	220	2	097YH5_SULIS	097YH5 sulfolobus
90	40	55.6	228	2	06SN45_CALJA	06SN45 calithrix
91	40	55.6	251	2	05OUX2_ENTHI	05OUX2 entamoeba h
92	40	55.6	308	2	08VGA4_MOUSE	08VGA4 mus musculu
93	40	55.6	315	2	07TR60_MOUSE	07TR60 mus musculu
94	40	55.6	315	2	07TS12_MOUSE	07TS12 mus musculu
95	40	55.6	315	2	07TS13_MOUSE	07TS13 mus musculu
96	40	55.6	315	2	08VP61_MOUSE	08VP61 mus musculu
97	40	55.6	317	2	08VP60_MOUSE	08VP60 mus musculu
98	40	55.6	322	2	023547_CABEL	023547 caenorhabdi
99	40	55.6	323	2	08EWH9_MYCPE	08EWH9 mycoplasma
100	40	55.6	334	2	033796_EMENTI	033796 emericella
101	40	55.6	338	2	05LIDG7_BACFN	05LIDG7 bacteroides
102	40	55.6	338	2	064U06_BACFR	064U06 bacteroides
103	40	55.6	371	2	06CKJ0_KLUTA	06CKJ0 kluyveromyc
104	40	55.6	398	2	06CX73_KLUTA	06CX73 kluyveromyc

105	40	55.6	411	2	Q4MK21	BACCE	Q4mk21	178	39	54.2	922	2	Q887R0	PSESM	Q887r0	pseudomonas
106	40	55.6	438	2	Q4IPH3	GIBBE	Q4iph3	179	39	54.2	923	2	Q74833	SCHPO	Q74833	schizosacch
107	40	55.6	468	2	Q569B4	RAT	Q569b4	180	39	54.2	923	2	Q4ZTS1	PSESY	Q4ztS1	pseudomonas
108	40	55.6	479	2	Q5BK12	RAT	Q5bk12	181	39	54.2	927	2	Q4ZXL5	PSESY	Q4zxl5	pseudomonas
109	40	55.6	484	2	Q51G07	ENTHI	Q51g07	182	39	54.2	1048	2	Q9XT27	SHEEP	Q9xt27	ovis aries
110	40	55.6	508	2	Q51G07	ENTHI	Q51g07	183	39	54.2	1051	2	Q86142	DICDI	Q86142	dictyosteli
111	40	55.6	520	2	Q13411	AMAMU	Q13411	184	39	54.2	1059	1	CERU RAT			
112	40	55.6	524	2	Q51G09	ENTHI	Q51g09	185	39	54.2	1061	1	CERU RAT			
113	40	55.6	524	2	Q50R83	ENTHI	Q50r83	186	39	54.2	1062	1	CERU MOUSE			
114	40	55.6	539	2	Q755M1	ASHGO	Q755m1	187	39	54.2	1065	1	CERU HUMAN			
115	40	55.6	540	2	Q41UG7	GIBBE	Q41ug7	188	39	54.2	1084	2	Q9UL57	RAT	Q9ul57	rat
116	40	55.6	542	1	LNT-CHIMU		Q9pjK8	189	39	54.2	1175	2	Q5Q0P1	PRUNG	Q5q0p1	oplinomyces
117	40	55.6	550	2	Q9RB11	ACTAD	Q9rb11	190	39	54.2	1429	2	Q4N2V1	THEPA	Q4n2v1	theileria p
118	40	55.6	550	2	Q6EFC3	ACTAD	Q6efc3	191	39	54.2	1491	2	Q96W9	GIBPU	Q96w9	gibberella
119	40	55.6	554	2	Q8A793	BACCN	Q8a793	192	39	54.2	1697	2	Q81119	PLAF7	Q81119	plasmidium
120	40	55.6	589	2	Q9REC7	CIOTM	Q9rec7	193	39	54.2	3474	2	Q673F7	TRYCR	Q673f7	trypanosoma
121	40	55.6	591	2	Q9F1T9	CIOTM	Q9f1t9	194	39	54.2	4837	2	Q54M05	DICDI	Q54m05	dictyosteli
122	40	55.6	670	2	Q88BY2	PSEBP	Q88by2	195	38.5	53.5	236	2	Q9U7H7	PLAFA	Q9u7h7	plasmidium
123	40	55.6	715	2	Q5ZD98	ORYSA	Q5zd98	196	38.5	53.5	276	1	Q9JHW2	MOUSE	Q9jhw2	mus musculus
124	40	55.6	956	2	Q4ZYW6	PSEBSY	Q4zyw6	197	38.5	53.5	432	1	GSAB LISIN		GSAB LISIN	listeria in
125	40	55.6	1413	2	Q582N5	PTERYP	Q582n5	198	38.5	53.5	432	1	GSAB LISMF		GSAB LISMF	listeria mo
126	40	55.6	1455	2	Q8PTJ8	STRMU	Q8d4j8	199	38.5	53.5	432	1	GSAB LISMO		GSAB LISMO	listeria mo
127	40	55.6	1489	2	Q41DX8	GIBBE	Q41dx8	200	38.5	53.5	434	2	Q5WIE9	BACSK	Q5wie9	bacillus cl
128	39.5	54.9	337	2	Q16470	CABEL	Q16470	201	38.5	53.5	682	2	Q6EMU2	GLILI	Q6emu2	giobba curt
129	39	54.2	119	2	Q55V06	CRYNE	Q55v06	202	38	52.8	31	2	Q49248	MYCGE	Q49248	mycoplasma
130	39	54.2	169	2	Q6C139	YARLI	Q6c139	203	38	52.8	35	2	Q4XWY6	PLACH	Q4xwy6	plasmidium
131	39	54.2	209	2	Q9ZB51	STRPY	Q9zb51	204	38	52.8	70	2	Q9WUM9	MUSCR	Q9wum9	mus caroli
132	39	54.2	220	2	Q7Y1J1	PTULM	Q7y1j1	205	38	52.8	95	2	Q6MCU2	PARUM	Q6mcu2	parachlamyd
133	39	54.2	228	2	Q6SNM6	PAPPA	Q6snm6	206	38	52.8	103	2	Q8KSP1	XENNE	Q8ksp1	xenothabdis
134	39	54.2	232	1	ICMT RAT		Q9wm4	207	38	52.8	123	2	Q819M7	ARATH	Q819m7	arabidopsis
135	39	54.2	274	2	Q6G5D0	BARHE	Q6g5d0	208	38	52.8	127	2	Q81LY4	PLAF7	Q81ly4	plasmidium
136	39	54.2	283	1	ICMT MOUSE		Q9e6k7	209	38	52.8	128	2	Q4YSS0	PLABE	Q4yss0	plasmidium
137	39	54.2	285	2	Q879P7	STRP3	Q879p7	210	38	52.8	133	1	Y961	THEYO	Y961	theryom
138	39	54.2	303	2	Q54C20	DICDI	Q54c20	211	38	52.8	145	2	Q9D546	MOUSE	Q9d546	mus musculus
139	39	54.2	307	2	Q7MWU6	PORGI	Q7mwj6	212	38	52.8	152	2	Q8CA26	MOUSE	Q8ca26	mus musculus
140	39	54.2	309	2	Q9STYV	ARATH	Q9stvy	213	38	52.8	154	2	Q8ZYU3	PRAB	Q8zyu3	pyrobaculum
141	39	54.2	317	1	Q13C3	HUMAN	Q8ngs6	214	38	52.8	182	2	Q5LEK0	BACFN	Q5lek0	bacteroides
142	39	54.2	318	1	Q13C4	HUMAN	Q8ngs5	215	38	52.8	184	2	Q977Y8	CIOAB	Q977y8	clostridium
143	39	54.2	318	1	Q61F51	HUMAN	Q61f51	216	38	52.8	199	1	PVAA STRP3		PVAA STRP3	streptococc
144	39	54.2	319	1	Q8R2S1	HUMAN	Q8rqn1	217	38	52.8	199	1	PVAA STRP6		PVAA STRP6	streptococc
145	39	54.2	320	1	Q13C8	HUMAN	Q8ng87	218	38	52.8	199	1	PVAA STRP8		PVAA STRP8	streptococc
146	39	54.2	347	2	Q61F52	HUMAN	Q61f52	219	38	52.8	199	1	PVAA STRPY		PVAA STRPY	streptococc
147	39	54.2	348	2	Q9RN13	HAENI	Q9rn13	220	38	52.8	202	2	Q25546	HELPU	Q25546	helipomyce
148	39	54.2	348	2	Q4QL27	HAENI	Q4ql27	221	38	52.8	209	2	Q8VCT8	MOUSE	Q8vct8	mus musculus
149	39	54.2	352	1	Y1598	HAENI	P456f57	222	38	52.8	215	2	Q74N52	NANEO	Q74n52	nanoarchaeu
150	39	54.2	362	1	PGUR2	ASPTU	P19805	223	38	52.8	228	2	Q6SNK9	CEBANP	Q6snk9	cebap apell
151	39	54.2	362	2	Q8NK96	ASPKA	Q8nk98	224	38	52.8	232	2	Q8HNA6	BRUMA	Q8hna6	brugia mala
152	39	54.2	362	2	Q9P359	ASPAW	Q9p359	225	38	52.8	240	2	Q5L5D4	CHLAB	Q5l5d4	chlamydomo
153	39	54.2	362	2	Q24972	GIALA	Q24972	226	38	52.8	240	2	Q822B0	CHLCV	Q822b0	chlamydomo
154	39	54.2	362	2	Q7QUX0	GIALA	Q7qux0	227	38	52.8	241	2	Q4R323	MACFA	Q4r323	macaca fasc
155	39	54.2	376	2	Q5L7U3	BACFN	Q5l7u3	228	38	52.8	243	2	Q9ZKK2	HELPU	Q9zkk2	helicobacte
156	39	54.2	379	2	Q64N14	BACFR	Q64n14	229	38	52.8	277	2	Q97110	SULFO	Q97110	sulfolobus
157	39	54.2	393	2	Q11412	GADEN	Q11412	230	38	52.8	280	2	Q69939	STRCO	Q69939	streptomyce
158	39	54.2	395	2	Q8TNU2	METAC	Q8tnl2	231	38	52.8	280	2	Q69808	STRCO	Q69808	streptomyce
159	39	54.2	401	2	Q8RP48	STRPY	Q8rp48	232	38	52.8	280	2	Q821Q7	STRAW	Q821q7	streptomyce
160	39	54.2	401	2	Q8RKU2	STRP3	Q8rk82	233	38	52.8	280	2	Q821R0	STRAW	Q821r0	streptomyce
161	39	54.2	401	2	Q8P2V8	STRP8	Q8p2v8	234	38	52.8	299	2	Q5M0F7	SPRT1	Q5m0f7	streptococc
162	39	54.2	411	2	Q81G99	BACCR	Q81gf9	235	38	52.8	299	2	Q5M504	SPRT2	Q5m504	streptococc
163	39	54.2	450	2	Q8PT25	METMA	Q8pt25	236	38	52.8	310	2	Q7TQR3	MOUSE	Q7tqr3	mus musculus
164	39	54.2	459	1	STC-IDTLO		Q5qyp3	237	38	52.8	310	2	Q8VFW4	MOUSE	Q8vfw4	mus musculus
165	39	54.2	459	1	Q25796	HELPU	Q25796	238	38	52.8	315	2	Q7R954	PLAYO	Q7r954	plasmidium
166	39	54.2	486	2	Q91Z07	MOUSE	Q91z07	239	38	52.8	315	2	Q8VGR1	MOUSE	Q8vgr1	mus musculus
167	39	54.2	498	2	Q553Z5	DICDI	Q553z5	240	38	52.8	315	2	Q8VGS9	MOUSE	Q8vgs9	mus musculus
168	39	54.2	516	2	Q8BV47	MOUSE	Q8bv47	241	38	52.8	324	2	Q7MTF9	PORGI	Q7mtf9	porphyromon
169	39	54.2	516	2	Q55Q13	CRYNE	Q55q13	242	38	52.8	324	2	Q8HMT5	GYELE	Q8hmt5	carapus ber
170	39	54.2	516	2	Q5KDE8	CRYNE	Q5kde8	243	38	52.8	330	1	Q842	MOUSE	Q842	mus musculus
171	39	54.2	520	2	Q6IN17	XENIA	Q6in17	244	38	52.8	342	2	Q4XJ4	PSESY	Q4xj4	pseudomonas
172	39	54.2	531	2	Q7S8Z7	XENIA	Q7s8z7	245	38	52.8	342	2	Q4KHV4	PSEFS	Q4khv4	pseudomonas
173	39	54.2	539	2	Q6MMW6	NEICR	Q6mmw6	246	38	52.8	342	2	Q88NB5	PSEBP	Q88nb5	pseudomonas
174	39	54.2	548	2	Q9RW08	DEIRA	Q9rw08	247	38	52.8	342	2	Q887N6	PSESM	Q887n6	pseudomonas
175	39	54.2	548	1	RCO3 NEUCR		Q92253	248	38	52.8	351	2	Q7QHT4	ANOGA	Q7qht4	anopheles g
176	39	54.2	621	1	GLGB RHOMR		Q93nu3	249	38	52.8	358	1	CCR3	CAVPO	CCR3	cavia porce
177	39	54.2	697	2	Q5AMZ1	EMENI	Q5awz1	250	38	52.8	370	2	Q75JL1	DICDI	Q75jl1	dictyosteli

251	38	52.8	382	2	Q70RL0_GIALA	Q70rl0 giardia lam	324	38	52.8	1016	2	Q6Q1Y_XENNE	Q6q1y xenorhabdus
252	38	52.8	411	2	Q20336_CAEEL	Q20336 caenorhabdi	325	38	52.8	1043	2	Q85157_PHOLU	Q85157 photorhabdu
253	38	52.8	420	2	Q8B9C9_NPYRO	Q8b9c9 nectophorus	326	38	52.8	1043	2	Q7MZV7_PHOLL	Q7mzv7 photorhabdu
254	38	52.8	423	2	Q8Y5H6_LISMO	Q8y5h6 listeria mo	327	38	52.8	1045	2	Q693A0_YEREN	Q693a0 yersinia en
255	38	52.8	423	2	Q71X58_LISMP	Q71x58 listeria mo	328	38	52.8	1142	2	Q8A0A0_BACTN	Q8a0a0 bacteroides
256	38	52.8	430	1	B10A_HAEIN	P44426 haemophilus	329	38	52.8	1173	2	Q4YU83_PLABE	Q4yu83 plasmid
257	38	52.8	430	2	Q4QKR4_HAB18	Q4qkr4 haemophilus	330	38	52.8	1190	2	Q782R4_9ALPH	Q782r4 gallid hepp
258	38	52.8	440	2	Q8M2C3_PYRRU	Q8m2c3 haemophilus	331	38	52.8	1190	2	Q9WSY3_9ALPH	Q9wsy3 marek b dis
259	38	52.8	467	2	Q9RSR9_DEIRA	Q9rsr9 haemophilus	332	38	52.8	1343	2	Q8A358_BACTN	Q8a358 bacteroides
260	38	52.8	468	2	Q834U1_ENTPA	Q834u1 enterococcus	333	38	52.8	1944	2	Q99PS9_MOUSE	Q99ps9 mus musculu
261	38	52.8	488	2	Q6UB92_STPAU	Q6ub92 enterococcus	334	38	52.8	2254	2	Q7R6B9_GIALA	Q7r6b9 giardia lam
262	38	52.8	489	2	Q94YL3_ARATH	Q94yl3 arabidopsis	335	38	52.8	4249	2	Q80ZK4_MOUSE	Q80zk4 mus musculu
263	38	52.8	490	2	Q54A47_TERTG	Q54a47 tetraodon n	336	38	52.8	4530	2	Q812K6_PLAPF	Q812k6 plasmid
264	38	52.8	507	2	Q5Z3R8_NOCFA	Q5z3r8 nocardia fa	337	37.5	52.1	341	1	R1R2_HELPD	R1r2 helpd
265	38	52.8	511	2	Q8R166_FUSNN	Q8r166 fusobacteri	338	37.5	52.1	341	1	R1R2_HELPD	R1r2 helpd
266	38	52.8	516	2	Q88843_LACPL	Q88843 lactobacilli	339	37.5	52.1	349	2	Q5WDM9_BACSK	Q5wdm9 bacteroides
267	38	52.8	517	2	Q5B084_EMENT	Q5b084 aspergillus	340	37.5	52.1	426	2	Q5WDM9_BACSK	Q5wdm9 bacteroides
268	38	52.8	519	2	Q5ZMT7_CHICK	Q5zmt7 gallus gall	341	37.5	52.1	441	2	Q97VBS_SULSO	Q97vbs sulfobas
269	38	52.8	522	2	Q96VF4_UROFA	Q96vf4 uromyces fa	342	37.5	52.1	444	2	Q54FP3_DICDI	Q54fp3 dictyosteli
270	38	52.8	525	2	Q8BRD9_MOUSE	Q8brd9 m mus muscu	343	37.5	52.1	498	2	Q6EMU3_GILTI	Q6emu3 hedychium f
271	38	52.8	526	2	Q7NSJ8_CHRYO	Q7nsj8 chromobacte	344	37.5	52.1	694	2	Q6EMU3_GILTI	Q6emu3 hedychium f
272	38	52.8	527	2	Q7S9U8_NEUCR	Q7s9u8 neurospora	345	37.5	52.1	694	2	Q6EMU3_GILTI	Q6emu3 hedychium f
273	38	52.8	539	2	Q7RWH1_NEUCR	Q7rwh1 neurospora	346	37.5	52.1	58	2	Q4XWD3_PLACH	Q4xwd3 plasmid
274	38	52.8	541	2	Q6S512_PICAN	Q6s512 picchia angu	347	37	51.4	98	2	Q64XZ9_BACFR	Q64xz9 bacteroides
275	38	52.8	542	2	Q9VQ85_DROME	Q9vq85 drosophila	348	37	51.4	118	2	Q6Y5K2_9APHY	Q6y5k2 nigroporus
276	38	52.8	552	2	Q5KM76_CRYNE	Q5km76 cryptococcu	349	37	51.4	118	2	Q35595_PHYPO	Q35595 phyvarum po
277	38	52.8	555	2	Q55XR4_CRYNE	Q55xr4 cryptococcu	350	37	51.4	119	2	Q6Y5J1_TRAVE	Q6y5j1 traneetes ve
278	38	52.8	556	2	Q4HMD0_GDEIO	Q4hmd0 deinococcus	351	37	51.4	119	2	Q6Y5J3_GHOMO	Q6y5j3 streptom ost
279	38	52.8	576	1	NUSM_ANOQU	P33510 anophelies q	352	37	51.4	119	2	Q6Y5J3_GHOMO	Q6y5j3 streptom ost
280	38	52.8	593	2	Q826F7_STRAW	Q826f7 streptomyce	353	37	51.4	119	2	Q6Y5J3_GHOMO	Q6y5j3 streptom ost
281	38	52.8	662	2	Q7S4B3_NEUCR	Q7s4b3 neurospora	354	37	51.4	119	2	Q6Y5L8_9AGAR	Q6y5l8 coprinopsis
282	38	52.8	683	2	Q9N091_MACPA	Q9n091 macaca fasc	355	37	51.4	119	2	Q6Y5L8_9AGAR	Q6y5l8 coprinopsis
283	38	52.8	685	2	Q7RHP1_PLAYO	Q7rhp1 plasmid	356	37	51.4	119	2	Q6Y5M0_9AGAR	Q6y5m0 coprinopsis
284	38	52.8	696	2	Q9S751_ARATH	Q9s751 arabidopsis	357	37	51.4	119	2	Q6Y5M0_9AGAR	Q6y5m0 coprinopsis
285	38	52.8	698	2	Q8WX19_HUMAN	Q8wx19 homo sapien	358	37	51.4	120	2	Q6Y5M3_9AGAR	Q6y5m3 amanita coc
286	38	52.8	703	2	Q5T3M4_HUMAN	Q5t3m4 homo sapien	359	37	51.4	120	2	Q6Y5J2_GHOMO	Q6y5j2 sullus pic
287	38	52.8	722	1	YC06_KLEPN	Q48452 klebsiella	360	37	51.4	120	2	Q6Y5L2_TREPLA	Q6y5l2 irpex lacte
288	38	52.8	747	2	Q6N2K8_MOUSE	Q6n2k8 mus musculu	361	37	51.4	121	1	HV01_MOUSE	P01745 mus musculu
289	38	52.8	754	2	Q6N2K8_MOUSE	Q6n2k8 mus musculu	362	37	51.4	121	1	Q6Y5K6_9AGAR	Q6y5k6 marasmius r
290	38	52.8	754	2	Q81WM1_HUMAN	Q81wm1 homo sapien	363	37	51.4	121	2	Q6Y5L1_9AGAR	Q6y5l1 lactarius l
291	38	52.8	787	2	Q417E3_GIBZE	Q417e3 gibberella	364	37	51.4	123	2	Q6Y5K0_PLEROS	Q6y5k0 pleurotus o
292	38	52.8	800	2	Q5HRB2_STAFB	Q5hdb2 staphylococ	365	37	51.4	131	2	Q08927_YEAST	Q08927 saccharomyc
293	38	52.8	800	2	Q8CQ50_STAFB	Q8cq50 staphylococ	366	37	51.4	135	2	Q55FT0_DICDI	Q55ft0 dictyosteli
294	38	52.8	812	2	Q51P19_MAGAR	Q51p19 magnaporthe	367	37	51.4	140	2	Q54Q32_DICDI	Q54q32 dictyosteli
295	38	52.8	824	2	Q4KRG3_PSEBS	Q4krg3 pseudomonas	368	37	51.4	145	2	Q97XU9_SULSO	Q97xu9 sulfobas
296	38	52.8	874	2	Q8ZE71_YERPE	Q8ze71 yersinia pe	369	37	51.4	152	1	Y830_PASMG	Y830 pasteurella
297	38	52.8	881	2	Q4ZP54_PSEBS	Q4zps4 pseudomonas	370	37	51.4	155	2	Q5JPE2_PYRKO	Q5jpe2 pyrococcus
298	38	52.8	886	2	Q87X45_PSEBS	Q87x45 pseudomonas	371	37	51.4	155	2	Q5JPE2_PYRKO	Q5jpe2 pyrococcus
299	38	52.8	886	2	Q87X45_PSEBS	Q87x45 pseudomonas	372	37	51.4	155	2	Q5JPE2_PYRKO	Q5jpe2 pyrococcus
300	38	52.8	889	2	Q4PBS8_USTMA	Q4pbs8 usciilago ma	373	37	51.4	160	2	Q68S80_9AGAR	Q68s80 pleurotus d
301	38	52.8	915	2	Q7N7Z1_PHOLL	Q7n7z1 photorhabdu	374	37	51.4	162	2	P70028_XENILA	P70028 xenopus lae
302	38	52.8	918	2	Q61BR3_CAEER	Q61br3 caenorhabdi	375	37	51.4	166	2	Q88M06_LACPL	Q88m06 lactobacilli
303	38	52.8	920	2	Q4ZP60_PSEBS	Q4zps6 pseudomonas	376	37	51.4	169	2	Q8T198_MERAC	Q8t198 methanocarc
304	38	52.8	936	2	Q7M220_PHOLL	Q7m220 photorhabdu	377	37	51.4	175	2	Q6Y5U6_9AGAR	Q6y5u6 auricularia
305	38	52.8	937	2	Q6MBT0_PARUM	Q6mbt0 parschlamyd	378	37	51.4	175	2	Q9B4A5_ANOAL	Q9b4a5 anophelies a
306	38	52.8	938	2	Q8GFP1_PHOLL	Q8gfp1 photorhabdu	379	37	51.4	175	2	Q9B4A6_ANOAL	Q9b4a6 anophelies a
307	38	52.8	938	2	Q7N7Y7_PHOLL	Q7n7y7 photorhabdu	380	37	51.4	177	2	Q4M162_9BUREX	Q4m162 burkholderia
308	38	52.8	939	2	Q4ZP59_PSEBS	Q4zps9 pseudomonas	381	37	51.4	180	2	Q4M162_9BUREX	Q4m162 burkholderia
309	38	52.8	940	2	Q87X48_PSEBS	Q87x48 yersinia pe	382	37	51.4	186	2	Q97SV1_SUITO	Q97sv1 sulfolobus
310	38	52.8	943	2	Q8D1P5_YERPE	Q8d1p5 yersinia pe	383	37	51.4	187	2	Q4Y1U6_PLABE	Q4y1u6 plasmid
311	38	52.8	949	2	Q8GFP5_PHOLL	Q8gfp5 photorhabdu	384	37	51.4	187	2	Q4Y1U6_PLABE	Q4y1u6 plasmid
312	38	52.8	952	2	Q655G1_YERPS	Q655g1 yersinia ps	385	37	51.4	189	2	Q815V1_PLAPF	Q815v1 plasmid
313	38	52.8	952	2	Q8ZAV9_YERPE	Q8zav9 yersinia pe	386	37	51.4	193	2	Q6Y5J4_9AGAR	Q6y5j4 schizophy11
314	38	52.8	955	2	Q4ZP55_PSEBS	Q4zps5 pseudomonas	387	37	51.4	203	2	Q6Y5J4_9AGAR	Q6y5j4 schizophy11
315	38	52.8	959	2	Q7N7X5_PHOLL	Q7n7x5 photorhabdu	388	37	51.4	211	2	Q86B18_DROME	Q86b18 drosophila
316	38	52.8	960	2	Q8GFP7_PHOLL	Q8gfp7 photorhabdu	389	37	51.4	211	2	Q892Y6_BACTN	Q892y6 bacteroides
317	38	52.8	965	2	Q7MZU2_PHOLL	Q7mzu2 photorhabdu	390	37	51.4	221	1	Y1211_STRMU	Y1211 streptococ
318	38	52.8	970	2	Q7N7Y4_PHOLL	Q7n7y4 photorhabdu	391	37	51.4	221	2	Q5M0B2_STRT1	Q5m0b2 streptococ
319	38	52.8	982	2	Q6XPS5_YERPR	Q6xps5 yersinia pr	392	37	51.4	221	2	Q5M4V9_STRT2	Q5m4v9 streptococ
320	38	52.8	982	2	Q6A3A8_YERPS	Q6a3a8 yersinia ps	393	37	51.4	222	2	Q6SMA2_EULMO	Q6sma2 eulemur mon
321	38	52.8	984	2	Q8ZE10_YERPE	Q8ze10 yersinia pe	394	37	51.4	222	2	Q6SNC7_ALOCA	Q6snc7 alouatta ca
322	38	52.8	994	2	Q6A9A9_YERPE	Q6a9a9 yersinia pe	395	37	51.4	222	2	Q6SNC7_ALOCA	Q6snc7 alouatta ca
323	38	52.8	1011	2	Q8ZAV8_YERPE	Q8zav8 yersinia pe	396	37	51.4	223	2	Q6W079_MOUSE	Q6w079 mus musculu

397	37	51.4	226	2	Q6RGM4_ACICA	Q6rgm4_acinecobact	470	37	51.4	530	2	Q6J0V1_ASPPG	Q6J0v1_aspergillus
398	37	51.4	250	2	Q67S49_SYMTH	Q67s49_symbiobace	471	37	51.4	531	2	Q4WD6_ASFPV	Q4wd6_aspergillus
399	37	51.4	256	2	Q9LMS5_ARATH	Q9lms5_arabidopsi	472	37	51.4	534	2	Q5AYG1_EMENT	Q5ayg1_aspergillus
400	37	51.4	262	2	Q5CPB2_CRPV	Q5cpb2_cryptospori	473	37	51.4	535	2	Q9XG37_GUITH	Q9xg37_guillardia
401	37	51.4	265	2	Q9P450_SCHCO	Q9p450_schizospori	474	37	51.4	546	2	Q82CW3_STRAW	Q82cw3_streptomyce
402	37	51.4	274	2	Q6FZM9_BAQU	Q6fzm9_bartonella	475	37	51.4	548	2	Q5CU48_CRPV	Q5cu48_cryptospori
403	37	51.4	277	2	Q4XUZ6_PLACH	Q4xuz6_plasmodium	476	37	51.4	559	2	Q8R136_MOUSE	Q8r136_mus musculu
404	37	51.4	288	2	Q8GJ81_MYCSM	Q8gj81_mycobacteri	477	37	51.4	560	2	Q7NM99_GLOVI	Q7nm99_gloeobacter
405	37	51.4	293	2	Q82MJ7_NITRU	Q82mj7_nitrosomoma	478	37	51.4	564	1	HXTI3_YEAST	Hxti3_yeast
406	37	51.4	294	2	Q6OAS9_MENCA	Q6oas9_methylococc	479	37	51.4	564	1	HXTI7_YEAST	Hxti7_yeast
407	37	51.4	300	2	Q7NXT2_CHRVO	Q7nxt2_chromobacte	480	37	51.4	565	2	Q4IGZ6_GIBZE	Q4igz6_gibberella
408	37	51.4	301	2	Q9GE19_9MYRT	Q9ge19_citriolema ob	481	37	51.4	567	1	HXTI5_YEAST	Hxti5_yeast
409	37	51.4	311	2	Q7TOP7_MOUSE	Q7top7_mus musculu	482	37	51.4	567	1	HXTI6_YEAST	Hxti6_yeast
410	37	51.4	311	2	Q8VF68_MOUSE	Q8vf68_mus musculu	483	37	51.4	581	2	Q43856_VICFA	Q43856_vicia faba
411	37	51.4	315	2	Q7TRH2_MOUSE	Q7trh2_mus musculu	484	37	51.4	591	2	Q6ONN1_PLACH	Q6onn1_phanerocha
412	37	51.4	315	2	Q8VFU3_MOUSE	Q8vfuz_mus musculu	485	37	51.4	596	2	Q5ONM9_ENTHI	Q5onm9_entamoeba h
413	37	51.4	315	2	Q8VFU4_MOUSE	Q8vfua_mus musculu	486	37	51.4	605	2	Q8BH65_MOUSE	Q8bh65_mus muscu
414	37	51.4	325	2	Q7NA07_PHOL	Q7na07_phototrabu	487	37	51.4	608	2	Q8IWF6_HUMAN	Q8iwf6_homo sapien
415	37	51.4	333	2	Q6C5J0_YARLI	Q6c5j0_yarrowia li	488	37	51.4	610	2	Q5IDZ5_ENTHI	Q5idz5_entamoeba h
416	37	51.4	333	2	Q4PKG2_9BACT	Q4pkg2_uncultured	489	37	51.4	614	2	Q9CANS_ARATH	Q9cans_arabidopsi
417	37	51.4	341	2	Q6AVC3_ORYSA	Q6avc3_oryza sativ	490	37	51.4	624	2	Q6KAP4_MOUSE	Q6kap4_mus musculu
418	37	51.4	341	2	Q6DAK8_ERWCT	Q6dak8_erwinia car	491	37	51.4	627	2	Q8TBG8_HUMAN	Q8tbg8_homo sapien
419	37	51.4	345	1	Y146A_HABTN	Q66241_haemophilus	492	37	51.4	639	2	Q5KJ06_CRYNE	Q5kj06_cryptococcu
420	37	51.4	345	2	Q7M8B0_WOLSU	Q7m8b0_wolfinella s	493	37	51.4	648	1	BGLR_CERAE	Bglr_cerale
421	37	51.4	359	2	Q6GDS8_STAR	Q6gds8_staphylococ	494	37	51.4	651	1	BGLR_CANPA	Bglr_canpa
422	37	51.4	361	2	Q6W262_RHTSN	Q6w262_rhizobium s	495	37	51.4	651	1	BGLR_HUMAN	Bglr_human
423	37	51.4	363	2	Q6FM08_CANGA	Q6fm08_candida gla	496	37	51.4	651	2	Q549T0_HUMAN	Q549t0_homo sapien
424	37	51.4	367	2	Q6MT62_MYCNS	Q6mt62_mycoplasma	497	37	51.4	651	2	Q5RSN6_PONPY	Q5rsn6_pongo pygma
425	37	51.4	370	2	Q8GPD84_STTRC	Q8gpd84_streptococ	498	37	51.4	651	2	Q5RBA1_PONPY	Q5rba1_pongo pygma
426	37	51.4	381	2	Q4JAW8_SULAC	Q4jaw8_sulfolobus	499	37	51.4	651	2	Q8RBA1_PONPY	Q8rba1_pongo pygma
427	37	51.4	383	2	Q560F2_CRYNE	Q560f2_cryptococcu	500	37	51.4	659	2	Q895D9_CLOTE	Q895d9_clostridium
428	37	51.4	383	2	Q5KRP4_CRYNE	Q5krp4_cryptococcu	501	37	51.4	659	2	Q4TSG2_TETNG	Q4tsg2_tetradodon n
429	37	51.4	390	2	Q4SSS2_TETNG	Q4sss2_tetradodon n	502	37	51.4	700	2	Q8TG16_DICDI	Q8tg16_dicystosteli
430	37	51.4	391	2	Q9N6C3_CAREL	Q9n6c3_caenorhabdi	503	37	51.4	712	2	Q7S0X9_NEUCR	Q7s0x9_neurospora
431	37	51.4	400	2	Q98PQ7_RHILLO	Q98pq7_rhizobium l	504	37	51.4	726	1	AMSA_BRMAM	Q46631_erwinia amy
432	37	51.4	403	2	Q4KGI9_PSEBF	Q4kgi9_pseudomonas	505	37	51.4	726	2	Q8YVH8_ERWPY	Q8yv8_erwinia pyr
433	37	51.4	404	2	Q7QCL0_ANOGA	Q7qcl0_anopheles g	506	37	51.4	735	2	Q6UWB0_HUMAN	Q6uwb0_homo sapien
434	37	51.4	417	2	Q9DJR5_MOUSE	Q9djr5_m mus muscu	507	37	51.4	737	2	Q6P9E3_HUMAN	Q6p9e3_homo sapien
435	37	51.4	417	2	Q9D3Y8_MOUSE	Q9d3y8_m mus muscu	508	37	51.4	738	2	Q5JRP0_HUMAN	Q5jrp0_homo sapien
436	37	51.4	418	2	Q4P7J9_USTMA	Q4p7j9_usellulago ma	509	37	51.4	742	2	Q8ABK3_BACTN	Q8abk3_bacteroides
437	37	51.4	418	2	Q6AXV7_RAT	Q6axv7_rattus norv	510	37	51.4	752	2	Q8SAB1_SORHI	Q8sab1_sorghum bic
438	37	51.4	430	2	Q5I0I3_MAGGR	Q5i0i3_magnaporthe	511	37	51.4	760	2	Q6YMB4_9AGAR	Q6ymb4_leucosagari
439	37	51.4	441	2	Q4Z4D2_PLABE	Q4z4d2_plasmodium	512	37	51.4	761	2	Q6FWB8_CANGA	Q6fwb8_candida gla
440	37	51.4	444	2	Q4JBS5_SULAC	Q4jbs5_sulfolobus	513	37	51.4	772	1	PMP_YEAST	Pmp_yeast
441	37	51.4	444	2	Q6ONM9_PHACH	Q6onm9_phanerocha	514	37	51.4	772	2	Q6Y5M7_9AGAR	Q6y5m7_coprinopsis
442	37	51.4	456	2	Q5I3B7_ENTHI	Q5i3b7_entamoeba h	515	37	51.4	773	2	Q6Y5M6_9AGAR	Q6y5m6_coprinellus
443	37	51.4	457	2	Q9H191_TREAC	Q9h191_thermoplaem	516	37	51.4	773	2	Q4I8M2_GIBZE	Q4i8m2_gibberella
444	37	51.4	470	2	Q4Y4M5_PLACH	Q4y4m5_plasmodium	517	37	51.4	785	1	PMP_SCHCO	Pmp_schco
445	37	51.4	480	2	Q9JAW9_CAREL	Q9jaw9_caenorhabdi	518	37	51.4	785	2	Q6Y5M5_9AGAR	Q6y5m5_pleurocua d
446	37	51.4	480	2	Q7KSV2_PLAYO	Q7ksv2_plasmodium	519	37	51.4	786	2	Q9MA83_ARATH	Q9ma83_arabidopsi
447	37	51.4	480	2	Q95NKL_9APIC	Q95nkl_plasmodium	520	37	51.4	802	2	Q4S2S0_TETNG	Q4s2s0_tetradodon n
448	37	51.4	484	2	Q9U9P0_HYDAT	Q9u9p0_hydra atten	521	37	51.4	820	2	Q8I2T3_PLAF7	Q8i2t3_plasmodium
449	37	51.4	487	2	Q8IIN9_DRONE	Q8iin9_drosophila	522	37	51.4	834	2	Q75K20_DICDI	Q75k20_dicystosteli
450	37	51.4	489	2	Q4JMW9_9BACT	Q4jmw9_uncultured	523	37	51.4	834	2	Q552P3_DICDI	Q552p3_dicystosteli
451	37	51.4	491	2	Q5RPM8_PONPY	Q5rpm8_pongo pygma	524	37	51.4	836	2	Q86G87_ORYTR	Q86g87_oryzaria t
452	37	51.4	494	2	Q6CCU1_YARLI	Q6ccu1_yarrowia li	525	37	51.4	854	2	Q6UYJ4_9CAUD	Q6uyj4_burkholderi
453	37	51.4	495	2	Q8DMX4_STBAS	Q8dmx4_streptococc	526	37	51.4	854	2	Q5V0I8_HALMA	Q5v0i8_haloarcula
454	37	51.4	500	2	Q7MDJ5_VIBVY	Q7mdj5_vibrio vuln	527	37	51.4	893	2	Q886I5_ORYSA	Q886i5_oryza sativ
455	37	51.4	503	2	Q6IYH4_CASBR	Q6iyh4_caenorhabdi	528	37	51.4	897	2	Q85661_PROMI	Q85661_proteus mir
456	37	51.4	505	1	Y1620_METVA	Q59015_methanococc	529	37	51.4	903	1	ADAI12_MOUSE	Q41824_mus musculu
457	37	51.4	508	2	Q09408_CABEL	Q09408_caenorhabdi	530	37	51.4	909	1	ADAI12_HUMAN	Q41814_homo sapien
458	37	51.4	512	2	Q5BCD3_EMENT	Q5bcd3_aspergillus	531	37	51.4	917	2	Q5JRP1_HUMAN	Q5jrp1_homo sapien
459	37	51.4	513	2	Q8E2S5_STEBA	Q8e2s5_streptococc	532	37	51.4	920	2	Q75PP9_BOVIN	Q75pp9_bov tauru
460	37	51.4	522	2	Q5CEJ7_CRYHO	Q5cej7_cryptospori	533	37	51.4	922	2	Q7NBYO_CHRVO	Q7nbyo_chromobacte
461	37	51.4	524	2	Q4SEB0_TETNG	Q4seb0_tetradodon n	534	37	51.4	922	2	Q8UVP2_COTCO	Q8uv2_coccuriux co
462	37	51.4	525	2	Q577U2_BRUAB	Q577u2_brucella ab	535	37	51.4	932	2	Q90YD3_ANGAN	Q90yd3_angilla an
463	37	51.4	525	2	Q8FMB9_BRUSU	Q8fmb9_brucella su	536	37	51.4	993	2	Q4T9J5_TETNG	Q4t9j5_tetradodon n
464	37	51.4	525	2	Q8YCW0_BRUME	Q8ycw0_brucella me	537	37	51.4	1075	2	Q75Q01_ORYLA	Q75q01_oryzias lat
465	37	51.4	526	2	Q54FQ9_DICDI	Q54fq9_dicystosteli	538	37	51.4	1082	2	Q96YK5_SULFO	Q96yk5_sulfolobus
466	37	51.4	526	2	Q9HMT7_PSRAB	Q9hmt7_pseudomonas	539	37	51.4	1086	2	Q54JZ0_DICDI	Q54jz0_dicystosteli
467	37	51.4	527	2	Q5ASJ3_EMENT	Q5asj3_aspergillus	540	37	51.4	1203	2	Q8IACO_PLAF7	Q8iaco_plasmodium
468	37	51.4	527	2	Q8JZ20_EMENT	Q8jz20_emeritella	541	37	51.4	1316	2	Q8A692_BACTN	Q8a692_bacteroides
469	37	51.4	528	2	Q5I0C5_MAGGR	Q5i0c5_magnaporthe	542	37	51.4	1467	2	Q4IMH6_GIBZE	Q4imh6_gibberella

543	37	51.4	1487	2	Q7RBD9_PLAYAO	Q7xb9 plasmidium	616	36	50.0	221	2	Q4YU3_PLABE	Q4uy3 plasmidium
544	37	51.4	1637	2	Q6LOY1_PICTO	Q6loy1 picrophilus	617	36	50.0	226	2	Q51B2_STPAU	Q51b2 staphylococ
545	37	51.4	1866	2	Q7XHI2_ORYSA	Q7xh2 oryza sativ	618	36	50.0	226	2	Q5198_STPAU	Q5198 staphylococ
546	37	51.4	1866	2	Q8SSR3_ORYSA	Q8ssr3 oryza sativ	619	36	50.0	226	2	Q8CU5_STPAB	Q8cu5 staphylococ
547	37	51.4	2009	2	Q7OSX2_GMLA	Q7osx2 gladiola lam	620	36	50.0	231	1	ARAD_BACDH	Q9ubq4 bacillus ha
548	37	51.4	2027	2	Q84T51_ORYSA	Q84t51 oryza sativ	621	36	50.0	231	2	Q4440_9RH12	Q4440 agrobacteri
549	37	51.4	2554	2	Q72OR5_LBPIIC	Q72or5 leptospira	622	36	50.0	232	2	Q47580_ONCVO	Q47580 onchocerca
550	37	51.4	7059	1	RIAB_CVBO	Q8vw7 b replicase	623	36	50.0	232	2	Q70UR8_DIRIM	Q70ur8 dirifilaria
551	37	51.4	7094	1	RIAB_CVBN	Q8vaw7 b replicase	624	36	50.0	233	2	Q9B862_ANAPU	Q9b862 anadara bro
552	37	51.4	7094	1	RIAB_CVBUTU	Q8vaw7 b replicase	625	36	50.0	234	2	Q4WDE ANAPU	Q4wde aspergillus
553	37	51.4	7094	1	RIAB_CVBM	Q8vaw7 b replicase	626	36	50.0	234	2	Q8GR9_98PFO	Q8gr9 borrelia du
554	37	51.4	7095	2	Q6TNG2_CVHOC	Q6tng2 human coron	627	36	50.0	241	2	Q8CUI8_OCEIH	Q8cui8 oceanobacil
555	37	51.4	7095	2	Q696Q1_CVHOC	Q6tng2 human coron	628	36	50.0	245	2	Q8LNB9_ORYSA	Q8lnb9 oryza sativ
556	37	51.4	7095	2	Q4VID8_CVHOC	Q696q1 human coron	629	36	50.0	250	2	Q8T3H1_CABEL	Q8t3h1 caenorhabdi
557	37	51.4	7095	2	Q4VIE7_CVHOC	Q4vid8 human coron	630	36	50.0	250	2	Q8REO8_FUSNL	Q8req8 fusobacteri
558	36.5	50.7	1113	2	Q4YH2_PLABE	Q4yeh2 human coron	631	36	50.0	252	2	Q5H863_9SOLN	Q5h863 solanum kha
559	36.5	50.7	174	2	Q4LYK3_9BURK	Q4lyk3 burkholderi	632	36	50.0	252	2	Q5H866_SOLTU	Q5h866 solanum tub
560	36.5	50.7	255	2	Q9U7H6_PLAFA	Q9u7h6 plasmidium	633	36	50.0	258	2	Q8MAH3_9RHOD	Q8mah3 rhodochaete
561	36.5	50.7	301	2	Q8Z2T3_PYRAE	Q8z2t3 pyrobaculum	634	36	50.0	258	2	Q6ZHE6_BURMA	Q6zeh6 burkholderi
562	36.5	50.7	317	2	Q4XRLO_PLACH	Q4xrlo plasmidium	635	36	50.0	261	2	Q6ZE10_ORYSA	Q6zeh10 oryza sativ
563	36.5	50.7	390	2	Q8DC99_VIBVU	Q8dce9 vibrio vuln	636	36	50.0	262	2	Q85UH4_CIOSA	Q85uh4 clona savig
564	36.5	50.7	390	2	Q7MHF9_VIBVY	Q7mf9 vibrio vuln	637	36	50.0	272	2	Q63R16_BURPS	Q63r16 burkholderi
565	36.5	50.7	434	2	Q8BRP0_OCEIH	Q8brp0 oceanobacil	638	36	50.0	276	2	Q60VW6_CABER	Q60vw6 caenorhabdi
566	36.5	50.7	472	2	Q6ATC5_ORYSA	Q6atc5 oryza sativ	639	36	50.0	276	2	Q9X8N3_BACHR	Q9x8n3 bacillus ha
567	36.5	50.7	545	2	Q4IRT8_GIBZB	Q4irt8 gibberella	640	36	50.0	276	2	Q61R61_XENLA	Q61r61 xenopus lae
568	36.5	50.7	593	2	Q6BJR1_DEBMA	Q6bjr1 debaryomyce	641	36	50.0	278	2	Q633D7_BACCZ	Q633d7 bacillus lae
569	36.5	50.7	686	2	Q63169_BURMA	Q63169 burkholderi	642	36	50.0	278	2	Q61NK2_XENLA	Q61nk2 xenopus lae
570	36.5	50.7	686	2	Q63V75_BURPS	Q63v75 burkholderi	643	36	50.0	279	2	Q4Q8W4_LEIMA	Q4q8w4 leishmania
571	36.5	50.7	981	2	Q7SCA4_ASHGO	Q7sca4 ashbya goss	644	36	50.0	283	2	Q4SM82_TETNG	Q4sm82 tetradon n
572	36	50.0	80	2	Q5SDU5_DICDI	Q5sdu5 dictyostell	645	36	50.0	288	1	ICMT_XENLA	Q12947 x protein-s
573	36	50.0	88	2	Q81PK4_BACCR	Q81pk4 bacillus ce	646	36	50.0	294	2	Q8UBU4_AGR75	Q8ubu4 agrobacteri
574	36	50.0	92	2	Q51D14_ENTHI	Q51d14 entamoeba h	647	36	50.0	296	2	Q8SVC6_ENCCU	Q8svc6 encyphalito
575	36	50.0	93	2	Q6A9K8_PROAC	Q6a9k8 propionibac	648	36	50.0	296	2	Q5WM25_LEGPA	Q5wm25 legionella
576	36	50.0	95	2	Q5C8Q0_CRIPI	Q5c8q0 cryptospori	649	36	50.0	296	2	Q5X4N4_LEGPA	Q5x4n4 legionella
577	36	50.0	98	2	Q9K195_NEIIB	Q9k195 neisseria m	650	36	50.0	296	2	Q6ZUX2_LEGPA	Q6zux2 legionella
578	36	50.0	103	2	Q4MS22_BACCE	Q4ms22 bacillus ce	651	36	50.0	300	2	Q5DUD9_PIRKO	Q5dud9 pyrococcus
579	36	50.0	103	2	Q6HCK9_BACHK	Q6hck9 bacillus th	652	36	50.0	305	2	Q7UBD9_SHIFL	Q7ubd9 shigella fl
580	36	50.0	103	2	Q63DP8_BACCC	Q63df8 bacillus ce	653	36	50.0	306	2	Q93ZD1_ARATH	Q93zd1 arabidopsis
581	36	50.0	107	2	Q58514_PYRHO	Q58514 pyrococcus	654	36	50.0	306	2	Q7TS42_MOUSE	Q7ts42 mus musculu
582	36	50.0	110	1	LIOX_BOVIN	P33072 bos taurus	655	36	50.0	306	2	Q8VFCO_MOUSE	Q8vfc0 mus musculu
583	36	50.0	111	2	Q6YSJ9_BRANA	Q6ysj9 brassica na	656	36	50.0	307	2	Q7Z133_CABEL	Q7z133 caenorhabdi
584	36	50.0	121	2	Q686V7_PLAFA	Q686v7 plasmidium	657	36	50.0	309	2	Q8VFE2_MOUSE	Q8vfe2 mus musculu
585	36	50.0	122	2	Q8SPA0_PLAFA	Q8spa0 plasmidium	658	36	50.0	310	2	Q51297_BORBU	Q51297 borrelia du
586	36	50.0	124	2	Q12631_METAN	Q12631 metarhizium	659	36	50.0	310	2	Q661U8_BORGA	P47592 mycoplasma
587	36	50.0	137	2	Q851I8_ORYSA	Q851i8 oryza sativ	660	36	50.0	311	1	Y350_MYCGB	Q9kjh7 burkholderi
588	36	50.0	142	2	Q9TINK0_9BRIO	Q9tink0 sphagnum fa	661	36	50.0	314	2	Q9KJH7_BURCE	Q9kd6 daucus caro
589	36	50.0	143	1	COX4_CORF	Q8ting8 corynebacte	662	36	50.0	315	2	Q9SDX6_DAUCA	Q8tkq0 mechanosarc
590	36	50.0	143	2	Q9TNJ5_9MARC	Q9tnj5 haplomitriu	663	36	50.0	316	2	Q8TKQ0_METAC	Q7cmv7 agrobacteri
591	36	50.0	145	2	Q8N7H8_HUMAN	Q8n7h8 homo sapien	664	36	50.0	316	2	Q7CWB7_AGR75	Q7my17 photothabdu
592	36	50.0	146	2	Q9TP82_STRPN	Q9tp82 streptococc	665	36	50.0	316	2	Q7MY17_PHOHL	Q8ngq2 homo sapien
593	36	50.0	149	2	Q9TTU5_PHYPA	Q9ttu5 physcomitre	666	36	50.0	317	1	Q8EOL1_HUMAN	Q8efh1 homo sapien
594	36	50.0	150	2	Q4YDW1_PLABE	Q4ydw1 plasmidium	667	36	50.0	317	2	Q61FHI_HUMAN	Q61fhi caenorhabdi
595	36	50.0	153	2	Q9TNL0_COANI	Q9tnl0 coleochaete	668	36	50.0	317	2	Q18947_CABEL	Q18947 caenorhabdi
596	36	50.0	156	2	Q73UNO_MYCPA	Q73uno mycobacteri	669	36	50.0	318	2	Q91ZU2_SUTSO	Q91zu2 sulfolobus
597	36	50.0	158	2	Q15616_HUMAN	Q15616 homo sapien	670	36	50.0	318	2	Q5D8Q9_SCHJA	Q5d8q9 schistosoma
598	36	50.0	158	2	P71105_CIOAB	P71105 clostridium	671	36	50.0	321	2	Q8VZS0_ARATH	Q8vzs0 arabidopsis
599	36	50.0	159	2	Q8B1G4_STRAS	Q8b1g4 streptococc	672	36	50.0	322	2	Q9MA90_ARATH	Q9ma90 arabidopsis
600	36	50.0	161	1	Q8B6Y1_STRAS	Q8b6y1 streptococc	673	36	50.0	322	2	Q8L9D8_ARATH	Q8l9d8 arabidopsis
601	36	50.0	167	2	Q7N9Y8_PHOHL	Q7n9y8 photorhabdu	674	36	50.0	326	2	Q8ZV85_PYRAE	Q8zv85 pyrobaculum
602	36	50.0	168	2	Q7M3F0_PIG	Q7m3f0 sus scrofa	675	36	50.0	326	2	Q5QNA3_ORYSA	Q5qna3 oryza sativ
603	36	50.0	175	2	Q01760_CABEL	Q01760 caenothrabi	676	36	50.0	327	2	Q4WFM6_ASPFU	Q4wfm6 aspergillus
604	36	50.0	175	2	Q8KZL2_9BACT	Q8kz2 uncultured	677	36	50.0	330	1	OR41_MOUSE	Q8vsw2 mus musculu
605	36	50.0	178	2	Q9F9Q4_BACAM	Q9f9q4 bacillus am	678	36	50.0	334	2	Q28312_ARCFU	Q28312 archaeoglob
606	36	50.0	185	2	Q8NPM1_PLAFA	Q8npy1 plasmidium	679	36	50.0	336	2	Q9FZ81_ARATH	Q9fz81 arabidopsis
607	36	50.0	194	2	Q8NGM3_HUMAN	Q8ngm3 homo sapien	680	36	50.0	341	1	YHDM_ECOLI	YHDM_ECOLI
608	36	50.0	195	2	Q7Q339_ANOGA	Q7q339 anopheles g	681	36	50.0	341	2	Q8CVN6_ECOL6	Q8cvn6 escherichia
609	36	50.0	196	2	Q4YME6_PLABE	Q4yme6 plasmidium	682	36	50.0	341	2	Q81ZJ0_SHIFL	Q81zj0 shigella fl
610	36	50.0	199	2	Q6YPV7_ONYPS	Q6ypv7 onion yello	683	36	50.0	342	2	Q5LWV5_SILBO	Q5lwy5 silibactace
611	36	50.0	210	2	Q6W6S6_CANPA	Q6w6s6 canis famli	684	36	50.0	342	2	Q4R3W1_MACPA	Q4r3w1 macaca fasc
612	36	50.0	212	2	Q82LR7_STRAW	Q82lr7 streptomyce	685	36	50.0	347	2	Q9P7X6_ECOLI	Q9p7x6 escherichia
613	36	50.0	220	2	Q4YP74_PLABE	Q4yp74 plasmidium	686	36	50.0	347	2	Q8FEK5_ECOL6	Q8fek5 escherichia
614	36	50.0	220	2	Q6R2L1_PENAM	Q6r2l1 penisetum	687	36	50.0	357	1	HIS7_CANBP	Q7vq8 candidatus
615	36	50.0	220	2			688	36	50.0				

689	36	50.0	357	2	Q4ZWM2_PSSBY	Q4ZWM2_pseudomonas	762	36	50.0	465	2	Q6LW21_GALSU	Q6LW21_galdieria s
690	36	50.0	357	2	Q8BBB4_PSSSM	Q8BBB4_pseudomonas	763	36	50.0	465	2	Q6MAR8_9EUKA	Q6MAR8_prymnesium
691	36	50.0	361	1	MTMD_MESOR	P93257 mesenterivant	764	36	50.0	465	2	Q6MAR9_PLEUCKA	Q6MAR9_pleurochrysis
692	36	50.0	362	2	Q4141A_STRHUT	Q41414 strephyllococ	765	36	50.0	465	2	Q8MAG6_9CRYP	Q8MAG6_pyrenomonas
693	36	50.0	367	2	Q61E13_CABBR	Q61E13 caenothabadi	766	36	50.0	465	2	Q8MAG9_PALRPL	Q8MAG9_palmaria pa
694	36	50.0	367	2	Q8BX08_MOUSE	Q8BX08 m mus muscu	767	36	50.0	465	2	Q6MAH0_CHOCR	Q6MAH0_chondrus cr
695	36	50.0	368	2	Q932B5_STRAM	Q932B5 strephyllococ	768	36	50.0	465	2	Q6MAH5_PORAE	Q6MAH5_porphyriliu
696	36	50.0	371	2	Q7UZFO_RHOBA	Q7UZFO rhodopirell	769	36	50.0	465	2	Q6MAH9_9RHOD	Q6MAH9_porphyrio
697	36	50.0	371	2	Q8BX16_STRAM	Q8BX16 strephyllococ	770	36	50.0	465	2	Q6MAI1_9RHOD	Q6MAI1_bangia fusc
698	36	50.0	372	2	Q5TUI1_ANOGA	Q5TUI1 anophalees g	771	36	50.0	465	2	Q6MAI2_BANAT	Q6MAI2_bangia atro
699	36	50.0	372	2	Q9LH88_ORISA	Q9LH88 oryza sativ	772	36	50.0	465	2	Q6MAI3_GALSU	Q6MAI3_galdieria s
700	36	50.0	374	2	Q9LHWE_ORISA	Q9LHWE oryza sativ	773	36	50.0	465	2	Q6JAL6_GALSU	Q6JAL6_cyanidiosch
701	36	50.0	374	2	Q97F42_CIOAB	Q97F42 clostridium	774	36	50.0	465	2	Q6JAL6_GALSU	Q6JAL6_galdieria s
702	36	50.0	375	2	Q5Z787_ORISA	Q5Z787 oryza sativ	775	36	50.0	465	2	Q6JAL8_GALSU	Q6JAL8_galdieria s
703	36	50.0	377	2	Q7M5X7_PHOIL	Q7M5X7 photorhabdu	776	36	50.0	465	2	Q6JAM1_CVACA	Q6JAM1_cyanidium c
704	36	50.0	377	2	Q6ZDI4_YERPE	Q6ZDI4 yersinia pe	777	36	50.0	465	2	Q52W90_9EUKA	Q52W90_glaucocystis
705	36	50.0	377	2	Q6EDG9_YERPS	Q6EDG9 yersinia ps	778	36	50.0	466	2	Q43526_LYCCEA	Q43526_lycoperisico
706	36	50.0	378	2	Q6BD13_YERPE	Q6BD13 yersinia pe	779	36	50.0	466	2	Q50499_STRCO	Q50499_streptomyce
707	36	50.0	384	2	Q9DM41_RCMVM	Q9DM41 rat cytoomeg	780	36	50.0	475	1	ARCID_LACRK	ARCID_lactobacilli
708	36	50.0	384	2	Q9LFB0_ARATH	Q9LFB0 arabidopsis	781	36	50.0	475	1	SYC_AERPE	SYC_aeropyrum p
709	36	50.0	385	2	Q9LFB0_ARATH	Q9LFB0 arabidopsis	782	36	50.0	475	2	Q9LYU0_ARATH	Q9LYU0_arabidopsis
710	36	50.0	386	2	Q4J6K7_SUIAC	Q4J6K7 sulfolobus	783	36	50.0	484	2	Q6SIX1_BACLD	Q6SIX1_bacillus li
711	36	50.0	387	2	Q97VJ5_SUIAC	Q97VJ5 sulfolobus	784	36	50.0	486	2	Q4W9A3_9EUKA	Q4W9A3_apeerygillus
712	36	50.0	388	2	Q61M24_CABBR	Q61M24 caenothabadi	785	36	50.0	486	2	Q4FRZ3_9EUKA	Q4FRZ3_apeerygillus
713	36	50.0	389	2	Q5LB12_BACFN	Q5LB12 bacteroides	786	36	50.0	492	1	SYC_TREDE	SYC_treponea d
714	36	50.0	389	2	Q64S15_BACFN	Q64S15 bacteroides	787	36	50.0	514	2	Q6EGTE_SHEON	Q6EGTE_shewanella
715	36	50.0	391	2	Q964D8_DICDI	Q964D8 dictyosteli	788	36	50.0	515	2	Q6CCU6_YARLI	Q6CCU6_yarrowia li
716	36	50.0	392	2	Q4YX19_PLABE	Q4YX19 plasmodium	789	36	50.0	518	2	Q6N030_HUMAN	Q6N030_homo sapien
717	36	50.0	411	1	LYOX_MOUSE	P28301 mus musculu	790	36	50.0	521	2	Q59P00_CANAL	Q59P00_candida alb
718	36	50.0	411	1	LYOX_RAT	P16636 rattus norv	791	36	50.0	523	2	Q7S3Q4_NEUCR	Q7S3Q4_neurospora
719	36	50.0	417	1	LYOX_HUMAN	P28300 homo sapien	792	36	50.0	524	2	Q6T7I5_VIBPA	Q6T7I5_vibrio para
720	36	50.0	417	2	Q96PQ9_HUMAN	Q96PQ9 homo sapien	793	36	50.0	525	2	Q9D0L4_MOUSE	Q9D0L4_mus muscu
721	36	50.0	417	2	Q5FWP0_HUMAN	Q5FWP0 homo sapien	794	36	50.0	526	2	Q5AFH4_CANAL	Q5AFH4_candida alb
722	36	50.0	418	2	Q9SL38_BOVIN	Q9SL38 bos taurus	795	36	50.0	526	2	Q8J2J7_CANAL	Q8J2J7_candida alb
723	36	50.0	420	1	LYOX_CHICK	Q05063 gallus gall	796	36	50.0	527	2	Q6BNE6_DBBHA	Q6BNE6_debaryomyce
724	36	50.0	420	2	Q8U459_PRRFU	Q8U459 pyrococcus	797	36	50.0	527	2	Q6PYQ5_GVXAN	Q6PYQ5_xestia c-ni
725	36	50.0	420	2	Q4RUV7_TETNG	Q4RUV7 tetraodon n	798	36	50.0	530	2	Q6KQF0_9RHOO	Q6KQF0_pseudomonas
726	36	50.0	423	1	CH11_ABPAL	P324170 aphanoeladi	799	36	50.0	534	2	Q5VJ90_9EUKA	Q5VJ90_brachyomonas
727	36	50.0	423	2	Q27626_MERTH	Q27626 methanobact	800	36	50.0	545	2	Q5OMG7_ENTHI	Q5OMG7_entrmeoba h
728	36	50.0	423	2	Q5MNU1_VERLE	Q5MNU1 verticilliu	801	36	50.0	551	2	Q7VMNO_HAEDU	Q7VMNO_haemophilus
729	36	50.0	423	2	Q5MNU2_VERLE	Q5MNU2 verticilliu	802	36	50.0	554	2	Q7SAVA_NEUCR	Q7SAVA_neurospora
730	36	50.0	427	2	Q757K7_ASHGO	Q757K7 ashba goss	803	36	50.0	555	2	Q6CLG7_KUTLA	Q6CLG7_kluyveromyc
731	36	50.0	434	2	Q8ABU7_BACTN	Q8ABU7 bacteroides	804	36	50.0	563	2	Q61YW7_CABBR	Q61YW7_caenothabadi
732	36	50.0	437	2	Q6CTUS_KUTLA	Q6CTUS kluyveromyc	805	36	50.0	565	2	Q6QHK9_PAROL	Q6QHK9_parallelchyl
733	36	50.0	439	2	Q4K9Z5_PSRFS	Q4K9Z5 pseudomonas	806	36	50.0	572	2	Q6CPW1_KUTLA	Q6CPW1_kluyveromyc
734	36	50.0	443	1	CD52_RAT	Q91XU8 r phosphati	807	36	50.0	574	1	MUPL_YEAST	P50276 saccharomyc
735	36	50.0	444	1	CD52_MOUSE	Q91XU8 r phosphati	808	36	50.0	581	2	Q4IKS6_GIBZE	Q4IKS6_gibberella
736	36	50.0	444	2	Q7SXPD_BRARE	Q7SXPD brachydanio	809	36	50.0	595	1	BTPT_CORGL	P54582 corynebacte
737	36	50.0	444	2	Q7ZUP2_BRARE	Q7ZUP2 brachydanio	810	36	50.0	595	2	Q4XSAT_PLACH	Q4XSAT_plasmodium
738	36	50.0	445	1	CD52_HUMAN	Q95674 h phosphati	811	36	50.0	598	2	Q6FR01_COREF	Q6FR01_corynebacte
739	36	50.0	445	2	Q4Q9M0_LEIMA	Q4Q9M0 leihsmania	812	36	50.0	610	2	Q72M04_LEPIC	Q72M04_leptospira
740	36	50.0	446	2	Q97U05_SUIAC	Q97U05 sulfolobus	813	36	50.0	621	2	Q8EYH8_LEPIN	Q8EYH8_leptospira
741	36	50.0	448	2	Q51W17_MAGGR	Q51W17 magaporthe	814	36	50.0	621	2	Q7S020_NEUCR	Q7S020_neurospora
742	36	50.0	450	2	Q4SAB5_TETNG	Q4SAB5 tetraodon n	815	36	50.0	622	2	Q9SSK1_DROME	Q9SSK1_drosophila
743	36	50.0	451	2	Q8MAG7_9CRYP	Q8MAG7 chroomonas	816	36	50.0	626	2	Q9V9U2_DRAME	Q9V9U2_drosophila
744	36	50.0	457	1	SYC2_PHOPE	Q6LH97 photobacter	817	36	50.0	632	2	Q4Z1A4_PLABE	Q4Z1A4_plasmodium
745	36	50.0	457	2	Q8MA10_9RHOD	Q8MA10 bangiopsis	818	36	50.0	643	2	Q75FW8_LEPIC	Q75FW8_leptospira
746	36	50.0	458	2	Q8MAG8_9RIOR	Q8MAG8 thorea viol	819	36	50.0	643	2	Q8EYX7_LEPIN	Q8EYX7_leptospira
747	36	50.0	459	2	Q8MAH4_RHOVL	Q8MAH4 rhodelia vi	820	36	50.0	644	2	Q4QHI7_LEIMA	Q4QHI7_leishmania
748	36	50.0	460	1	CD51_HUMAN	Q92A03 h phosphati	821	36	50.0	650	2	Q6WD69_9RIOR	Q6WD69_haliurus flo
749	36	50.0	461	1	CD51_MOUSE	P98191 r phosphati	822	36	50.0	650	2	Q6WD70_9RIOR	Q6WD70_griiffithsia
750	36	50.0	461	1	CD51_MOUSE	Q5052 r phosphati	823	36	50.0	650	2	Q6WD71_9RIOR	Q6WD71_griiffithsia
751	36	50.0	461	1	CD51_MOUSE	Q5052 r phosphati	824	36	50.0	650	2	Q6WD72_9RIOR	Q6WD72_griiffithsia
752	36	50.0	461	2	Q5R9Z3_PONPY	Q5R9Z3 pongo pygma	825	36	50.0	650	2	Q6WD73_GRIIPA	Q6WD73_griiffithsia
753	36	50.0	461	2	Q8MAH2_9RHOD	Q8MAH2 rhodospirub	826	36	50.0	650	2	Q6WD74_9RIOR	Q6WD74_griiffithsia
754	36	50.0	461	2	Q8MAH4_CYAME	Q8MAH4 cyanidiosch	827	36	50.0	650	2	Q6WD75_9RIOR	Q6WD75_griiffithsia
755	36	50.0	462	2	Q8MAG5_9CRYP	Q8MAG5 rhodomonas	828	36	50.0	650	2	Q6WD76_GRIJA	Q6WD76_griiffithsia
756	36	50.0	464	2	Q6JAL9_9RHOD	Q6JAL9 galdieria p	829	36	50.0	650	2	Q6WD77_9RIOR	Q6WD77_griiffithsia
757	36	50.0	464	2	Q6JAM0_9RHOD	Q6JAM0 galdieria d	830	36	50.0	650	2	Q6WD78_9RIOR	Q6WD78_griiffithsia
758	36	50.0	465	2	Q8MAH6_9RHOD	Q8MAH6 flintieria	831	36	50.0	650	2	Q6WD79_9RIOR	Q6WD79_anotrichium
759	36	50.0	465	2	Q6TPW0_9RHOD	Q6TPW0 galdieria m	832	36	50.0	650	2	Q6WD81_9RIOR	Q6WD81_anotrichium
760	36	50.0	465	2	Q6TPW0_9RHOD	Q6TPW0 cyanidium s	833	36	50.0	650	2	Q6WD82_9RIOR	Q6WD82_anotrichium
761	36	50.0	465	2	Q6TPW0_9RHOD	Q6TPW0 cyanidium s	834	36	50.0	650	2	Q6WD82_9RIOR	Q6WD82_anotrichium

835	36	50.0	650	2	Q6WD83_9FIOR	Q6w83 anotrichium	908	36	50.0	750	1	PSAA_ORINI	Q6enh4 oryza nivar
836	36	50.0	650	2	Q6WD84_9FIOR	Q6w84 anotrichium	909	36	50.0	750	1	PSAA_ORYSA	P12155 oryza sativ
837	36	50.0	651	2	Q6WD65_9FIOR	Q6w65 ceramium ko	910	36	50.0	750	1	PSAA_PANCI	Q66806 panax ginseng
838	36	50.0	651	2	Q6WD66_9FIOR	Q6w66 centrocercos	911	36	50.0	750	1	PSAA_PHYPA	Q8ftw3 physcomitre
839	36	50.0	651	2	Q6WD67_9FIOR	Q6w67 anthelmias	912	36	50.0	750	1	PSAA_PINKO	Q85w3 plus korai
840	36	50.0	652	2	Q6PH08_ARKTH	Q6fth8 arabidopsis	913	36	50.0	750	1	PSAA_PSTNU	Q9mu2 psilocum nu
841	36	50.0	659	2	Q8IMH9_DROME	Q8imh9 dirosophila	914	36	50.0	750	1	PSAA_SACHP	Q61398 saccharum h
842	36	50.0	661	2	Q8MFE8_ACCAL	Q8mfe8 accorus cala	915	36	50.0	750	1	PSAA_SACOF	Q6enw3 saccharum o
843	36	50.0	663	2	Q9M469_PHYPO	Q9m469 physarum po	916	36	50.0	750	1	PSAA_SORBI	Q9c216 sorgum bic
844	36	50.0	682	2	Q9HPZ0_HALISA	Q9hpz0 halobacteri	917	36	50.0	750	1	PSAA_SPIOL	P06511 spinacia ol
845	36	50.0	685	1	CRPI_PBRAM	Q25c41 periplaneta	918	36	50.0	750	1	PSAA_TOBAC	P06405 nicotiana t
846	36	50.0	685	2	Q7UM85_RHOBA	Q7um85 rhodoptrelli	919	36	50.0	750	1	PSAA_WHEAT	P53311 triticum ae
847	36	50.0	693	2	Q8M9F7_9LILI	Q8m9f7 liliun brow	920	36	50.0	750	2	Q8S6F6_ORYSA	Q8S6F6 oryza sativ
848	36	50.0	694	2	Q8NTH9_CORGL	Q8nth9 corynebacte	921	36	50.0	750	2	Q8S7T3_ORYSA	Q8S7T3 oryza sativ
849	36	50.0	711	2	Q8M8W3_TAXBR	Q8m8w3 taxus brevi	922	36	50.0	750	2	Q8S1Q4_ORYSA	Q8S1Q4 oryza sativ
850	36	50.0	711	2	Q8M9A5_NELINU	Q8m9a5 nelumbo nuc	923	36	50.0	750	2	Q4VZN3_CUCSA	Q4VZN3 cucumis sat
851	36	50.0	715	1	PSAA_HIPSO	Q9mu1 hupeyria sq	924	36	50.0	750	2	Q4FFJ6_9LILI	Q4ffj6 acorus amer
852	36	50.0	715	1	Q4MME9_ASBFU	Q4mme9 aspergillus	925	36	50.0	750	2	Q4FFJ5_GINBI	Q4ffj5 ginkgo blio
853	36	50.0	715	2	Q8M9R8_9MAGN	Q8m9r8 eupomatia l	926	36	50.0	750	2	Q4FFU4_9MAGN	Q4ffu4 ranunculus
854	36	50.0	715	2	Q8MA52_CRYJA	Q8ma52 cryptomeria	927	36	50.0	750	2	Q4FFU3_9MAGN	Q4ffj3 ranunculus
855	36	50.0	716	1	PSAA_ARAAA	Q9mu7 araucaria a	928	36	50.0	750	2	Q4FFJ2_TYPLA	Q4ffj2 typha latif
856	36	50.0	717	1	PSAA_CYCCE	Q9mu0 cycas revol	929	36	50.0	750	2	Q4FFJ1_9ASPA	Q4ffj1 yucca schid
857	36	50.0	717	1	PSAA_DRIMI	Q9mu9 drimys wint	930	36	50.0	751	1	PSAA_CHLRE	P12154 chlamydomon
858	36	50.0	718	2	Q8MAZ6_9MAGN	Q8maz6 chloranthus	931	36	50.0	751	1	PSAA_CHLUV	P53341 chlorella v
859	36	50.0	719	1	PSAA_ASPND	Q9mu2 chloranthus	932	36	50.0	751	1	PSAA_MAIZE	P04966 zea mays l
860	36	50.0	719	1	PSAA_ENICLR	Q9mu4 asplenium n	933	36	50.0	751	1	PSAA_NEPOL	P09466 nephrrolepis
861	36	50.0	719	1	PSAA_EOUPA	Q9mu6 encyphalart	934	36	50.0	751	1	PSAA_SYNY3	P29254 synchococyt
862	36	50.0	719	1	PSAA_TORCL	Q9mu7 araucaria a	935	36	50.0	752	1	PSAA_CYACA	Q9f1l5 cyanidium c
863	36	50.0	719	2	Q8MA47_9CONI	Q8ma47 cedrus liba	936	36	50.0	752	1	PSAA_GARAT	Q6B806 grecliarla
864	36	50.0	720	1	PSAA_EPHIT	Q9mu8 ephedra twe	937	36	50.0	752	1	PSAA_PORPU	P51284 porphyra pu
865	36	50.0	720	1	PSAA_MARBO	Q9mu1 marsilea bo	938	36	50.0	754	1	Q67QZ1_SYMTH	Q67qz1 synchobacte
866	36	50.0	720	1	PSAA_SEOSR	Q9muk3 sequoia sem	939	36	50.0	755	1	PSAA_SYNEL	P04406 synchococcc
867	36	50.0	720	1	PSAA_WEIMI	Q9muk3 welwitschia	940	36	50.0	755	1	PSAA_SYNNV	P25936 synchococcc
868	36	50.0	720	2	Q8M953_9CONI	Q8m953 pinus parvi	941	36	50.0	755	1	PSAA_SYNNV	P05310 pinum sativ
869	36	50.0	720	2	Q8M9D1_MAGGA	Q8m9d1 magnolia gr	942	36	50.0	758	1	PSAA_PEA	Q6QY10 ORYSA
870	36	50.0	721	1	PSAA_ANGEV	Q9muj5 angiopteris	943	36	50.0	765	2	Q6QY14 ORYSA	Q6Qy14 oryza sativ
871	36	50.0	721	1	PSAA_GINBI	Q9muk3 ginkgo blio	944	36	50.0	765	2	PURL_LEIXX	Q6ac33 leifsonia x
872	36	50.0	721	2	Q8M932_USEUD	Q8m932 pachysandra	945	36	50.0	772	1	Q5YOM4_9ARCH	Q5YOM4 uncultured
873	36	50.0	721	2	Q8MA50_USEUD	Q8ma50 copticis laci	946	36	50.0	772	2	Q6Q4Z9_DROBU	Q6Q4Z9 dirosophila
874	36	50.0	721	2	Q8M8T6_ZAMPU	Q8m8t6 zania pumil	947	36	50.0	773	2	Q64B34_9ARCH	Q64b34 uncultured
875	36	50.0	721	2	Q8M8Y3_9ARAB	Q8m8y3 spathiphyll	948	36	50.0	774	2	Q8WZT7_NEUCR	Q8wzt7 neurospora
876	36	50.0	721	2	Q8M900_SARCE	Q8m900 saururus ce	949	36	50.0	782	2	Q6TDL0_9VIRU	Q6tdl0 sulfolobus
877	36	50.0	721	2	Q8M937_9CONI	Q8m937 picea splin	950	36	50.0	793	2	Q7SDS5_NEUCR	Q7sds5 neurospora
878	36	50.0	721	2	Q8M9S0_9ERIC	Q8m9s0 enkianthus	951	36	50.0	805	2	Q8U6S5_AGRTS	Q8u6s5 agrobacteri
879	36	50.0	721	2	Q8MA40_CALOC	Q8ma40 calycanthus	952	36	50.0	812	2	Q54UR9_DICDI	Q54ur9 dictyosteli
880	36	50.0	721	2	Q8MC78_ACPBM	Q8mc78 acer palmat	953	36	50.0	819	2	Q7REO7_PLAYO	Q7reo7 plasmodium
881	36	50.0	722	2	Q8I408_PLAF7	Q8i408 plasmodium	954	36	50.0	850	2	Q7SOW0_ASHGO	Q7sow0 ashbya gos
882	36	50.0	722	2	Q8M944_USEUD	Q8m944 platanus ra	955	36	50.0	851	2	Q8YQI4_9ANAS	Q8YqI4 anabaena gp
883	36	50.0	722	2	Q8M928_9CONI	Q8m928 phyllocladu	956	36	50.0	854	2	Q869V0_DICDI	Q869v0 dictyosteli
884	36	50.0	722	2	Q8M9A3_9MAGN	Q8m9a3 nymphea sp	957	36	50.0	855	2	Q51D35_ENTHI	Q51d35 entameoba h
885	36	50.0	722	2	Q8M9A7_9MAGN	Q8m9a7 nuphar lute	958	36	50.0	870	2	DBOI_BACCA	Q04957 bacillus ca
886	36	50.0	722	2	Q8M9E4_LIOST	Q8m9e4 liquidambar	959	36	50.0	878	2	Q6X9S1_BACCL	Q6x9s1 bacillus ca
887	36	50.0	722	2	Q8MC74_9MAGN	Q8mc74 austrobaile	960	36	50.0	878	2	Q5KWCL_GROKA	Q5kwcl geobacillus
888	36	50.0	722	2	Q8M9M3_ISGAR	Q8m9m3 isometris ar	961	36	50.0	882	2	Q4PDJ4_USITMA	Q4pdj4 usellago ma
889	36	50.0	723	2	Q8M8Y6_SERRE	Q8m8y6 serenoia rep	962	36	50.0	883	2	Q5OR07_IDILO	Q5or07 idiomarina
890	36	50.0	723	2	Q8M966_9CONI	Q8m966 afrocarpus	963	36	50.0	893	2	Q51BR0_ENTHI	Q51br0 entameoba h
891	36	50.0	724	2	Q8M906_9ROSI	Q8m906 faqus grand	964	36	50.0	897	2	Q4PEMO_USITMA	Q4pem0 usellago ma
892	36	50.0	725	2	Q8M990_PERRAE	Q8m990 persea amer	965	36	50.0	932	2	Q6MD92_PARUM	Q6md92 paracchlamyd
893	36	50.0	737	2	Q64US5_BACFR	Q64us5 bacteroides	966	36	50.0	941	2	Q7PKX0_ANOGA	Q7pkx0 anophelis g
894	36	50.0	739	1	PSAA_SYNP	P17154 synchococcc	967	36	50.0	950	2	Q77329_PLAF7	Q77329 plasmodium
895	36	50.0	747	1	Q4ZGM4_ABDAB	Q4zgm4 aedes aegypt	968	36	50.0	955	2	Q8U5J7_AGRTS	Q8u5j7 agrobacteri
896	36	50.0	748	1	PSAA_CHAGL	Q8m9w0 chaetophae	969	36	50.0	972	2	Q8UHY9_AGRTS	Q8uhy9 agrobacteri
897	36	50.0	750	1	PSAA_CYAME	Q85fY7 cyanidiosch	970	36	50.0	994	2	Q756R4_ASHGO	Q756r4 ashbya gos
898	36	50.0	750	1	PSAA_ADICA	Q70yD3 adiantum ca	971	36	50.0	1011	2	Q5CR84_CRYPV	Q5cr84 cryptospori
899	36	50.0	750	1	PSAA_AMBTC	Q85s27 anthoceros	972	36	50.0	1025	2	Q7YNS9_EIMTE	Q7yns9 elmeria ten
900	36	50.0	750	1	PSAA_AANTFO	P56766 arabidopsis	973	36	50.0	1050	2	Q8ILD2_PLAF7	Q8ild2 plasmodium
901	36	50.0	750	1	PSAA_ARATH	Q868x4 atropa bell	974	36	50.0	1103	2	Q5JGP8_PYRKO	Q5jgp8 pyrococcus
902	36	50.0	750	1	PSAA_ATRBR	Q7Y1x2 calycanthus	975	36	50.0	1103	2	Q7QI46_ANOGA	Q7qi46 anophelis g
903	36	50.0	750	1	PSAA_CALFE	P58310 lotus japon	976	36	50.0	1133	2	Q65ZT6_BORGA	Q65zt6 borrelia ga
904	36	50.0	750	1	PSAA_IOTUA	P06406 marchantia	977	36	50.0	1181	2	Q54L55_DICDI	Q54l55 dictyosteli
905	36	50.0	750	1	PSAA_MARBO	Q9mu18 mesostigma	978	36	50.0	1199	2	Q18859_CABEL	Q18859 caenorhabdi
906	36	50.0	750	1	PSAA_MESVI	Q6ew48 nymphea al	979	36	50.0	1256	2	Q617W3_CABER	Q617w3 caenorhabdi
907	36	50.0	750	1	PSAA_NYMAL		980	36	50.0				

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981 36 50.0 1336 2 051555 ENTH1
982 36 50.0 1368 2 08XSJ7_RALSO
983 36 50.0 1491 2 04Q2T2_LEIMA
984 36 50.0 1664 2 05AX84_EMENT
985 36 50.0 1726 2 051EB8_ENTHI
986 36 50.0 1776 2 07RPB6_PLAYO
987 36 50.0 2343 2 075DB8_ASHGO
988 36 50.0 2649 2 07RAS7_PLAYO
989 36 50.0 2817 2 07KK42_CIOAB
990 36 50.0 3689 2 07PBP9_ANOAB
991 35.5 49.3 124 2 071J46_LACDL
992 35.5 49.3 136 2 06S8S3_PLAFA
993 35.5 49.3 185 2 0721T7_THET2
994 35.5 49.3 185 2 05S1F9_THET8
995 35.5 49.3 215 2 070Z66_CANPA
996 35.5 49.3 261 2 04W6G8_RHASC
997 35.5 49.3 261 2 05VHD2_9NEOB
998 35.5 49.3 365 1 COMT1_ROSCH
999 35.5 49.3 365 2 07X9J0_ROSCH
1000 35.5 49.3 365 2 09W602_FRAAN

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ALIGNMENTS

RESULT 1

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09C4Q2_METTL PRELIMINARY; PRT; 329 AA.
ID 09C4Q2_METTL PRELIMINARY; PRT; 329 AA.
AC 09C4Q2;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Flab1
GN Name=flab1;
OS Methanococcus thermolithotrophicus.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanothermococcus.
OX NCBI_TaxID=2186;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574152; PubMed=11717274;
RX DOI=10.1128/JB.183.24.7154-7164.2001;
RA Thomas N.A., Jarrell K.F.;
RT "Characterization of flagellum gene families of methanogenic archaea
RT and localization of novel flagellum accessory proteins.";
RL J. Bacteriol. 183:7154-7164(2001).
DR EMBL; AF333250; AAG50068.1; -; Genomic_DNA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0006928; P:cell motility; IEA.
DR InterPro; IPR002774; Arch_flagellin.
DR Pfam; PF01917; Arch_flagellin; 1.
SQ SEQUENCE 329 AA; 34929 MW; D5A3182D8929B22 CRC64;

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Query Match 65.3%; Score 47; DB 2; Length 329;
Best Local Similarity 80.0%; Pred. No. 16;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 2 IYFGTYTFD 11
Db 71 IYKYGTYTD 80

```

RESULT 2

```

09C4Q1_METTL
ID 09C4Q1_METTL PRELIMINARY; PRT; 435 AA.
AC 09C4Q1;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Flab2.
GN Name=flab2;
OS Methanococcus thermolithotrophicus.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;

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OC Methanococcaceae; Methanothermococcus.
OX NCBI_TaxID=2186;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574152; PubMed=11717274;
RX DOI=10.1128/JB.183.24.7154-7164.2001;
RA Thomas N.A., Jarrell K.F.;
RT "Characterization of flagellum gene families of methanogenic archaea
RT and localization of novel flagellum accessory proteins.";
RL J. Bacteriol. 183:7154-7164(2001).
DR EMBL; AF333250; AAG50069.1; -; Genomic_DNA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR002774; Arch_flagellin.
DR Pfam; PF01917; Arch_flagellin; 1.
SQ SEQUENCE 435 AA; 46259 MW; D707A8951DD80E99 CRC64;

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QY 2 IYFGTYTFD 11
Db 71 IYKYGTYTD 80

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RESULT 3

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SYT_BDBEA STANDARD; PRT; 656 AA.
ID SYT_BDBEA
AC 06MML0;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)
DE (ThrS).
GN Name=thrS; OrderedLocNames=Bdl617;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RX STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jacquet P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasks: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
CC -!- CATALYTIC ACTIVITY: ATP + L-threonine + tRNA(Thr) = AMP +
CC -!- diphosphate + L-threonyl-tRNA(Thr).
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the class-II aminoacyl-tRNA synthetase
CC family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; BX842650; CAE79494.1; -; Genomic_DNA.
CC HAMAP; MF_00184; -; 1.
CC InterPro; IPR004154; anticodon bd.
CC InterPro; IPR012675; Peridoxin_fold.
CC InterPro; IPR004095; TGS.
CC InterPro; IPR012676; TGS_1like.
CC InterPro; IPR002314; tRNA-synt_2b.
CC InterPro; IPR002320; tRNA-synt_thr.
CC InterPro; IPR006195; tRNA_ligase_II.

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SQ SEQUENCE 366 AA; 41163 MW; 006F1389E29DCBAD CRC64;
 Query Match 62.5%; Score 45; DB 2; Length 366;
 Best Local Similarity 87.5%; Pred. No. 38;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 YGTYTFDY 12
 |||||
 Db 59 YGTYTFDY 66
 RESULT 7
 Q6T4P0 HEVBR PRELIMINARY; PRT; 366 AA.
 ID Q6T4P0 HEVBR PRELIMINARY;
 AC Q6T4P0;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Major latex allergen Hev b 4 precursor.
 OS Hevea brasiliensis (Para rubber tree).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
 CC Microdeseae; Hevea.
 OC NCBI_TaxID=3981;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sunderasan E., Yeang H.Y.;
 RT "Hevea brasiliensis latex lectinase homolog.",
 RL Submitted (Oct-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY437086; AAR98518.1; -; mRNA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR InterPro; IPR001087; Lipase_GDSL.
 DR Pfam; PF00657; Lipase_GDSL; 1.
 KM Signal.
 FT SIGNAL. 1 24 Potential.
 SQ SEQUENCE 366 AA; 41177 MW; 5FD2BC136D7F8EE CRC64;
 Query Match 62.5%; Score 45; DB 2; Length 366;
 Best Local Similarity 87.5%; Pred. No. 38;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 YGTYTFDY 12
 |||||
 Db 59 YGTYTFDY 66
 RESULT 8
 Q568Y0 RAT PRELIMINARY; PRT; 598 AA.
 ID Q568Y0 RAT PRELIMINARY;
 AC Q568Y0;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE LOC229458 protein.
 GN Name=LOC229458;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Murioidea; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Tissue=Spleen.
 MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheffen C.F., Schuler G.D.,
 RA Alekshch S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
 RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Spleen.
 RG NIH MGC Project;
 RL Submitted (Apr-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC032661; AAB2661.1; -; mRNA.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 4.
 DR SMART; SM00408; IGcl; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
 SQ SEQUENCE 598 AA; 65920 MW; DB826961E1B3A36 CRC64;
 Query Match 62.5%; Score 45; DB 2; Length 598;
 Best Local Similarity 58.3%; Pred. No. 64;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GIFYGYTFDY 12
 |||||
 Db 121 GSYGYWYTFDY 132
 RESULT 9
 Q6E124 9HETE PRELIMINARY; PRT; 619 AA.
 ID Q6E124 9HETE PRELIMINARY;
 AC Q6E124;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Laccase.
 GN Name=lac1;
 OS Auricularia polytricha.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 CC Heterobasidiomycetidae; Auriculariales; Auriculariaceae; Auricularia.
 OC NCBI_TaxID=29893;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Yang J.-M., Cao H., Chen M.-J., Xing Z.-T., Tan O., Pan Y.-J.;
 RL Submitted (May-2004) to the EMBL/Genbank/DBJ databases.
 CC -1-COPACTOR: Binds 4 copper ions per monomer (By similarity).
 DR EMBL; AY615304; AAT73204.1; -; mRNA.
 DR GO; GO:0005507; F:copper ion binding; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR001117; Cu-oxidase.
 DR InterPro; IPR011706; Cu-oxidase_2.
 DR InterPro; IPR011707; Cu-oxidase_3.
 DR InterPro; IPR002355; Cu oxidase_Cu_BS.
 DR Pfam; PF00394; Cu-oxidase; 1.
 DR Pfam; PF07731; Cu-oxidase_2; 1.
 DR Pfam; PF07732; Cu-oxidase_3; 1.
 DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 2.

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DR PROSITE; PS00080; MULTICOPPER OXIDASE2; 1.
KW Copper; Metal-binding; Oxidoreductase; Repeat.
SQ SEQUENCE 619 AA; 68367 MW; 37716E0A58AB0B6 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 619;
Best Local Similarity 63.6%; Pred. No. 66;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVFYGTYYFD 11
Db 80 GMFFNGTSTYFD 90

RESULT 10
Q6E0Y2_9HETE PRELIMINARY; PRT; 620 AA.
ID Q6E0Y2_9HETE PRELIMINARY; PRT; 620 AA.
AC Q6E0Y2;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Laccase.
GN Name=IacI;
OS Auricularia polycricha.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Heterobasidiomycetidae; Auriculariales; Auriculariaceae; Auricularia.
OX NCBI_TaxID=29893;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang J.-M., Cao H., Chen M.-J., Xing Z.-T., Tan Q., Pan Y.-J.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- COPFCTOR: Binds 4 copper ions per monomer (by similarity).
DR EMBL; AY616035; AAT73205.1; -; Genomic DNA.
DR GO; GO:0005507; Fcopper ion binding; IEA.
DR GO; GO:0046872; Fmetal ion binding; IEA.
DR GO; GO:001491; Foxidoreductase activity; IEA.
DR InterPro; IPR011176; Cu-oxidase.
DR InterPro; IPR011707; Cu-oxidase.
DR InterPro; IPR002355; Cu-oxidase_3.
DR InterPro; IPR002355; Cu-oxidase_Cu_BS.
DR Pfam; PF00394; Cu-oxidase; 1.
DR Pfam; PF07731; Cu-oxidase_2; 1.
DR Pfam; PF07732; Cu-oxidase_3; 1.
DR PROSITE; PS00079; MULTICOPPER OXIDASE1; 2.
DR PROSITE; PS00080; MULTICOPPER OXIDASE2; 1.
KW Copper; Metal-binding; Oxidoreductase; Repeat.
SQ SEQUENCE 620 AA; 68514 MW; 4C953A44CDE54A2B CRC64;

Query Match 62.5%; Score 45; DB 2; Length 620;
Best Local Similarity 63.6%; Pred. No. 66;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVFYGTYYFD 11
Db 80 GMFFNGTSTYFD 90

RESULT 11
O28859_ARCFU PRELIMINARY; PRT; 2425 AA.
ID O28859_ARCFU PRELIMINARY; PRT; 2425 AA.
AC O28859;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Surface layer protein B (S19B-2).
GN OrderedlocusNames=AF1413;
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RC MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;
MEDLINE=98049343; PubMed=9389475; DOI=10.1038/37052;

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RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kexlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
RA Kirnesh E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Reich C.T., McNeil L.K., Badger J.H., Glodek A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.P., McDonald L.A.,
RA Ullrich T.R., Cotton M.D., Spriggs T., Artach P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Woese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
DR EMBL; AB001006; AAB89834.1; -; Genomic DNA.
DR PIR; D69426; D69426.
DR TIGR; AF1413; -.
DR InterPro; IPR006633; CASH.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR006626; Pbh1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00722; CASH; 6.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00710; Pbh1; 16.
DR PROSITE; PS50853; FN3; 1.
KW Complete proteome.
SQ SEQUENCE 2425 AA; 266571 MW; 97E3856843226E37 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 2425;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIVFYGTYYFD 11
Db 179 GVIYTGSSIFN 189

RESULT 12
HV07_MOUSE STANDARD; PRT; 139 AA.
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG heavy chain V region BI-8/186-2 precursor.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6;
RC MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
DE -1- MISCCELLANEOUS: The BI-8 mu chain mRNA was cloned from a hybridoma
DE making antibodies to the hapten (4-hydroxy-3-nitrophenyl)acetyl
DE (NPb antibodies).
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; J00529; AAA38170.1; -, mRNA.
CC PIR; A90809; MEMS18.
CC PDB; 1A6V; X-ray; H=20-139.
CC PDB; 1A6V; X-ray; H/I/J=20-139.

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DR PDB; 1A6W; X-ray; H=20-139.
DR PDB; INGP; X-ray; H=20-139.
DR PDB; INGO; X-ray; H=20-139.
DR PDB; 1NOB; X-ray; A/C=20-139.
DR Ensembl; ENSMUSG0000063737; Mus musculus.
DR InterPro; IPR007110; 19-1-like.
DR InterPro; IPR003596; 19_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 Ig heavy chain V region B1-6/186-2.
FT REGION 20 49 Framework-1.
FT REGION 50 54 Complementarity-determining-1.
FT REGION 55 68 Framework-2.
FT REGION 69 85 Complementarity-determining-2.
FT REGION 86 117 Framework-3.
FT REGION 118 124 D segment.
FT REGION 125 139 JH2 segment.
FT DISULFID 41 115 By similarity.
FT NON_TER 139 139
FT STRAND 22 24
FT STRAND 28 31
FT TURN 33 34
FT STRAND 37 44
FT HELIX 48 50
FT STRAND 52 58
FT TURN 60 61
FT STRAND 64 70
FT TURN 72 74
FT STRAND 77 79
FT HELIX 81 83
FT TURN 84 86
FT STRAND 87 92
FT TURN 93 96
FT STRAND 97 102
FT HELIX 107 109
FT STRAND 111 118
FT TURN 120 123
FT STRAND 129 129
FT STRAND 133 137
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 61.1%; Score 44; DB 1; Length 139;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 FYGTTYFDY 12
Db 120 YYGSSYFDY 128

RESULT 13
O92407_MOUSE PRELIMINARY; PRT; 145 AA.
ID O92407_MOUSE PRELIMINARY; PRT; 145 AA.
AC O92407;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB VHL86.2-D-J-C mu protein (Fragment).
GN Name=VHL86.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DDA databases.
RP NUCLEOTIDE SEQUENCE.

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RX PubMed=3135311;
RA Corbet S., Hirn M., Roth C., These J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
DR EMBL; AB067793; BAB63278.1; -, mRNA.
DR PIR; F28833; F28833.
DR PIR; PH105; PH105.
DR PIR; PH108; PH108.
DR PIR; PH114; PH114.
DR PIR; PH118; PH118.
DR PIR; PH119; PH119.
DR PIR; PH125; PH125.
DR PIR; PH126; PH126.
DR PIR; PH128; PH128.
DR PIR; PH129; PH129.
DR PIR; PH131; PH131.
DR PIR; PH134; PH134.
DR PIR; PH137; PH137.
DR PIR; PH139; PH139.
DR PIR; PH142; PH142.
DR PIR; PH144; PH144.
DR PIR; PH147; PH147.
DR PIR; PH149; PH149.
DR PIR; PH150; PH150.
DR PIR; PH151; PH151.
DR PIR; PH152; PH152.
DR PIR; PH153; PH153.
DR HSP; P01751; 1A6W.
DR SMR; Q92407; 1-136.
DR InterPro; IPR007110; 19-1-like.
DR InterPro; IPR003596; 19_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 145 145
FT NON_TER 145 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 61.1%; Score 44; DB 2; Length 145;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 FYGTTYFDY 12
Db 101 YYGSSYFDY 109

RESULT 14
Q8CUH8_OCEIH PRELIMINARY; PRT; 239 AA.
ID Q8CUH8_OCEIH PRELIMINARY; PRT; 239 AA.
AC Q8CUH8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Spore coat polysaccharide synthesis (Glucose-1-phosphate
DB thymidyltransferase).
GN Ordered locus Names=OB1129;
OS Oceanobacillus thelyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HT631 / DSM 14371 / JCM 11309;
RA MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus thelyensis isolated from the Itheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC13085.1; -, Genomic_DNA.
DR HSP; Q9H022; IFXO.
DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.

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DR GO: GO:0016740; P:transferase activity; IEA.
DR GO: GO:0009058; P:biosynthesis; IEA.
DR InterPro: IPR005835; NTP transferase.
DR Pfam: PF00483; NTP transferase; 1.
DR Complete proteome; Transferase.
SQ SEQUENCE 239 AA; 27107 MW; 6D12038297E70B35 CRC64;

Query Match
Best Local Similarity 61.1%; Score 44; DB 2; Length 239;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIFYGTYFYD 12
DB 172 GIHFVGTAYD 183

RESULT 15
Q8YD28 BRUME PRELIMINARY; PRT; 331 AA.
AC Q8YD28;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE GENERAL L-AMINO ACID-BINDING PERIPLASMIC PROTEIN AAPJ.
GN OrderedLocustNames=BMEI10349;
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=16M / ATCC 23456 / Biotype 1;
RX PubMed=11756688; DOI=10.1073/pnas.221575398;
RA DelVecchio V.G., Kapral V., Redkar R.J., Patra G., Wjjer C., Los T.,
RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
RA Jablonksi L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Lateson J.-J.,
RA Haselkorn R., Kyrides N.C., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis."
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL: AE009672; AAL53591.1; -; Genomic_DNA.
FIR: AD3553; AD3553.
DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR InterPro: IPR001311; SBP/glu receptor.
DR InterPro: IPR001638; SBP_bac_3.
DR SMART; SM00062; PBPb; 1.
KW Complete proteome.
SQ SEQUENCE 331 AA; 35751 MW; B4B762C471D65511 CRC64;

Query Match
Best Local Similarity 61.1%; Score 44; DB 2; Length 331;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTYFYD 11
DB 107 GIHFVGTAYD 117

RESULT 16
Q579G5 BRUB PRELIMINARY; PRT; 339 AA.
AC Q579G5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Amino acid ABC transporter, periplasmic amino acid-binding
DE protein.
GN OrderedLocustNames=Brub2_0285;
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

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OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=9-941 / Biovar 1;
RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuercher R.L.,
RA Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
RT "Completion of the genome sequence of Brucella abortus and comparison
RT to the highly similar genomes of Brucella melitensis and Brucella
RT suis."
RT J. Bacteriol. 187:2715-2726(2005).
RL EMBL: AE017224; AAX75719.1; -; Genomic_DNA.
DR Complete proteome.
KW SEQUENCE 339 AA; 36538 MW; EFAD2104P9FPA0B7 CRC64;

Query Match
Best Local Similarity 61.1%; Score 44; DB 2; Length 339;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTYFYD 11
DB 115 GIHFVGTAYD 125

RESULT 17
Q8FV98 BRUSU PRELIMINARY; PRT; 339 AA.
AC Q8FV98;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Amino acid ABC transporter, periplasmic amino acid-binding
DE protein.
GN OrderedLocustNames=BR0948;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1330 / Biovar 1;
RX PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umeyam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
EMBL: AE014292; AAN34119.1; -; Genomic_DNA.
DR TIGR: BR0948; -
DR GO: GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR InterPro: IPR001311; SBP/glu receptor.
DR InterPro: IPR001638; SBP_bac_3.
DR SMART; SM00062; PBPb; 1.
KW Complete proteome.
SQ SEQUENCE 339 AA; 36605 MW; 2790247F7C9F10C6 CRC64;

Query Match
Best Local Similarity 61.1%; Score 44; DB 2; Length 339;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTYFYD 11
DB 115 GIHFVGTAYD 125

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RESULT 18
097N14 STRPN PRELIMINARY; PRT: 227 AA.
ID 097N14 STRPN PRELIMINARY; PRT: 227 AA.
AC 097N14.
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE L-ribulose 5-phosphate 4-epimerase Arad, putative.
GN OrderedLocustNames=SP2033;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN-ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916; DOI=10.1126/science.1061217;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtapple E.K., Khouri H.M., Wolf A.M., Uitterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S.V., Dickinson T.,
RA Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
RL Science 293:498-506(2001).
DR EMBL; AB007492; AAK76098.1; -; Genomic_DNA.
DR PIR; A95238; A95238.
DR HSSP; P08203; 1K0W.
DR TIGR; SP2033; -.
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00596; Aldolase_II; 1.
DR Complete proteome.
SQ SEQUENCE 227 AA; 25572 MW; 5CED7825DPA560C CRC64;

Query Match 59.7%; Score 43; DB 2; Length 227;
Best Local Similarity 72.7%; Pred. NO. 50;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IYFGTYFDY 12
| | | | | : | |
| | | | | : | |
Db 106 IPFYGTHADY 116

RESULT 19
08DN99 STRR6 PRELIMINARY; PRT: 234 AA.
ID 08DN99 STRR6 PRELIMINARY; PRT: 234 AA.
AC 08DN99.
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE L-ribulose 5-phosphate 4-epimerase (EC 5.1.3.4).
GN Name=arad; OrderedLocustNames=SP1844;
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21429245; PubMed=11544234;
RX DOI=10.1126/jb.183.19.5709-5717.2001;
RA Hoefling J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., BURGESS S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmore R., Glaes J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz B.J., Lu J., Matsushita P.,
RA McLaren S.M., McHenry M., Mcleaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rokey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Kosteck P.R., Skatrud P.L.,
RA Glaes J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
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RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL; AB008549; AAL00647.1; -; Genomic_DNA.
DR PIR; B98102; B98102.
DR HSSP; P08203; 1JDI.
DR GO; GO:0008742; F:L-ribulose-phosphate 4-epimerase activity; IEA.
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00596; Aldolase_II; 1.
DR Complete proteome.
SQ SEQUENCE 234 AA; 26313 MW; EB3CB8586A7DBBC2 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 234;
Best Local Similarity 72.7%; Pred. NO. 52;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IYFGTYFDY 12
| | | | | : | |
| | | | | : | |
Db 113 IPFYGTHADY 123

RESULT 20
09A1N4 STRPY PRELIMINARY; PRT: 234 AA.
ID 09A1N4 STRPY PRELIMINARY; PRT: 234 AA.
AC 09A1N4.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative L-ribulose 5-phosphate 4-epimerase (EC 5.1.3.4).
GN Name=arad; OrderedLocustNames=SPY0179;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN-SP370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McCloughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AB006486; AAK33279.1; -; Genomic_DNA.
DR HSSP; P08203; 1JDI.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0008742; F:L-ribulose-phosphate 4-epimerase activity; IEA.
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00596; Aldolase_II; 1.
DR Complete proteome; Isomerase.
SQ SEQUENCE 234 AA; 26158 MW; BE17505DFE5EBB4B CRC64;

Query Match 59.7%; Score 43; DB 2; Length 234;
Best Local Similarity 72.7%; Pred. NO. 52;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IYFGTYFDY 12
| | | | | : | |
| | | | | : | |
Db 113 IPFYGTHADY 123

RESULT 21
08K8R7 STRP3 PRELIMINARY; PRT: 234 AA.
ID 08K8R7 STRP3 PRELIMINARY; PRT: 234 AA.
AC 08K8R7; 079YL7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Putative L-ribulose 5-phosphate 4-epimerase.
GN Name=arad; OrderedLocustNames=SP0143; SPYM3_0140;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301448;
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RN NUCLEOTIDE SEQUENCE.
RP STRAIN=MGAS315 / Serotype M3;
RC MEDLINE=22133808; PubMed=1122006; DOI=10.1073/pnas.152298499;
RX Beres S.B., Silva G.L., Barbican K.D., Lei B., Hoff U.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Perkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSI-1 / Serotype M3;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurikawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution."
RL Genome Res. 13:1042-1055(2003).
DR EMBL; AB014139; AAM78747.1; -; Genomic_DNA.
DR EMBL; BA000034; BAC63238.1; -; Genomic_DNA.
DR HSSP; P08203; 1K0W.
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00596; Aldolase_II; 1.
DR Complete Proteome.
SQ SEQUENCE 234 AA; 26102 MW; 92DA4C90F5D36C5 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 234;
Best Local Similarity 72.7%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFGTYFDY 12
| | | | | : | |
| | | | | : | |
Db 113 IPFYGTTTHADY 123

RESULT 22
Q8DXP0 STRA5 PRELIMINARY; PRT; 238 AA.
ID Q8DXP0 STRA5 PRELIMINARY;
AC Q8DXP0;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Carbohydrate isomerase, Arad/Fuca family.
DE OrderedLocNames=SAG1810;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tettelin H., Massignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Nelson K.B., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Pedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
RA Carey H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Jacobini E.T., Bretonni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappunli R., Telford J.L., Kasper D.L., Grandi G.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AS014274; AAN00673.1; -; Genomic_DNA.
DR HSSP; P08203; 1K0W.
DR TIGR; SAG1810; -
DR InterPro; IPR001303; Aldolase_II_N.

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DR Pfam; PF00596; Aldolase_II; 1.
KW Complete proteome.
SQ SEQUENCE 238 AA; 26719 MW; FA59E1290D24B84E CRC64;

Query Match 59.7%; Score 43; DB 2; Length 238;
Best Local Similarity 72.7%; Pred. No. 53;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFGTYFDY 12
| | | | | : | |
| | | | | : | |
Db 113 IPFYGTTTHADY 123

RESULT 23
Q8E3B0 STRA3 PRELIMINARY; PRT; 238 AA.
ID Q8E3B0 STRA3 PRELIMINARY;
AC Q8E3B0;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein gba1851.
DE OrderedLocNames=gba1851;
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaeser P., Rusniok C., Buchrieser C., Chevalier F., Frangoul L.,
RA Msadek T., Zouine M., Couve E., Lallouet L., Poyart C., Tieu-Cuot P.,
RA Kunat F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease."
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766853; CAD47510.1; -; Genomic_DNA.
DR HSSP; P08203; 1K0W.
DR Sageliet; gba1851; -
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00596; Aldolase_II; 1.
DR Complete Proteome.
SQ SEQUENCE 238 AA; 26719 MW; FA59E1290D24B84E CRC64;

Query Match 59.7%; Score 43; DB 2; Length 238;
Best Local Similarity 72.7%; Pred. No. 53;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFGTYFDY 12
| | | | | : | |
| | | | | : | |
Db 113 IPFYGTTTHADY 123

RESULT 24
O5XE29 STRP6 PRELIMINARY; PRT; 242 AA.
ID O5XE29 STRP6 PRELIMINARY;
AC O5XE29;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4).
DE OrderedLocNames=M6_Spy0199;
OS Streptococcus pyogenes (serotype M6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGAS10394;
RX PubMed=15272401; DOI=10.1086/422697;
RA Banks D.J., Porcella S.F., Barbican K.D., Beres S.B., Phillips L.B.,
RA Voyich J.M., Deleo F.R., Martin J.M., Somerville G.A., Musser J.M.;
RT "Progress toward characterization of the group A Streptococcus

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RT metagenome: complete genome sequence of a macrophide-resistant serotype
RT M6 strain.":
RL J. Infect. Dis. 190:727-738(2004).
DR EMBL; CP000003; AAT86334.1; -: Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0008742; F:L-ribulose-phosphate 4-epimerase activity; IEA.
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00596; Aldolase_II; 1.
KW Complete proteome; Isomerase.
SQ SEQUENCE 242 AA; 27224 MW; C47FAFB2DD3737DAF CRC64;

Query Match 59.7%; Score 43; DB 2; Length 242;
Best Local Similarity 72.7%; Pred. No. 53;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IYFGTTFDY 12
Db 121 IYFGTTHADY 131

RESULT 25
Q8P2S7_STRP8 PRELIMINARY; PRT; 255 AA.
ID Q8P2S7_STRP8 PRELIMINARY;
AC Q8P2S7;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Putative L-ribulose 5-phosphate.
GN OrderedLocusNames=spym18_0178;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=301451;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.B., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Betes S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
DR EMBL; AE009967; AAL96979.1; -: Genomic DNA.
DR HSSP; P08203; 1JDI.
DR InterPro; IPR001303; Aldolase_II_N.
DR Pfam; PF00596; Aldolase_II; 1.
KW Complete proteome.
SQ SEQUENCE 255 AA; 28750 MW; E42E2B9B12C3CDED CRC64;

Query Match 59.7%; Score 43; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 56;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IYFGTTFDY 12
Db 134 IYFGTTHADY 144

RESULT 26
Q9EP55_MOUSE PRELIMINARY; PRT; 310 AA.
ID Q9EP55_MOUSE PRELIMINARY;
AC Q9EP55;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE B3 olfactory receptor (Olfactory receptor Olfr710) (Olfactory receptor
DE MOR260-3).
GN Name=Olfr710;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SVJ;
RA Lane R.P., Cutforth T., Young J., Athanasou M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Rose J.A.,
RA Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
RT expression of over 400 genes, extensive alternate splicing and unequal
RT expression levels.";
RL Genome Biol. 4:R71-R71(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=21310002; PubMed=11416212; DOI=10.1073/pnas.131215398;
RA Lane R.P., Cutforth T., Young J., Athanasou M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RT loci.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=21676863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 5:124-133(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=21864068; PubMed=11875048; DOI=10.1093/hmg/11.5.535;
RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
RA Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human olfactory
RT receptor gene families.";
RL Hum. Mol. Genet. 11:535-546(2002).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF312336; AAG45203.1; -: Genomic DNA.
DR EMBL; AY317831; AAG71174.1; -: Genomic DNA.
DR EMBL; AF312334; AAG45191.1; -: Genomic DNA.
DR EMBL; AY073496; AAL61159.1; -: Genomic DNA.
DR Ensembl; ENSMUSG0000045581; Mus musculus.
DR MGI; MGI:3030544; Olfr710.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECPE_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECPE_F1_2; 1.
KW Receptor.
SQ SEQUENCE 310 AA; 35209 MW; F3EDC60C1B5A994 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 310;
Best Local Similarity 63.6%; Pred. No. 69;

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Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFDY 12
|:|:|:|:|
Db 249 IYFYGTTFY 259

RESULT 27

Q983V9_RHIL0 PRELIMINARY; PRT; 342 AA.

AC Q983V9;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ABC transporter, amino acid binding protein.
GN OrderedLocustNames=mlr18149;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFP303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Ideawara K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shingo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RT DNA Res. 7:331-338 (2000).
RL EMBL; BA000012; BMB53771.1; -; Genomic_DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0005215; F:transport activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR005768; Iys Arg Orn bind.
DR InterPro; IPR001311; SBP/glu_receptor.
DR InterPro; IPR001638; SBP_bac_3.
DR SMART; SM00062; PBPb; 1.
DR TIGRfams; TIGR01096; 3A0103603R.1.
KW Complete proteome.
SQ SEQUENCE 342 AA; 36564 MW; F983A7A1FAFBCA2C CRC64;

Query Match 59.7%; Score 43; DB 2; Length 342;
Best Local Similarity 63.6%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTTFDY 11
|:|:|:|:|
Db 114 GANFGTTFYD 124

RESULT 28

O73ME2_TREDE PRELIMINARY; PRT; 360 AA.

AC O73ME2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Conserved domain protein.
GN OrderedLocustNames=TD81566;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=0.1073/pnas.0307639101;
RA Sedshari R., Myers G.S.A., Tettein H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Holt D.H.,
RA Selenget J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,

RA Gebregorgis E., Geer K., Tsagaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajd D., Howell J.K., Pal S., Amin A.,
RA Vashisht P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
DR EMBL; AE017251; AAS12083.1; -; Genomic_DNA.
DR TIGR; TDE1566; -;
KW Complete proteome.
SQ SEQUENCE 360 AA; 41656 MW; 13C4C5F277BA65C8 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 360;
Best Local Similarity 54.5%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIFYGTTFDY 11
|:|:|:|:|
Db 101 GUYYGARYLD 111

RESULT 29

O8K8M4_STRP3 PRELIMINARY; PRT; 372 AA.

AC O8K8M4;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Putative polyacharide biosynthesis protein.
GN Name=rgpg; OrderedLocustNames=Spym3_0207;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301448;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
RL EMBL; AE014140; AAM78814.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR000715; Glyco_trans_4.
DR InterPro; IPR003524; PNAcPept_trans.
DR Pfam; PF00953; Glycos_transf_4_1.
DR PROSITE; PS01348; WRAY_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 372 AA; 40994 MW; 2D48DA70347DB9C2 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 372;
Best Local Similarity 58.3%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIFYGTTFDY 12
|:|:|:|:|
Db 58 GANFGQTFYFSY 69

RESULT 30

O879M1_STRP3 PRELIMINARY; PRT; 389 AA.

AC O879M1;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

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DE Putative competence protein.
GN OrderedLocustNames=SP0213;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301448;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SSI-1 / Serotype M3;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution.";
RL Genome Res. 13:1042-1055(2003).
DR EMBL; BA000034; BAC63308.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR000715; Glyco_trans_4.
DR InterPro; IPR003524; PNACPept_trans.
DR Pfam; PF00953; Glycos_transf_4; 1.
DR PROSITE; PS01348; MRAY_2; UNKNOWN_1.
SQ SEQUENCE 389 AA; 42891 MW; ABE3B0CE89CEECOD CRC64;

Query Match 59.7%; Score 43; DB 2; Length 389;
Best Local Similarity 58.3%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIFYGTYFDY 12
Db 75 GAMFFGQTFYSY 86

RESULT 31
OSXDV6_STRP6 PRELIMINARY; PRT; 389 AA.
AC 05XDV6_
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Undecaprenyl-phosphate alpha-N-acetylglucosaminophosphotransferase
DE (EC 2.7.8.-).
GN OrderedLocustNames=M6_Spy02272;
OS Streptococcus pyogenes (serotype M6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGA510394;
RX PubMed=15272401; DOI=10.1086/422697;
RA Banks D.J., Porcella S.F., Barbican K.D., Beres S.B., Phillips J.E.,
RA Voyich J.M., Deleo F.R., Martin J.M., Somerville G.A., Musser J.M.;
RT "Progress toward characterization of the group A Streptococcus
RT metagenome: complete genome sequence of a macrolide-resistant serotype
RT M6 strain.";
RL M6 strain.
RL J. Infect. Dis. 190:727-738(2004).
DR EMBL; CP000003; AAT8407.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008963; F:phospho-N-acetylmuramoyl-pentapeptide-trans. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR000715; Glyco_trans_4.
DR InterPro; IPR003524; PNACPept_trans.
DR Pfam; PF00953; Glycos_transf_4; 1.
DR PROSITE; PS01348; MRAY_2; UNKNOWN_1.
RW Complete proteome; transferase.
SQ SEQUENCE 389 AA; 42937 MW; 636F7356B84FE081 CRC64;

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Query Match 59.7%; Score 43; DB 2; Length 389;
Best Local Similarity 58.3%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIFYGTYFDY 12
Db 75 GAMFFGQTFYSY 86

RESULT 32
OSXDV6_STRP8 PRELIMINARY; PRT; 389 AA.
AC 09AIG6_
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possibly involved in regulation of genetic competence.
GN Name=ixpg; OrderedLocustNames=SPy0282;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar P.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006494; AAK33354.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR000715; Glyco_trans_4.
DR InterPro; IPR003524; PNACPept_trans.
DR Pfam; PF00953; Glycos_transf_4; 1.
DR PROSITE; PS01348; MRAY_2; UNKNOWN_1.
RW Complete proteome.
SQ SEQUENCE 389 AA; 42891 MW; ABE3B0CE89CEECOD CRC64;

Query Match 59.7%; Score 43; DB 2; Length 389;
Best Local Similarity 58.3%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIFYGTYFDY 12
Db 75 GAMFFGQTFYSY 86

RESULT 33
OSXDV6_STRP8 PRELIMINARY; PRT; 389 AA.
AC 08P2M6_
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative regulator of genetic competence.
GN Name=ixpg; OrderedLocustNames=SPyM18_0270;
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301451;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGA58232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;

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RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A *Streptococcus* strains associated with acute rheumatic fever
RT outbreaks";
RT
RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR EMBL; AE009974; AAL97048.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR000715; Glyco_trans_4.
DR InterPro; IPR003524; PNAcPept_trans.
DR Pfam; PF00953; Glycos_transf_4; 1.
DR PROSITE; PS01348; MRAY_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 389 AA; 42907 MW; 32FE57C5CF34FP44 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 389;
Best Local Similarity 58.3%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIFYGTTYDY 12
| | | | |
Db 75 GAMFFGQTFYSY 86

RESULT 34
09ZK32_HELPJ PRELIMINARY; PRT; 459 AA.
AC 09ZK32;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative.
GN OrderedlocusNames=JHP1110;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteriaceae; Helicobacter.
OX NCBI_TaxID=85963; [1]
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99120557; PubMed=9923662; DOI=10.1038/16495.
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Gaid B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.B., Voris G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori";
RL Nature 397:176-180 (1999).
DR EMBL; AE001538; AAD06682.1; -; Genomic_DNA.
DR PIR; A71849; A71849.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; P:antipporter activity; IEA.
DR GO; GO:0015238; P:drug transporter activity; IEA.
DR GO; GO:0006855; P:multidrug transport; IEA.
DR InterPro; IPR002528; MATE.
DR Pfam; PF01554; MATE; 2.
KW Complete proteome.
SQ SEQUENCE 459 AA; 51643 MW; 15F9911F7F19B84E CRC64;

Query Match 59.7%; Score 43; DB 2; Length 459;
Best Local Similarity 70.0%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GIFYGTTYDY 10
| | | | |
Db 325 GIFYGAYYF 324

RESULT 35
061BF5_CAEBR PRELIMINARY; PRT; 492 AA.
ID 061BF5_CAEBR PRELIMINARY; PRT; 492 AA.
AC 061BF5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG13373.
GN Name=CBG13373;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6238; [1]
RN
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAACO100064; CAB57795.1; -; Genomic_DNA.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011583; Chitinase_II.
DR InterPro; IPR001223; Glyco_hydro_18.
DR Pfam; PF00704; Glyco_hydro_18; 2.
DR SMART; SM00636; Glyco_18; 1.
KW Hypothetical protein.
SQ SEQUENCE 492 AA; 57010 MW; 60A3531238BC4B40 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 492;
Best Local Similarity 77.8%; Pred. No. 11e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIFYGTTY 9
| | | | |
Db 249 GVAFYGTTY 257

RESULT 36
041289_GIBZE PRELIMINARY; PRT; 799 AA.
ID 041289_GIBZE PRELIMINARY; PRT; 799 AA.
AC 041289;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG08669.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533; [1]
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choquel Y., Collymore A., Cook A., Cooke P., Corum B., DeRellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gaidyna S., Gierke S., Graham L., Grand-Pierre N., Hatz N.,
RA Hagopian D., Hages B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kella C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Muccio E., McCarthy M., Meldrum J., Menes L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Piere N., Purcell S.,
RA Rachenk A., Ramasamy U., Raymond C., Reta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talama J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

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CC      preliminary data.
DR      EMBL: AAC01000349; EAA72259.1; -, Genomic_DNA.
KN      Hypothetical protein.
SQ      SEQUENCE 799 AA; 90306 MW; CD41C1B61E378606 CRC64;

Query Match
Best Local Similarity 59.7%; Score 43; DB 2; Length 799;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GIFYGYGYFPD 12
Db      369 GIHFTGTWYADY 380

RESULT 37
Q73ME8 TREDE PRELIMINARY; PRT; 1126 AA.
AC      Q73ME8;
DT      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE      YD repeat protein.
GN      OrderedLocustNames=TDE1560;
OS      Treponema denticola.
OC      Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX      NCBI_TaxID=158;
[1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=ATCC 35405 / DSM 14222;
RX      PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA      Dodson R.J., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA      Seehadri R., Davidson T.M., Debey R.T., Fouts D.E., Haft D.H.,
RA      Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA      Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA      Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA      Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA      Vaishish P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA      Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT      "Comparison of the genome of the oral pathogen Treponema denticola
RT      with other spirochete genomes.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR      EMBL: AE017251; AAS12077.1; -, Genomic_DNA.
DR      TIGR: TDE1560; -.
DR      InterPro: IPR006530; YD.
DR      Pfam: PF05593; Rhs_repeat; 5.
DR      TIGRFAMs: TIGR01643; YD_repeat_2x; 3.
KW      Complete proteome.
SQ      SEQUENCE 1126 AA; 129197 MW; C6F34E209PD6AD03 CRC64;

Query Match
Best Local Similarity 59.7%; Score 43; DB 2; Length 1126;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GIFYGYGYFPD 11
Db      866 GUYGYGARYLD 876

RESULT 38
Q73L45 TREDE PRELIMINARY; PRT; 1140 AA.
AC      Q73L45;
DT      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE      YD repeat protein.
GN      OrderedLocustNames=TDE2020;
OS      Treponema denticola.
OC      Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX      NCBI_TaxID=158;
[1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=ATCC 35405 / DSM 14222;
RX      PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA      Dodson R.J., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA      Seehadri R., Davidson T.M., Debey R.T., Fouts D.E., Haft D.H.,
RA      Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA      Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA      Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA      Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA      Vaishish P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA      Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT      "Comparison of the genome of the oral pathogen Treponema denticola
RT      with other spirochete genomes.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR      EMBL: AE017252; AAS12536.1; -, Genomic_DNA.
DR      TIGR: TDE2022; -.
DR      InterPro: IPR006530; YD.
DR      Pfam: PF05593; Rhs_repeat; 7.
DR      TIGRFAMs: TIGR01643; YD_repeat_2x; 5.
KW      Complete proteome.
SQ      SEQUENCE 1488 AA; 170910 MW; 7052CEADf162EDB6 CRC64;

Query Match
Best Local Similarity 59.7%; Score 43; DB 2; Length 1488;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GIFYGYGYFPD 11
Db      1225 GUYGYGARYLD 1235

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RX      PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA      Seehadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA      Dodson R.J., Davidson T.M., Debey R.T., Fouts D.E., Haft D.H.,
RA      Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA      Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA      Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA      Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA      Vaishish P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA      Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT      "Comparison of the genome of the oral pathogen Treponema denticola
RT      with other spirochete genomes.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR      EMBL: AE017252; AAS12534.1; -, Genomic_DNA.
DR      TIGR: TDE2020; -.
DR      InterPro: IPR006530; YD.
DR      Pfam: PF05593; Rhs_repeat; 6.
DR      TIGRFAMs: TIGR01643; YD_repeat_2x; 4.
KW      Complete proteome.
SQ      SEQUENCE 1140 AA; 130329 MW; AAB083C3BC1CA2MA CRC64;

Query Match
Best Local Similarity 59.7%; Score 43; DB 2; Length 1140;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GIFYGYGYFPD 11
Db      868 GUYGYGARYLD 878

RESULT 39
Q73L43 TREDE PRELIMINARY; PRT; 1488 AA.
AC      Q73L43;
DT      05-JUL-2004 (TREMBLrel. 27, Created)
DT      05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE      YD repeat protein.
GN      OrderedLocustNames=TDE2022;
OS      Treponema denticola.
OC      Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX      NCBI_TaxID=158;
[1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=ATCC 35405 / DSM 14222;
RX      PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA      Dodson R.J., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA      Seehadri R., Davidson T.M., Debey R.T., Fouts D.E., Haft D.H.,
RA      Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA      Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA      Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA      Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA      Vaishish P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA      Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT      "Comparison of the genome of the oral pathogen Treponema denticola
RT      with other spirochete genomes.";
RL      Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR      EMBL: AE017252; AAS12536.1; -, Genomic_DNA.
DR      TIGR: TDE2022; -.
DR      InterPro: IPR006530; YD.
DR      Pfam: PF05593; Rhs_repeat; 7.
DR      TIGRFAMs: TIGR01643; YD_repeat_2x; 5.
KW      Complete proteome.
SQ      SEQUENCE 1488 AA; 170910 MW; 7052CEADf162EDB6 CRC64;

Query Match
Best Local Similarity 59.7%; Score 43; DB 2; Length 1488;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GIFYGYGYFPD 11
Db      1225 GUYGYGARYLD 1235

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RESULT 40
O73MF0 TREDE PRELIMINARY; PRT; 3320 AA.
ID O73MF0;
AC O73MF0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE YD repeat protein.
GN OrderedlocusNames=TDE1558;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DebRoy R.T., Fouts D.E., Haft D.H.,
RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebreyes G., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashishth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
RT with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR EMBL; AF017251; AAS12075.1; -; Genomic_DNA.
DR TIGR; TDE1558; -
DR GO; GO:0008305; C:integrin complex; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPR000413; Integrin_alpha.
DR InterPro; IPR006530; YD.
DR Pfam; PF01839; FG-GAP; 2.
DR Pfam; PF05593; RMS_repeat; 5.
DR TIGRFAMs; TIGR01643; YD_repeat_2x; 4.
KW Complete proteome.
SQ SEQUENCE 3320 AA; 377975 MW; 20DCBFI39415306D CRC64;

Query Match 59.7%; Score 43; DB 2; Length 3320;
Best Local Similarity 54.5%; Pred. No. 8.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYFGTTFD 11
|:|:|
Db 3040 GLYTGARYLD 3050

RESULT 41
O60QT7 CAEBR PRELIMINARY; PRT; 336 AA.
ID O60QT7;
AC O60QT7;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG21682 (Fragment).
GN Name=CBG21682;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC0100124; CAF74032.1; -; Genomic_DNA.
DR InterPro; IPR003839; DUF215.
DR Pfam; PF02688; DUF215; 1.
KW Hypothetical protein.
FT NON_TER 336

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SQ SEQUENCE 336 AA; 39216 MW; DED8E982DC9B7E2 CRC64;

Query Match 59.0%; Score 42.5; DB 2; Length 336;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 IFYGTTFD 12
|:|:|
Db 278 IFYGTTFD 289

RESULT 42
O950Y0 TETTH PRELIMINARY; PRT; 89 AA.
ID O950Y0;
AC O950Y0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Ymf70.
GN Name=ymf70;
OS Tetrahymena thermophila.
OC Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenida; Tetrahymenidae; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SB210;
RX MEDLINE=22514407; PubMed=12626709; DOI=10.1093/nar/gkg270;
RA Brunk C.F., Lee L.C., Tran A.B., Li J.;
RT "Complete sequence of the mitochondrial genome of Tetrahymena
RT thermophila and comparative methods for identifying highly divergent
RT genes.";
RL Nucleic Acids Res. 31:1673-1682(2003).
DR EMBL; AF396436; AAK77605.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
SQ SEQUENCE 89 AA; 10882 MW; A58BB9FAB910B65 CRC64;

Query Match 58.3%; Score 42; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 FYGTTFD 12
|:|:|
Db 59 FYGTTFD 67

RESULT 43
O9XMR7 TETPY PRELIMINARY; PRT; 89 AA.
ID O9XMR7;
AC O9XMR7;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Orf89.
GN Name=orf89;
OS Tetrahymena pyriformis.
OC Mitochondrion.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenida; Tetrahymenidae; Tetrahymena.
OX NCBI_TaxID=5908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20181866; PubMed=10715208; DOI=10.1006/jmbi.2000.3530;
RA Edqvist J., Burger G., Gray M.W.;
RT "Expression of mitochondrial protein-coding genes in Tetrahymena
RT pyriformis.";
RL J. Mol. Biol. 297:381-393(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20181865; PubMed=10715207; DOI=10.1006/jmbi.2000.3529;
RA Burger G., Zhu Y., Littlejohn T.G., Greenwood S.J., Schnare M.N.,

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RA Lang B.F., Gray M.W.,
 RT "Complete sequence of the mitochondrial genome of Tetrahymena
 RL pyloformia and comparison with Paramacium aurelia mitochondrial DNA."
 DR J. Mol. Biol. 297:365-380(2000).
 DR EMBL; AF160864; AAD1954.1; -; Genomic_DNA.
 KW GO; GO:0005739; C:mitochondrion; IEA.
 SQ SEQUENCE 89 AA; 10899 MW; 2B8727697FAE1BBF CRC64;

Query Match 58.3%; Score 42; DB 2; Length 89;
 Best Local Similarity 77.8%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 FYGTYFPDY 12
 |||||
 Db 59 FYKNTYFPDY 67

RESULT 44

Q7P319 FUSNV PRELIMINARY; PRT; 92 AA.
 AC Q7P319_2
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=FWV1517;
 OS Fusoobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusoobacteriia; Fusoobacteriales; Fusoobacteriaceae;
 CC Fusoobacterium.
 RX NCBI_TaxID=209882;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 49256;
 RA Karpachal V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AABF0100013; EAA24851.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 92 AA; 11306 MW; 400C16430B84646A CRC64;

Query Match 58.3%; Score 42; DB 2; Length 92;
 Best Local Similarity 54.5%; Pred. No. 28;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTYFPD 11
 |||||
 Db 45 GINTYGNITYFE 55

RESULT 45

O81SP5 BACAN PRELIMINARY; PRT; 103 AA.
 ID O81SP5_2
 AC O81SP5_2
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Lipoprotein, putative.
 GN OrderedLocusNames=BA1601, BAS1485, GBAA1601;
 OS Bacillus anthracis.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 RX NCBI_TaxID=1392;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ames / isolate Porton;
 DR MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Bailly L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

RA Holtzapfel E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nielsen W.C.,
 RA Hazen A.C., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.B., Fraser C.M.,
 RA "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria."
 RL Nature 423:81-86(2003).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ames / isolate 0581;
 RA Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.,
 RT "Bacillus anthracis comparative genomics."
 RL Submitted (MAY-2004) to the EMBL/Genbank/DBJ databases.
 RN [3]

RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
 RC STRAIN=Stearne; Bruce D., Chalacombe J.F., Gilna P., Han C., Hill K.,
 RA Bretlin T.S., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.,
 RT "Complete genome sequence of Bacillus anthracis Sterne."
 RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AE017029; AAP25536.1; -; Genomic_DNA.
 DR EMBL; AE017334; AAT30700.1; -; Genomic_DNA.
 DR EMBL; AE017225; AAT53805.1; -; Genomic_DNA.
 DR TIGR; BAI601; -.
 DR TIGR; GBA1601; -.
 KW Complete proteome; Lipoprotein.
 SQ SEQUENCE 103 AA; 11226 MW; 72F63414963B5C72 CRC64;

Query Match 58.3%; Score 42; DB 2; Length 103;
 Best Local Similarity 70.0%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTYFP 10
 |||||
 Db 59 GHYFGTYFP 68

RESULT 46

O6Y5L0 9APHY PRELIMINARY; PRT; 120 AA.
 ID O6Y5L0_2
 AC O6Y5L0_2
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Mitochondrial intermediate peptidase (EC 3.4.24.55) (Fragment).
 GN Name=mip;
 OS Lenticaria sp. TJ00/28.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Gomphaceae; Lenticaria.
 RX NCBI_TaxID=222707;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=14761798; DOI=10.1016/j.fgb.2003.11.008;
 RA James T.Y., Kues U., Rehner S.A., Vilgalys R.,
 RT "Evolution of the gene encoding mitochondrial intermediate peptidase
 RT and its cosegregation with the A mating-type locus of mushroom
 RT fungi."
 RL Fungal Genet. Biol. 41:381-390(2004).
 DR EMBL; AY179578; AAO61517.1; -; Genomic_DNA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004243; F:mitochondrial intermediate peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001567; Pept_M3A_M3B.
 DR Pfam; PF01432; Peptidase_M5; I.
 KW Hydrolase.

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FT  NON TER      1      1
FT  NON TER      120     120
SQ  SEQUENCE     120 AA; 13178 MW;  CADD3A5A724ED120 CRC64;

Query Match
Best Local Similarity 58.3%; Score 42; DB 2; Length 120;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 IYFYGTYPDY 12
DB      86 IYSGATYYSY 96

RESULT 47
Q8RCV8_FUSNN PRELIMINARY; PRT; 135 AA.
ID  Q8RCV8_FUSNN PRELIMINARY; PRT; 135 AA.
AC  Q8RCV8;
DT  01-JUN-2002 (TREMBLrel. 21, Created)
DT  01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE  Hypothetical protein FN0169.
GN  OrderedLocustNames=FN0169;
OC  Fusobacterium nucleatum (subsp. nucleatum).
OC  Bacteria; Fusobacteriales; Fusobacteriaceae;
OC  Fusobacterium.
OX  NCBI_Taxid=76856;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC 25586;
RX  MEDLINE=2186394; PubMed=11889109;
RA  DOI=10.1128/JB.184.7.2005-2018.2002;
RA  Kapteitl V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA  Bhattacharya A., Battman A., Gardner W., Grechkin G., Zhu L.,
RA  Vassileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA  Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA  Fongstein M., Kyriades N.C., Overbeek R.,
RA  "Genome sequence and analysis of the oral bacterium Fusobacterium
RT  nucleatum strain ATCC 25586."
RT  J. Bacteriol. 184(2005-2018(2002)).
DR  EMBL; AE009951; AAL94375.1; -; Genomic DNA.
SQ  COMPLETE proteome; Hypothetical protein.
SQ  SEQUENCE 135 AA; 16507 MW; A27PBD3179D2E865 CRC64;

Query Match
Best Local Similarity 58.3%; Score 42; DB 2; Length 135;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 GIFYGTYPDY 11
DB      45 GINYGYNTYFE 55

RESULT 48
Q728W2_DESVH PRELIMINARY; PRT; 274 AA.
ID  Q728W2_DESVH PRELIMINARY; PRT; 274 AA.
AC  Q728W2;
DT  05-JUL-2004 (TREMBLrel. 27, Created)
DT  05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE  Histidinol-phosphatase, putative.
GN  OrderedLocustNames=DVU2490;
OS  Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS  8303).
OC  Bacteria; Proteobacteria; DeltaProteobacteria; Desulfovibrionales;
OC  Desulfovibrionaceae; Desulfovibrio.
OX  NCBI_Taxid=882;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  PubMed=15077118; DOI=10.1038/nbt959;
RA  Heidelberg J.F., Seshadri R., Haveman S.A., Heme C.L., Paulsen I.T.,
RA  Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA  Daugherty S.C., Deboy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA  Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,

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RA  Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
RA  Dimitrov G., Hane M., Tran K., Khouri H.M., Gill J., Uterback T.R.,
RA  Feldblum T.V., Wall J.D., Voordouw G., Fraser C.M.,
RT  "The genome sequence of the anaerobic, sulfate-reducing bacterium
RT  Desulfovibrio vulgaris Hildenborough."
RT  Nat. Biotechnol. 22:554-559(2004).
RL  EMBL; AE017317; AAS96962.1; -; Genomic DNA.
DR  TIGR; DVU2490; -.
DR  GO; GO:0004401; F:histidinol-phosphatase activity; IEA.
DR  GO; GO:0000105; P:histidine biosynthesis; IEA.
DR  InterPro; IPR010140; PHP_fam.
DR  Pfam; PF02811; PHP_1.
DR  TIGRFAMs; TIGR01856; hisJ_fam; 1.
DR  Complete proteome.
SQ  SEQUENCE 274 AA; 31060 MW; 7978D96B22C75B4 CRC64;

Query Match
Best Local Similarity 58.3%; Score 42; DB 2; Length 274;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 GIFYGTYPDY 12
DB      111 GIHFLGTWGPDY 122

RESULT 49
Q8ETW2_HUMAN PRELIMINARY; PRT; 341 AA.
ID  Q8ETW2_HUMAN PRELIMINARY; PRT; 341 AA.
AC  Q8ETW2;
DT  01-JUN-2003 (TREMBLrel. 24, Created)
DT  01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT  01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE  Full-length cDNA clone CS0D1087YN05 of Placenta of Homo sapiens
DE  (human) (Fragment).
OS  Homo sapiens (Human).
OS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC  Homo.
OX  NCBI_Taxid=9606;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Placenta;
RA  Li W.B., Gruber C., Jessee J., Polayes D.,
RL  Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Placenta;
RA  Genoscope;
RL  Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.
DR  EMBL; BX248292; CAD62620.1; -; mRNA.
DR  Ensembl; ENSG00000063761; Homo sapiens.
DR  GO; GO:0005524; P:ATP binding; IEA.
DR  GO; GO:0004672; P:protein kinase activity; IEA.
DR  GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR  InterPro; IPR004147; ABC_1.
DR  InterPro; IPR000719; Prot_kinase.
DR  Pfam; PF03109; ABC1, 1.
DR  PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
FT  NON TER      1      1
FT  NON TER      341     341
SQ  SEQUENCE 341 AA; 38764 MW; 28BE7D460A5D896 CRC64;

Query Match
Best Local Similarity 58.3%; Score 42; DB 2; Length 341;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GIFYGTYPDY 11
DB      40 GIFYSNKRLD 50

RESULT 50

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O9UIE6 HUMAN
ID O9UIE6 HUMAN PRELIMINARY; PRT; 455 AA.
AC O9UIE6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN Name=ADCK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OC NCBI_TaxID=9606;
OX
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rowen L., Madan A., Qin S., Abbasi N., Baradaran L., Birditt B.,
RA Bloom S., Dots M., Dickhoff R., Fleetwood P., Harrison G., James R.,
RA Kaur A., Madan A., Owen M.P., Ratcliffe A., Shaffer T., Hood L.,
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC008372; AAF23326.1; -; Genomic DNA.
DR Ensembl; ENSG0000063761; Homo sapiens.
DR HGNC; HGNC:19038; ADCK1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR004147; ABC_1.
DR InterPro; IPR000719; Prot_Kinase.
DR Pfam; PF03109; ABC1; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
KW Hypothetical protein.
SQ
SEQUENCE 455 AA; 51999 MW; E2B3FD7B4E5AAC7C CRC64;

Query Match 58.3%; Score 42; DB 2; Length 455;
Best Local Similarity 63.6%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1 GIYPYGTTFD 11
|||
Db 20 GIYPYSNKYLD 30

```

Search completed: January 17, 2006, 12:05:42
 Job time : 95.6364 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:50:24 : Search time 20.7273 Seconds
(without alignments)
47.865 Million cell updates/sec

Title: US-10-665-658-12

Perfect score: 72

Sequence: 1 GIFYGTYFPD 12

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5 COMB.pep:*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/prodata/1/iaa/H.COMB.pep:*
4: /cgn2_6/prodata/1/iaa/PCUS.COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PC.COMB.pep:*
6: /cgn2_6/prodata/1/iaa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	12	2	US-08-974-899-12
2	72	100.0	12	2	US-09-795-798-12
3	72	100.0	116	2	US-09-027-449-50
4	72	100.0	116	2	US-08-804-444-50
5	72	100.0	116	2	US-09-026-985-50
6	72	100.0	116	2	US-09-121-952A-50
7	72	100.0	116	2	US-09-234-340A-50
8	72	100.0	116	2	US-09-355-014-50
9	72	100.0	121	2	US-08-974-899-4
10	72	100.0	121	2	US-08-974-899-4
11	72	100.0	121	2	US-08-974-899-24
12	72	100.0	121	2	US-09-795-798-4
13	72	100.0	121	2	US-09-795-798-4
14	72	100.0	121	2	US-09-795-798-24
15	72	100.0	121	2	US-08-497-112-26
16	72	100.0	120	1	US-08-497-112-28
17	72	100.0	120	1	US-08-497-112-28
18	72	100.0	120	1	US-08-497-112-28
19	72	100.0	120	1	US-08-497-112-28
20	72	100.0	120	1	US-08-497-112-28
21	72	100.0	120	1	US-08-497-112-28
22	72	100.0	120	1	US-08-497-112-28
23	72	100.0	120	1	US-08-497-112-28
24	72	100.0	120	1	US-08-497-112-28
25	72	100.0	120	1	US-08-497-112-28
26	72	100.0	120	1	US-08-497-112-28
27	72	100.0	120	1	US-08-497-112-28

28	43	59.7	234	2	US-09-583-110-4749	Sequence 4749, Ap
29	43	59.7	236	2	US-09-107-433-3704	Sequence 3704, Ap
30	42	58.3	142	1	US-08-678-194-8	Sequence 8, Appl1
31	42	58.3	142	2	US-08-890-011-8	Sequence 8, Appl1
32	42	58.3	142	2	US-09-262-724-8	Sequence 4012, Ap
33	42	58.3	142	2	US-09-621-976-4012	Sequence 4, Appl1
34	42	58.3	353	2	US-09-203-958A-8	Sequence 5825, A
35	41.5	57.6	26	2	US-09-270-767-58255	Sequence 7, Appl1
36	39	54.2	10	2	US-09-406-535-7	Sequence 2, Appl1
37	39	54.2	119	2	US-09-406-535-2	Sequence 214, App
38	39	54.2	121	2	US-10-014-012-214	Sequence 213, App
39	39	54.2	122	2	US-10-014-012-213	Sequence 7, Appl1
40	39	54.2	142	1	US-08-860-174A-7	Sequence 12, Appl
41	39	54.2	274	1	US-08-860-174A-12	Sequence 10, Appl
42	39	54.2	282	1	US-08-860-174A-10	Sequence 3513, Ap
43	39	54.2	486	2	US-09-540-236-3513	Sequence 2, Appl1
44	39	54.2	621	2	US-09-514-245-2	Sequence 2, Appl1
45	39	54.2	621	2	US-09-537-120-2	Sequence 55, Appl
46	38	52.8	18	2	US-09-563-222C-55	Sequence 21665, A
47	38	52.8	95	2	US-09-248-796A-21665	Sequence 14, Appl
48	38	52.8	132	2	US-08-434-000A-14	Sequence 14, Appl
49	38	52.8	132	2	US-09-312-157-14	Sequence 14, Appl
50	38	52.8	132	2	US-09-717-888-14	Sequence 14914, A
51	38	52.8	377	2	US-09-902-540-14914	Sequence 4768, Ap
52	38	52.8	468	2	US-09-134-000C-4768	Sequence 5655, Ap
53	38	52.8	800	2	US-09-134-001C-5655	Sequence 6, Appl1
54	38	52.8	915	2	US-09-817-514A-6	Sequence 12, Appl
55	38	52.8	954	2	US-09-251-645-12	Sequence 61, Appl
56	38	52.8	1043	2	US-08-851-567B-61	Sequence 125, App
57	37	51.4	13	2	US-08-908-469-58	Sequence 125, App
58	37	51.4	14	2	US-08-908-469-129	Sequence 125, App
59	37	51.4	19	2	US-09-563-222C-61	Sequence 61, Appl
60	37	51.4	21	1	US-08-471-780C-125	Sequence 125, App
61	37	51.4	21	1	US-08-467-282B-125	Sequence 125, App
62	37	51.4	21	1	US-08-471-282B-125	Sequence 125, App
63	37	51.4	21	1	US-08-466-710C-125	Sequence 125, App
64	37	51.4	21	1	US-08-468-739C-125	Sequence 125, App
65	37	51.4	21	2	US-09-293-769A-125	Sequence 114, App
66	37	51.4	118	2	US-08-908-469-116	Sequence 116, App
67	37	51.4	118	2	US-08-908-469-116	Sequence 118, App
68	37	51.4	118	2	US-08-908-469-118	Sequence 13, Appl
69	37	51.4	121	2	US-08-537-871A-13	Sequence 17, Appl
70	37	51.4	122	2	US-09-868-352-17	Sequence 18, Appl
71	37	51.4	137	1	US-08-379-057-18	Sequence 17, Appl
72	37	51.4	367	1	US-08-655-704B-17	Sequence 4512, Ap
73	37	51.4	367	2	US-09-107-755-17	Sequence 11657, A
74	37	51.4	482	2	US-09-107-532A-4512	Sequence 24056, A
75	37	51.4	500	2	US-09-949-016-11697	Sequence 5, Appl1
76	37	51.4	555	2	US-09-252-991A-24056	Sequence 16, Appl
77	37	51.4	613	2	US-09-149-727-5	Sequence 2, Appl1
78	37	51.4	613	2	US-09-270-957-16	Sequence 5291, Ap
79	37	51.4	651	2	US-09-715-858-2	Sequence 74, Appl
80	37	51.4	735	2	US-09-999-833A-74	Sequence 4249, Ap
81	37	51.4	735	2	US-10-020-445A-74	Sequence 6370, Ap
82	37	51.4	897	2	US-09-543-681A-4249	Sequence 8, Appl1
83	37	51.4	909	2	US-09-949-016-6370	Sequence 12, Appl
84	37	51.4	919	1	US-08-553-497A-12	Sequence 52, Appl
85	36.5	50.7	119	1	US-08-553-497A-12	Sequence 52, Appl
86	36.5	50.7	119	1	US-08-553-497A-12	Sequence 52, Appl
87	36	50.0	19	2	US-09-563-222C-55	Sequence 24732, A
88	36	50.0	75	2	US-09-248-796A-24732	Sequence 1672, Ap
89	36	50.0	143	2	US-09-069-628-7	Sequence 1672, Ap
90	36	50.0	145	2	US-09-702-705-1672	Sequence 1672, Ap
91	36	50.0	145	2	US-09-736-457-1672	Sequence 1672, Ap
92	36	50.0	145	2	US-09-671-325-1672	Sequence 1672, Ap
93	36	50.0	145	2	US-09-658-824-1672	Sequence 1672, Ap
94	36	50.0	145	2	US-10-017-754-1672	Sequence 1672, Ap
95	36	50.0	145	2	US-09-651-563-1672	Sequence 2256, A
96	36	50.0	169	2	US-09-248-796A-2256	Sequence 4887, Ap
97	36	50.0	194	2	US-09-328-352-4887	Sequence 2961, Ap
98	36	50.0	243	2	US-09-134-001C-2961	Sequence 202, App
99	36	50.0	257	2	US-09-830-230A-202	Sequence 8, Appl1
100	36	50.0	288	2	US-09-095-758-8	

101	36	50.0	288	2	US-09-422-968-8	Sequence 8, Appl1	174	35	48.6	118	2	US-08-913-555-11	Sequence 11, Appl1
102	36	50.0	288	2	US-09-708-015A-8	Sequence 8, Appl1	175	35	48.6	119	1	US-08-192-102-5	Sequence 5, Appl1
103	36	50.0	303	2	US-09-543-681A-7946	Sequence 7946, Ap	176	35	48.6	119	1	US-08-324-799-5	Sequence 5, Appl1
104	36	50.0	310	2	US-09-830-230A-201	Sequence 201, App	177	35	48.6	119	1	US-08-360-125-5	Sequence 5, Appl1
105	36	50.0	315	2	US-09-602-787A-454	Sequence 454, App	178	35	48.6	119	1	US-08-450-578-5	Sequence 5, Appl1
106	36	50.0	389	1	US-07-939-501A-1	Sequence 1, Appl1	179	35	48.6	119	1	US-08-318-157B-12	Sequence 12, Appl1
107	36	50.0	389	2	US-08-448-398-7	Sequence 7, Appl1	180	35	48.6	119	1	US-08-318-157B-13	Sequence 13, Appl1
108	36	50.0	391	2	US-09-242-095-4	Sequence 4, Appl1	181	35	48.6	119	1	US-08-318-157B-14	Sequence 14, Appl1
109	36	50.0	392	2	US-09-489-039A-7806	Sequence 7806, Ap	182	35	48.6	119	1	US-08-318-157B-15	Sequence 15, Appl1
110	36	50.0	417	2	US-09-276-400-5	Sequence 5, Appl1	183	35	48.6	119	1	US-08-192-861A-5	Sequence 5, Appl1
111	36	50.0	417	2	US-09-242-095-2	Sequence 2, Appl1	184	35	48.6	119	1	US-09-017-628-5	Sequence 5, Appl1
112	36	50.0	417	2	US-09-448-076-5	Sequence 5, Appl1	185	35	48.6	119	1	US-09-014-880-5	Sequence 5, Appl1
113	36	50.0	417	2	US-09-702-572-5	Sequence 5, Appl1	186	35	48.6	119	2	US-08-851-362D-42	Sequence 42, Appl1
114	36	50.0	423	1	US-07-939-501A-10	Sequence 10, Appl1	187	35	48.6	119	2	US-08-133-119-5	Sequence 5, Appl1
115	36	50.0	423	1	US-07-939-501A-12	Sequence 12, Appl1	188	35	48.6	119	2	US-08-192-093A-5	Sequence 5, Appl1
116	36	50.0	431	2	US-09-949-016-10182	Sequence 10182, A	189	35	48.6	119	2	US-08-450-363-5	Sequence 5, Appl1
117	36	50.0	445	2	US-09-282-218A-12	Sequence 12, Appl1	190	35	48.6	119	2	US-09-253-794-12	Sequence 12, Appl1
118	36	50.0	461	1	US-08-672-814D-2	Sequence 2, Appl1	191	35	48.6	119	2	US-09-253-794-13	Sequence 13, Appl1
119	36	50.0	461	2	US-09-333-696-2	Sequence 2, Appl1	192	35	48.6	119	2	US-09-253-794-14	Sequence 14, Appl1
120	36	50.0	461	2	US-09-282-218A-2	Sequence 2, Appl1	193	35	48.6	119	2	US-09-253-794-15	Sequence 15, Appl1
121	36	50.0	471	2	US-09-106-464-2	Sequence 2, Appl1	194	35	48.6	119	2	US-09-253-794-17	Sequence 17, Appl1
122	36	50.0	471	2	US-09-107-532A-4028	Sequence 4028, Ap	195	35	48.6	119	2	US-09-467-903-5	Sequence 5, Appl1
123	36	50.0	484	2	US-09-602-787A-452	Sequence 452, App	196	35	48.6	119	2	US-09-756-301B-5	Sequence 5, Appl1
124	36	50.0	516	2	US-09-949-016-11239	Sequence 11239, A	197	35	48.6	119	2	US-09-756-301B-5	Sequence 5, Appl1
125	36	50.0	536	1	US-08-208-036-17	Sequence 17, Appl1	198	35	48.6	119	2	US-08-360-125-11	Sequence 11, Appl1
126	36	50.0	593	1	US-08-428-823-17	Sequence 17, Appl1	199	35	48.6	122	1	US-08-450-578-11	Sequence 11, Appl1
127	36	50.0	694	2	US-10-029-180-22	Sequence 22, Appl1	200	35	48.6	122	1	US-09-017-628-11	Sequence 11, Appl1
128	36	50.0	876	1	US-08-633-476-2	Sequence 2, Appl1	201	35	48.6	122	1	US-09-014-880-11	Sequence 11, Appl1
129	36	50.0	877	1	US-08-208-036-14	Sequence 14, Appl1	202	35	48.6	122	1	US-08-450-363-11	Sequence 11, Appl1
130	36	50.0	877	1	US-08-428-823-14	Sequence 14, Appl1	203	35	48.6	122	2	US-08-466-193-7	Sequence 7, Appl1
131	35	48.6	14	1	US-08-360-125-23	Sequence 23, Appl1	204	35	48.6	122	2	US-09-467-903-11	Sequence 11, Appl1
132	35	48.6	14	1	US-08-450-578-23	Sequence 23, Appl1	205	35	48.6	137	2	US-08-466-153B-7	Sequence 7, Appl1
133	35	48.6	14	1	US-09-017-628-23	Sequence 23, Appl1	206	35	48.6	137	2	US-08-466-163B-7	Sequence 7, Appl1
134	35	48.6	14	1	US-09-014-880-23	Sequence 23, Appl1	207	35	48.6	137	2	US-09-802-096-7	Sequence 7, Appl1
135	35	48.6	14	2	US-08-450-363-23	Sequence 23, Appl1	208	35	48.6	137	2	US-09-802-077-7	Sequence 7, Appl1
136	35	48.6	14	2	US-09-467-903-23	Sequence 23, Appl1	209	35	48.6	137	2	US-09-925-179-7	Sequence 7, Appl1
137	35	48.6	58	2	US-08-858-207A-385	Sequence 385, App	210	35	48.6	150	2	US-09-582-337-14	Sequence 14, Appl1
138	35	48.6	76	2	US-08-851-362D-19	Sequence 19, Appl1	211	35	48.6	172	2	US-09-467-087-7	Sequence 7, Appl1
139	35	48.6	76	2	US-09-472-087-85	Sequence 85, Appl1	212	35	48.6	152	2	US-09-472-087-7	Sequence 7, Appl1
140	35	48.6	82	2	US-09-134-000C-3963	Sequence 3963, Ap	213	35	48.6	172	2	US-09-472-087-86	Sequence 86, Appl1
141	35	48.6	97	2	US-08-851-362D-29	Sequence 29, Appl1	214	35	48.6	200	2	US-09-270-767-4543	Sequence 42543, A
142	35	48.6	97	2	US-09-905-243-16	Sequence 16, Appl1	215	35	48.6	207	2	US-09-270-767-6161	Sequence 62161, A
143	35	48.6	98	1	US-08-478-039-75	Sequence 75, Appl1	216	35	48.6	212	2	US-09-902-540-15355	Sequence 15355, A
144	35	48.6	98	1	US-08-476-349A-75	Sequence 75, Appl1	217	35	48.6	241	2	US-09-710-279-3148	Sequence 3148, Ap
145	35	48.6	98	2	US-08-851-362D-23	Sequence 23, Appl1	218	35	48.6	245	2	US-09-202-548B-9	Sequence 9, Appl1
146	35	48.6	98	2	US-10-194-975-35	Sequence 35, Appl1	219	35	48.6	245	2	US-09-942-858-9	Sequence 9, Appl1
147	35	48.6	98	2	US-10-330-613A-78	Sequence 78, Appl1	220	35	48.6	245	2	US-10-461-180-9	Sequence 9, Appl1
148	35	48.6	99	2	US-10-194-975-36	Sequence 36, Appl1	221	35	48.6	258	2	US-09-134-001C-5336	Sequence 3536, Ap
149	35	48.6	99	2	US-10-194-975-38	Sequence 38, Appl1	222	35	48.6	259	2	US-09-134-001C-4468	Sequence 4468, Ap
150	35	48.6	99	2	US-10-194-975-39	Sequence 39, Appl1	223	35	48.6	278	2	US-09-260-527-3	Sequence 3, Appl1
151	35	48.6	99	2	US-10-194-975-41	Sequence 41, Appl1	224	35	48.6	282	2	US-09-583-110-3800	Sequence 3800, Ap
152	35	48.6	99	2	US-10-330-613A-45	Sequence 45, Appl1	225	35	48.6	284	2	US-09-095-758-5	Sequence 5, Appl1
153	35	48.6	99	2	US-10-330-613A-46	Sequence 46, Appl1	226	35	48.6	284	2	US-09-422-968-5	Sequence 5, Appl1
154	35	48.6	99	2	US-10-330-613A-57	Sequence 57, Appl1	227	35	48.6	284	2	US-09-708-015A-5	Sequence 5, Appl1
155	35	48.6	99	2	US-10-330-613A-65	Sequence 65, Appl1	228	35	48.6	287	2	US-09-147-433-4120	Sequence 4120, Ap
156	35	48.6	99	2	US-10-330-613A-73	Sequence 73, Appl1	229	35	48.6	298	2	US-09-949-016-7653	Sequence 7653, Ap
157	35	48.6	99	2	US-10-330-613A-73	Sequence 73, Appl1	230	35	48.6	317	2	US-09-902-540-11936	Sequence 11936, A
158	35	48.6	117	1	US-08-290-592E-17	Sequence 17, Appl1	231	35	48.6	329	2	US-09-902-540-13659	Sequence 13659, A
159	35	48.6	117	1	US-08-290-592E-18	Sequence 18, Appl1	232	35	48.6	345	2	US-09-107-532A-4426	Sequence 4426, Ap
160	35	48.6	117	2	US-08-545-809A-114	Sequence 114, App	233	35	48.6	350	2	US-09-668-097A-26	Sequence 9903, Ap
161	35	48.6	117	2	US-10-330-613A-5	Sequence 5, Appl1	234	35	48.6	380	2	US-09-668-097A-26	Sequence 26, Appl1
162	35	48.6	117	2	US-10-330-613A-13	Sequence 13, Appl1	235	35	48.6	400	2	US-09-248-796A-15048	Sequence 15048, A
163	35	48.6	117	2	US-09-515-697-114	Sequence 114, App	236	35	48.6	420	2	US-09-248-796A-19301	Sequence 19301, A
164	35	48.6	117	4	PCT-US95-10053-14	Sequence 14, Appl1	237	35	48.6	420	2	US-09-107-532A-4094	Sequence 4094, Ap
165	35	48.6	117	4	PCT-US95-10053-15	Sequence 15, Appl1	238	35	48.6	520	2	US-09-194-945A-15	Sequence 15, Appl1
166	35	48.6	117	4	PCT-US96-09448-17	Sequence 17, Appl1	239	35	48.6	631	2	US-09-620-412C-325	Sequence 325, App
167	35	48.6	117	4	PCT-US96-09448-18	Sequence 18, Appl1	240	35	48.6	664	2	US-09-598-419-335	Sequence 168, App
168	35	48.6	118	2	US-09-065-059-11	Sequence 11, Appl1	241	35	48.6	675	2	US-09-489-039A-9046	Sequence 9046, Ap
169	35	48.6	118	2	US-08-545-809A-116	Sequence 116, App	242	35	48.6	816	1	US-08-190-802A-54	Sequence 54, Appl1
170	35	48.6	118	2	US-08-545-809A-123	Sequence 123, App	243	35	48.6	816	1	US-08-477-346-54	Sequence 54, Appl1
171	35	48.6	118	2	US-08-851-362D-45	Sequence 45, Appl1	244	35	48.6	816	2	US-08-473-089-54	Sequence 54, Appl1
172	35	48.6	118	2	US-09-515-697-116	Sequence 116, App	245	35	48.6	816	2	US-08-487-072A-54	Sequence 54, Appl1
173	35	48.6	118	2	US-09-515-697-123	Sequence 123, App	246	35	48.6	816	2		

247	35	48.6	1016	2	US-10-197-220-95	Sequence 95, Appl	320	34	47.2	363	2	US-09-270-767-35641	Sequence 35641, A
248	35	48.6	1049	2	US-09-538-092-72	Sequence 72, Appl	321	34	47.2	369	2	US-09-270-767-50858	Sequence 50858, A
249	35	48.6	1084	1	US-08-117-515-6	Sequence 6, Appl	322	34	47.2	373	2	US-09-339-159B-16	Sequence 16, Appl
250	35	48.6	1276	1	US-08-117-515-8	Sequence 8, Appl	323	34	47.2	378	2	US-09-057-9669-6	Sequence 6, Appl
251	34.5	47.9	1119	1	US-08-553-497A-4	Sequence 4, Appl	324	34	47.2	382	2	US-09-607-787A-432	Sequence 432, App
252	34.5	47.9	119	2	US-10-268-883-3	Sequence 3, Appl	325	34	47.2	397	2	US-09-328-352-7357	Sequence 7357, Ap
253	34.5	47.9	120	2	US-08-554-840-5	Sequence 5, Appl	326	34	47.2	401	2	US-09-270-767-56710	Sequence 56710, A
254	34.5	47.9	120	2	US-08-554-840-6	Sequence 6, Appl	327	34	47.2	405	2	US-09-248-796A-15148	Sequence 15148, A
255	34.5	47.9	120	2	US-08-554-840-7	Sequence 7, Appl	328	34	47.2	411	1	US-08-232-532-1	Sequence 1, Appl
256	34.5	47.9	120	2	US-08-554-840-8	Sequence 8, Appl	329	34	47.2	411	1	US-08-748-150-1	Sequence 1, Appl
257	34.5	47.9	120	2	US-08-925-339-5	Sequence 5, Appl	330	34	47.2	411	2	US-09-347-877-1	Sequence 1, Appl
258	34.5	47.9	120	2	US-08-925-339-6	Sequence 6, Appl	331	34	47.2	411	2	US-09-912-740A-1	Sequence 1, Appl
259	34.5	47.9	120	2	US-08-925-339-7	Sequence 7, Appl	332	34	47.2	411	2	US-09-912-741B-1	Sequence 1, Appl
260	34.5	47.9	120	2	US-08-925-339-8	Sequence 8, Appl	333	34	47.2	411	4	PCT-US95-05168-1	Sequence 1, Appl
261	34.5	47.9	120	2	US-09-332-595-5	Sequence 5, Appl	334	34	47.2	423	2	US-09-824-551-2	Sequence 2, Appl
262	34.5	47.9	120	2	US-09-332-595-6	Sequence 6, Appl	335	34	47.2	449	2	US-09-949-016-9614	Sequence 9614, Ap
263	34.5	47.9	120	2	US-09-332-595-7	Sequence 7, Appl	336	34	47.2	449	2	US-09-949-016-9615	Sequence 9615, Ap
264	34.5	47.9	120	2	US-09-332-595-8	Sequence 8, Appl	337	34	47.2	453	1	US-08-206-176-6	Sequence 6, Appl
265	34.5	47.9	138	2	US-10-268-883-2	Sequence 2, Appl	338	34	47.2	454	2	US-08-434-099A-27	Sequence 27, Appl
266	34.5	47.2	12	1	US-08-360-125-14	Sequence 14, Appl	339	34	47.2	457	2	US-09-057-969-5	Sequence 5, Appl
267	34	47.2	12	1	US-08-450-578-17	Sequence 17, Appl	340	34	47.2	457	2	US-09-949-016-8584	Sequence 8584, Ap
268	34	47.2	12	1	US-08-450-578-17	Sequence 17, Appl	341	34	47.2	465	2	US-09-339-159B-4	Sequence 4, Appl
269	34	47.2	12	1	US-08-450-578-17	Sequence 17, Appl	342	34	47.2	476	2	US-09-270-767-60873	Sequence 60873, A
270	34	47.2	12	1	US-09-017-628-14	Sequence 14, Appl	343	34	47.2	484	2	US-09-339-159B-2	Sequence 2, Appl
271	34	47.2	12	1	US-09-017-628-14	Sequence 14, Appl	344	34	47.2	507	2	US-09-248-796A-19164	Sequence 19164, A
272	34	47.2	12	1	US-09-014-880-14	Sequence 14, Appl	345	34	47.2	509	2	US-09-252-991A-20470	Sequence 20470, A
273	34	47.2	12	1	US-08-450-578-14	Sequence 14, Appl	346	34	47.2	524	1	US-08-928-692-12	Sequence 12, Appl
274	34	47.2	12	2	US-08-450-578-14	Sequence 14, Appl	347	34	47.2	524	1	US-09-339-972-12	Sequence 12, Appl
275	34	47.2	12	2	US-08-450-578-14	Sequence 14, Appl	348	34	47.2	524	2	US-09-057-969-4	Sequence 4, Appl
276	34	47.2	12	2	US-09-467-903-14	Sequence 14, Appl	349	34	47.2	539	2	US-09-538-092-581	Sequence 581, App
277	34	47.2	12	2	US-09-467-903-17	Sequence 17, Appl	350	34	47.2	566	2	US-09-487-556B-418	Sequence 418, App
278	34	47.2	15	2	US-08-469-141A-14	Sequence 14, Appl	351	34	47.2	566	2	US-08-642-664-2	Sequence 2, Appl
279	34	47.2	15	4	PCT-US95-13794-14	Sequence 14, Appl	352	34	47.2	587	1	US-08-642-664-23	Sequence 23, Appl
280	34	47.2	18	1	US-07-654-839-3	Sequence 3, Appl	353	34	47.2	587	1	US-08-436-664-23	Sequence 23, Appl
281	34	47.2	20	2	US-09-664-945-37	Sequence 37, Appl	354	34	47.2	587	2	US-09-135-664-23	Sequence 23, Appl
282	34	47.2	20	2	US-09-664-945-38	Sequence 38, Appl	355	34	47.2	587	2	US-08-394-232A-23	Sequence 23, Appl
283	34	47.2	20	2	US-09-962-756-832	Sequence 832, App	356	34	47.2	587	2	US-09-157-397-2	Sequence 2, Appl
284	34	47.2	20	2	US-10-372-735-37	Sequence 37, Appl	357	34	47.2	587	2	US-09-517-871-22	Sequence 22, Appl
285	34	47.2	20	2	US-10-372-735-38	Sequence 38, Appl	358	34	47.2	587	2	US-09-512-021-2	Sequence 2, Appl
286	34	47.2	21	2	US-09-180-570A-5	Sequence 5, Appl	359	34	47.2	587	2	US-09-512-021-2	Sequence 2, Appl
287	34	47.2	27	2	US-09-664-945-98	Sequence 98, Appl	360	34	47.2	587	2	PCT-US95-04080-23	Sequence 23, Appl
288	34	47.2	27	2	US-09-664-945-99	Sequence 99, Appl	361	34	47.2	588	1	US-08-436-664-25	Sequence 25, Appl
289	34	47.2	27	2	US-10-372-735-110	Sequence 110, App	362	34	47.2	588	1	US-09-135-664-25	Sequence 25, Appl
290	34	47.2	27	2	US-10-372-735-111	Sequence 111, App	363	34	47.2	588	2	US-08-394-232A-25	Sequence 25, Appl
291	34	47.2	62	2	US-09-248-796A-24053	Sequence 24053, A	364	34	47.2	588	2	US-09-157-397-4	Sequence 4, Appl
292	34	47.2	96	2	US-08-851-362D-27	Sequence 27, Appl	365	34	47.2	588	2	US-09-517-871-6	Sequence 6, Appl
293	34	47.2	97	2	US-08-851-362D-31	Sequence 31, Appl	366	34	47.2	588	2	US-09-512-021-4	Sequence 4, Appl
294	34	47.2	117	2	US-08-851-362D-44	Sequence 44, Appl	367	34	47.2	588	2	US-09-517-871-6	Sequence 6, Appl
295	34	47.2	118	2	US-08-851-362D-46	Sequence 46, Appl	368	34	47.2	588	2	US-09-517-871-6	Sequence 6, Appl
296	34	47.2	121	2	US-10-330-613A-37	Sequence 37, Appl	369	34	47.2	588	4	PCT-US95-04080-25	Sequence 25, Appl
297	34	47.2	193	2	US-09-393-627B-20	Sequence 20, Appl	370	34	47.2	589	1	US-08-642-664-4	Sequence 4, Appl
298	34	47.2	193	2	US-09-393-627B-24	Sequence 24, Appl	371	34	47.2	590	1	US-08-436-664-27	Sequence 27, Appl
299	34	47.2	206	2	US-09-107-383-15	Sequence 15, Appl	372	34	47.2	590	2	US-09-135-664-27	Sequence 27, Appl
300	34	47.2	206	2	US-09-643-914-15	Sequence 15, Appl	373	34	47.2	590	2	US-08-394-232A-27	Sequence 27, Appl
301	34	47.2	206	2	US-09-742-361A-15	Sequence 15, Appl	374	34	47.2	590	4	PCT-US95-04080-27	Sequence 27, Appl
302	34	47.2	213	2	US-09-107-383-14	Sequence 14, Appl	375	34	47.2	590	4	US-09-517-871-4	Sequence 4, Appl
303	34	47.2	213	2	US-09-643-914-14	Sequence 14, Appl	376	34	47.2	592	2	US-09-517-871-4	Sequence 4, Appl
304	34	47.2	213	2	US-09-742-361A-14	Sequence 14, Appl	377	34	47.2	592	2	US-09-517-871-4	Sequence 4, Appl
305	34	47.2	231	2	US-09-172-952-33	Sequence 33, Appl	378	34	47.2	612	2	US-09-252-991A-31248	Sequence 31248, A
306	34	47.2	238	2	US-09-004-730A-112	Sequence 112, App	379	34	47.2	624	2	US-09-057-966-3	Sequence 3, Appl
307	34	47.2	238	2	US-08-981-799A-112	Sequence 112, App	380	34	47.2	668	2	US-09-270-767-41490	Sequence 41490, A
308	34	47.2	242	2	US-09-004-730A-119	Sequence 119, App	381	34	47.2	717	2	US-09-107-532A-6350	Sequence 6350, Ap
309	34	47.2	242	2	US-08-981-799A-119	Sequence 119, App	382	34	47.2	764	2	US-09-489-039A-8823	Sequence 8823, Ap
310	34	47.2	245	2	US-09-198-452A-1091	Sequence 1091, Ap	383	34	47.2	801	2	US-09-538-099-258	Sequence 258, App
311	34	47.2	245	2	US-09-338-185A-1019	Sequence 1019, Ap	384	34	47.2	876	1	US-08-510-215A-2	Sequence 2, Appl
312	34	47.2	248	2	US-09-393-627B-32	Sequence 32, Appl	385	34	47.2	876	1	US-08-436-664-32	Sequence 32, Appl
313	34	47.2	264	2	US-08-564-164A-4	Sequence 4, Appl	386	34	47.2	876	1	US-08-436-664-34	Sequence 34, Appl
314	34	47.2	264	2	US-09-004-730A-115	Sequence 115, App	387	34	47.2	876	1	US-09-135-664-32	Sequence 32, Appl
315	34	47.2	264	2	US-08-981-799A-115	Sequence 115, App	388	34	47.2	876	2	US-09-135-664-32	Sequence 32, Appl
316	34	47.2	294	2	US-09-057-969-7	Sequence 7, Appl	389	34	47.2	876	2	US-09-135-664-34	Sequence 34, Appl
317	34	47.2	329	2	US-09-370-767-46040	Sequence 46040, A	390	34	47.2	876	2	US-08-394-232A-30	Sequence 30, Appl
318	34	47.2	332	2	US-09-135-121B-7	Sequence 7, Appl	391	34	47.2	876	2	US-08-394-232A-30	Sequence 30, Appl
319	34	47.2	353	2	US-09-248-796A-20008	Sequence 20008, A	392	34	47.2	876	2	US-08-394-232A-32	Sequence 32, Appl

393	34	47.2	876	2	US-08-394-232A-34	Sequence 34, Appl	466	33	45.8	245	2	US-09-248-796A-17929	Sequence 17929, A
394	34	47.2	876	2	US-09-517-871-2	Sequence 20, Appl	467	33	45.8	246	1	US-08-553-497A-24	Sequence 24, Appl
395	34	47.2	876	2	US-09-517-871-20	Sequence 20, Appl	468	33	45.8	246	1	US-09-134-000C-5831	Sequence 5831, Ap
396	34	47.2	876	2	US-09-517-439-2	Sequence 20, Appl	469	33	45.8	265	2	US-09-248-796A-14982	Sequence 14982, A
397	34	47.2	876	4	PCT-US95-04080-20	Sequence 20, Appl	470	33	45.8	265	2	US-09-248-796A-14982	Sequence 14982, A
398	34	47.2	876	4	PCT-US95-04080-32	Sequence 32, Appl	471	33	45.8	269	2	US-09-270-767-57645	Sequence 57645, A
399	34	47.2	876	4	PCT-US95-04080-34	Sequence 34, Appl	472	33	45.8	286	2	US-09-205-258-1012	Sequence 1012, Ap
400	34	47.2	917	2	US-09-538-092-1364	Sequence 1364, Ap	473	33	45.8	286	2	US-10-004-860-1012	Sequence 1012, Ap
401	34	47.2	918	2	US-09-538-092-1364	Sequence 1364, Ap	474	33	45.8	291	2	US-10-004-860-1012	Sequence 1012, Ap
402	34	47.2	954	2	US-09-270-767-45370	Sequence 45370, A	475	33	45.8	292	2	US-09-107-532A-6914	Sequence 6914, Ap
403	34	47.2	954	2	US-09-057-969-2	Sequence 2, Appl	476	33	45.8	292	2	US-09-107-532A-6914	Sequence 6914, Ap
404	34	47.2	990	2	US-09-248-796A-20230	Sequence 20230, A	477	33	45.8	293	2	US-09-902-540-9955	Sequence 9956, Ap
405	34	47.2	1025	1	US-08-530-792D-23	Sequence 23, Appl	478	33	45.8	294	2	US-09-543-681A-4399	Sequence 4399, Ap
406	34	47.2	1026	1	US-08-530-792D-22	Sequence 22, Appl	479	33	45.8	311	2	US-09-248-796A-20933	Sequence 20933, A
407	34	47.2	1382	1	US-08-737-715-2	Sequence 7, Appl	480	33	45.8	310	1	US-09-134-000C-5598	Sequence 5598, Ap
408	34	47.2	1382	1	US-09-457-040B-7	Sequence 7, Appl	481	33	45.8	330	2	US-08-838-543-3	Sequence 3, Appl
409	34	47.2	1665	2	US-09-583-110-4667	Sequence 4667, Ap	482	33	45.8	332	2	US-09-270-767-58031	Sequence 38031, A
410	34	47.2	1653	2	US-09-107-443-4155	Sequence 4155, Ap	483	33	45.8	332	2	US-09-270-767-58031	Sequence 38031, A
411	33.5	46.5	94	2	US-09-513-999C-4101	Sequence 4101, Ap	484	33	45.8	363	2	US-09-173-300-20	Sequence 52348, A
412	33.5	46.5	250	2	US-09-710-279-1124	Sequence 1124, Ap	485	33	45.8	363	2	US-10-027-430-20	Sequence 20, Appl
413	33.5	46.5	263	2	US-09-069-821-3	Sequence 3, Appl	486	33	45.8	370	2	US-09-252-991A-19518	Sequence 19518, A
414	33.5	46.5	263	2	US-09-956-086-3	Sequence 3, Appl	487	33	45.8	372	2	US-09-668-097A-14	Sequence 14, Appl
415	33.5	46.5	263	2	US-09-956-086-3	Sequence 3, Appl	488	33	45.8	376	2	US-09-902-540-13960	Sequence 13960, A
416	33.5	46.5	283	2	US-09-420-592A-6	Sequence 6, Appl	489	33	45.8	414	2	US-09-902-540-11308	Sequence 11308, A
417	33.5	46.5	283	2	US-09-985-442-6	Sequence 6, Appl	490	33	45.8	434	2	US-09-771-161A-92	Sequence 92, Appl
418	33.5	46.5	283	2	US-09-983-580-6	Sequence 6, Appl	491	33	45.8	443	2	US-09-328-352-7069	Sequence 7069, Ap
419	33.5	46.5	376	2	US-09-710-279-490	Sequence 490, App	492	33	45.8	449	2	US-09-769-787-110	Sequence 110, App
420	33.5	46.5	439	1	US-09-710-279-2260	Sequence 2260, Ap	493	33	45.8	468	2	US-09-248-796A-15571	Sequence 15571, A
421	33.5	46.5	439	1	US-07-952-817-13	Sequence 13, Appl	494	33	45.8	480	2	US-09-438-185A-934	Sequence 934, App
422	33.5	46.5	439	1	US-09-538-092-843	Sequence 843, App	495	33	45.8	495	2	US-09-948-004-18	Sequence 18, Appl
423	33.5	46.5	439	6	5210025-6	Sequence 843, App	496	33	45.8	504	2	US-09-134-000C-5485	Sequence 5485, Ap
424	33	45.8	449	2	US-09-949-016-10515	Sequence 10515, A	497	33	45.8	511	1	US-08-480-604A-20	Sequence 20, Appl
425	33	45.8	9	2	US-09-527-487-3	Sequence 3, Appl	498	33	45.8	511	1	US-08-480-604A-20	Sequence 20, Appl
426	33	45.8	10	1	US-09-948-004-34	Sequence 34, Appl	499	33	45.8	511	2	US-08-915-136-20	Sequence 20, Appl
427	33	45.8	12	2	US-07-946-421-6	Sequence 6, Appl	500	33	45.8	511	2	US-08-957-310-20	Sequence 20, Appl
428	33	45.8	20	2	US-09-962-756-881	Sequence 881, App	501	33	45.8	511	2	US-10-011-366-20	Sequence 20, Appl
429	33	45.8	68	2	US-09-134-000C-3348	Sequence 4348, Ap	502	33	45.8	516	1	US-09-084-517-20	Sequence 20, Appl
430	33	45.8	77	2	US-09-248-796A-26555	Sequence 26555, A	503	33	45.8	527	2	US-09-603-208A-52	Sequence 30, Appl
431	33	45.8	95	2	US-09-270-767-34376	Sequence 34376, A	504	33	45.8	554	2	US-09-438-185A-924	Sequence 924, App
432	33	45.8	95	2	US-09-270-767-49593	Sequence 49593, A	505	33	45.8	565	2	US-09-710-279-2608	Sequence 2608, Ap
433	33	45.8	111	2	US-09-471-276-840	Sequence 840, App	506	33	45.8	565	2	US-09-198-482A-994	Sequence 994, App
434	33	45.8	114	1	US-08-436-463-16	Sequence 16, Appl	507	33	45.8	599	2	US-09-248-796A-17744	Sequence 17744, A
435	33	45.8	114	1	US-08-483-749A-10	Sequence 10, Appl	508	33	45.8	608	1	US-08-480-604A-21	Sequence 21, Appl
436	33	45.8	119	1	US-08-318-157B-58	Sequence 58, Appl	509	33	45.8	608	1	US-08-480-604A-21	Sequence 21, Appl
437	33	45.8	119	1	US-09-253-794-58	Sequence 58, Appl	510	33	45.8	608	2	US-08-915-136-21	Sequence 21, Appl
438	33	45.8	121	2	US-09-254-180C-7	Sequence 7, Appl	511	33	45.8	608	2	US-08-957-310-21	Sequence 21, Appl
439	33	45.8	123	2	US-09-726-653-4	Sequence 4, Appl	512	33	45.8	608	2	US-10-011-366-21	Sequence 21, Appl
440	33	45.8	124	1	US-07-958-140-4	Sequence 4, Appl	513	33	45.8	608	2	US-09-084-517-21	Sequence 21, Appl
441	33	45.8	124	4	PCT-US93-0916-4	Sequence 19, Appl	514	33	45.8	609	1	US-08-480-604A-30	Sequence 30, Appl
442	33	45.8	125	2	US-09-726-653-19	Sequence 61, Appl	515	33	45.8	609	2	US-08-915-136-30	Sequence 30, Appl
443	33	45.8	137	1	US-08-331-398A-61	Sequence 61, Appl	516	33	45.8	609	2	US-09-084-517-30	Sequence 30, Appl
444	33	45.8	137	1	US-08-331-397B-61	Sequence 61, Appl	517	33	45.8	631	2	US-09-545-773-4	Sequence 4, Appl
445	33	45.8	137	1	US-08-759-804A-60	Sequence 60, Appl	518	33	45.8	631	2	US-10-223-038-4	Sequence 4, Appl
446	33	45.8	140	1	US-09-948-004-14	Sequence 14, Appl	519	33	45.8	632	2	US-09-634-228-249	Sequence 24, App
447	33	45.8	140	1	US-07-946-421-24	Sequence 24, Appl	520	33	45.8	639	2	US-09-902-540-14902	Sequence 14902, A
448	33	45.8	141	2	US-07-946-421-28	Sequence 28, Appl	521	33	45.8	640	2	US-09-336-115C-14	Sequence 14, Appl
449	33	45.8	143	4	US-08-589-939-5	Sequence 5, Appl	522	33	45.8	642	2	US-09-336-115C-16	Sequence 16, Appl
450	33	45.8	143	4	US-08-236-520-7	Sequence 7, Appl	523	33	45.8	645	1	US-09-902-540-16286	Sequence 16286, A
451	33	45.8	147	2	PCT-US95-05262-7	Sequence 7, Appl	524	33	45.8	645	1	US-08-785-430-2	Sequence 2, Appl
452	33	45.8	147	2	US-09-270-767-37343	Sequence 37343, A	525	33	45.8	645	1	US-08-996-800-2	Sequence 19, Appl
453	33	45.8	147	2	US-09-270-767-3560	Sequence 3560, A	526	33	45.8	645	2	US-09-336-115C-18	Sequence 18, Appl
454	33	45.8	163	2	US-09-605-703B-2018	Sequence 2018, Ap	527	33	45.8	645	2	US-09-710-279-1770	Sequence 1770, Ap
455	33	45.8	167	2	US-09-248-796A-24968	Sequence 24968, A	528	33	45.8	650	2	US-09-134-001C-3781	Sequence 3781, Ap
456	33	45.8	169	2	US-09-328-352-4314	Sequence 4314, Ap	529	33	45.8	652	2	US-09-336-115C-16	Sequence 16, Appl
457	33	45.8	221	2	US-09-270-767-36040	Sequence 36040, A	530	33	45.8	659	2	US-09-134-001C-5537	Sequence 5537, Ap
458	33	45.8	221	2	US-09-270-767-51257	Sequence 51257, A	531	33	45.8	672	2	US-09-336-115C-10	Sequence 10, Appl
459	33	45.8	222	2	US-09-198-452A-1005	Sequence 1005, Ap	532	33	45.8	681	2	US-09-252-991A-28831	Sequence 28831, A
460	33	45.8	236	2	US-08-886-265-4	Sequence 4, Appl	533	33	45.8	682	2	US-09-134-000C-5288	Sequence 5288, Ap
461	33	45.8	242	1	US-09-167-647-5	Sequence 5, Appl	534	33	45.8	690	2	US-09-336-115C-22	Sequence 22, Appl
462	33	45.8	242	1	US-08-553-497A-26	Sequence 26, Appl	535	33	45.8	711	2	US-09-336-115C-12	Sequence 12, Appl
463	33	45.8	243	2	US-08-553-497A-38	Sequence 38, Appl	536	33	45.8	743	2	US-09-107-532A-4219	Sequence 4219, Ap
464	33	45.8	244	1	US-09-328-352-7321	Sequence 7321, Ap	537	33	45.8	977	2	US-09-489-039A-11073	Sequence 11073, A
465	33	45.8	244	1	US-08-553-497A-50	Sequence 50, Appl	538	33	45.8	1006	2	US-09-771-161A-183	Sequence 183, App
					US-08-553-497A-22	Sequence 22, Appl						US-09-949-016-10730	Sequence 10730, A

539	33	45.8	1120	2	US-09-792-024-86	Sequence 86, Appl	612	32	44.4	178	2	US-09-624-670-25	Sequence 25, Appl
540	33	45.8	1666	2	US-09-949-016-8322	Sequence 8322, Ap	613	32	44.4	180	6	US-09-270-767-31574	Sequence 31574, A
541	33	45.8	1968	1	US-07-745-206A-7	Sequence 7, Appl	614	32	44.4	181	2	US-09-270-767-31574	Sequence 33574, A
542	33	45.8	1968	1	US-08-455-543A-45	Sequence 45, Appl	615	32	44.4	196	2	US-09-270-767-58891	Sequence 58891, A
543	33	45.8	1968	1	US-08-223-305C-45	Sequence 45, Appl	616	32	44.4	199	2	US-09-583-110-3127	Sequence 3127, Ap
544	33	45.8	1968	1	US-08-311-363-7	Sequence 7, Appl	617	32	44.4	204	2	US-09-903-456-39	Sequence 39, Appl
545	33	45.8	2366	1	US-08-480-604A-10	Sequence 10, Appl	618	32	44.4	204	2	US-10-101-464A-190	Sequence 790, App
546	33	45.8	2366	1	US-08-405-496A-10	Sequence 10, Appl	619	32	44.4	205	2	US-09-624-670-38	Sequence 38, Appl
547	33	45.8	2366	2	US-08-915-136-10	Sequence 10, Appl	620	32	44.4	206	2	US-09-769-787-46	Sequence 46, Appl
548	33	45.8	2366	2	US-08-957-310-10	Sequence 10, Appl	621	32	44.4	206	2	US-09-270-767-38740	Sequence 38740, A
549	33	45.8	2366	2	US-10-011-366-10	Sequence 10, Appl	622	32	44.4	208	2	US-09-107-433-4691	Sequence 4691, Ap
550	33	45.8	2366	2	US-09-084-517-10	Sequence 10, Appl	623	32	44.4	217	2	US-09-252-991A-19722	Sequence 19722, A
551	33	45.8	2532	2	US-09-215-694-10	Sequence 10, Appl	624	32	44.4	217	2	US-09-903-456-49	Sequence 49, Appl
552	33	45.8	2532	2	US-10-109-310-10	Sequence 10, Appl	625	32	44.4	217	2	US-09-624-670-48	Sequence 48, Appl
553	33	45.8	4544	1	US-08-469-486-52	Sequence 52, Appl	626	32	44.4	219	2	US-09-903-456-38	Sequence 38, Appl
554	33	45.8	4544	1	US-08-469-658-52	Sequence 52, Appl	627	32	44.4	219	2	US-09-270-767-37049	Sequence 37049, A
555	33	45.8	6239	2	US-09-914-286-4	Sequence 4, Appl	628	32	44.4	219	2	US-09-270-767-52266	Sequence 52266, A
556	32.5	45.1	22	4	US-08-221-580-5	Sequence 5, Appl	629	32	44.4	219	2	US-09-624-670-37	Sequence 37, Appl
557	32.5	45.1	22	4	PCT-US95-04018-67	Sequence 67, Appl	630	32	44.4	223	2	US-09-465-901-38	Sequence 38, Appl
558	32.5	45.1	122	4	US-08-336-520-9	Sequence 9, Appl	631	32	44.4	223	2	US-09-681-432-1	Sequence 1, Appl
559	32.5	45.1	122	4	PCT-US95-05262-9	Sequence 9, Appl	632	32	44.4	231	1	US-08-681-432-1	Sequence 20052, A
560	32.5	45.1	135	2	US-08-284-516C-46	Sequence 46, Appl	633	32	44.4	231	2	US-09-248-796A-20052	Sequence 16060, A
561	32.5	45.1	135	2	US-09-537-911A-46	Sequence 46, Appl	634	32	44.4	249	2	US-09-489-039A-17755	Sequence 7755, Ap
562	32.5	45.1	183	2	US-09-105-343A-8	Sequence 8, Appl	635	32	44.4	253	2	US-09-320-424-11	Sequence 11, Appl
563	32.5	45.1	291	1	US-08-670-354-6	Sequence 6, Appl	636	32	44.4	253	2	US-09-825-563-11	Sequence 11, Appl
564	32.5	45.1	291	2	US-09-320-424-6	Sequence 6, Appl	637	32	44.4	254	2	US-09-586-106D-75	Sequence 75, Appl
565	32.5	45.1	291	2	US-09-825-563-6	Sequence 6, Appl	638	32	44.4	254	2	US-10-799-870-75	Sequence 4, Appl
566	32.5	45.1	291	4	PCT-US96-10895-6	Sequence 6, Appl	639	32	44.4	255	1	US-07-690-192-4	Sequence 13, Appl
567	32.5	45.1	315	2	US-09-134-001C-4771	Sequence 4771, Ap	640	32	44.4	256	2	US-09-320-424-13	Sequence 13, Appl
568	32.5	45.1	429	2	US-09-710-279-322	Sequence 322, App	641	32	44.4	256	2	US-09-825-563-13	Sequence 13, Appl
569	32.5	45.1	431	2	US-09-543-681A-6232	Sequence 6232, Ap	642	32	44.4	266	2	US-09-825-563-13	Sequence 13, Appl
570	32.5	45.1	825	2	US-09-538-092-523	Sequence 523, App	643	32	44.4	266	6	US-09-645-415A-10	Sequence 10, Appl
571	32	44.4	13	2	US-08-908-469-62	Sequence 62, Appl	644	32	44.4	266	6	5223610-5	Patent No. 5223610
572	32	44.4	13	2	US-08-908-469-83	Sequence 83, Appl	645	32	44.4	269	6	5244657-5	Patent No. 5244657
573	32	44.4	15	2	US-08-992-877-53	Sequence 53, Appl	646	32	44.4	269	6	5433945-5	Patent No. 5433945
574	32	44.4	31	2	US-09-770-767-58852	Sequence 58852, A	647	32	44.4	271	2	US-09-563-611C-30	Sequence 30, Appl
575	32	44.4	40	1	US-08-472-244-3	Sequence 3, Appl	648	32	44.4	276	2	US-09-903-456-37	Sequence 37, Appl
576	32	44.4	43	2	US-09-962-756-1433	Sequence 1433, Ap	649	32	44.4	276	2	US-09-624-670-36	Sequence 36, Appl
577	32	44.4	47	1	US-08-994-189-15	Sequence 15, Appl	650	32	44.4	279	2	US-09-072-993C-3	Sequence 3, Appl
578	32	44.4	62	2	US-09-107-532A-7047	Sequence 7047, Ap	651	32	44.4	280	2	US-09-145-828A-21	Sequence 21, Appl
579	32	44.4	64	2	US-09-621-976-6986	Sequence 6986, Ap	652	32	44.4	280	2	US-09-149-476-415	Sequence 415, App
580	32	44.4	64	2	US-08-302-756E-14	Sequence 14, Appl	653	32	44.4	280	2	US-09-903-456-28	Sequence 28, Appl
581	32	44.4	65	2	US-09-448-796A-27478	Sequence 27478, A	654	32	44.4	281	1	US-08-670-354-2	Sequence 27, Appl
582	32	44.4	73	2	US-09-513-999C-7157	Sequence 7157, Ap	655	32	44.4	281	2	US-08-670-354-2	Sequence 2, Appl
583	32	44.4	82	2	US-09-370-767-58568	Sequence 58568, A	656	32	44.4	281	2	US-08-584-031-1	Sequence 1, Appl
584	32	44.4	85	2	US-09-131-827A-13	Sequence 13, Appl	657	32	44.4	281	2	US-08-780-496-1	Sequence 1, Appl
585	32	44.4	85	2	US-09-632-287A-12	Sequence 12, Appl	658	32	44.4	281	2	US-08-883-086-10	Sequence 10, Appl
586	32	44.4	85	2	US-10-286-696-12	Sequence 12, Appl	659	32	44.4	281	2	US-09-320-424-2	Sequence 6, Appl
587	32	44.4	87	2	US-09-632-287A-13	Sequence 13, Appl	660	32	44.4	281	2	US-09-333-593A-6	Sequence 6, Appl
588	32	44.4	87	2	US-10-286-696-13	Sequence 13, Appl	661	32	44.4	281	2	US-09-157-864-11	Sequence 11, Appl
589	32	44.4	99	2	US-09-248-796A-17758	Sequence 17758, A	662	32	44.4	283	2	US-09-825-563-2	Sequence 2, Appl
590	32	44.4	110	2	US-09-328-352-5550	Sequence 5550, Ap	663	32	44.4	283	2	US-09-919-029-118	Sequence 118, App
591	32	44.4	113	2	US-09-434-870-4	Sequence 4, Appl	664	32	44.4	283	2	US-09-582-450-1	Sequence 1, Appl
592	32	44.4	120	2	US-08-436-463-14	Sequence 2, Appl	665	32	44.4	281	2	US-09-934-465-1	Sequence 1, Appl
593	32	44.4	122	1	US-08-436-463-14	Sequence 14, Appl	666	32	44.4	281	4	US-10-011-125A-4	Sequence 4, Appl
594	32	44.4	123	2	US-09-252-991A-28722	Sequence 28722, A	667	32	44.4	283	2	PCT-US96-10895-2	Sequence 2, Appl
595	32	44.4	123	2	US-09-640-459-91	Sequence 91, Appl	668	32	44.4	284	2	US-09-902-540-13146	Sequence 13146, A
596	32	44.4	123	2	US-09-497-625A-91	Sequence 91, Appl	669	32	44.4	286	2	US-08-564-164A-2	Sequence 2, Appl
597	32	44.4	126	2	US-09-605-703B-2778	Sequence 2778, Ap	670	32	44.4	286	2	US-09-903-456-55	Sequence 59, Appl
598	32	44.4	129	2	US-09-912-161-2	Sequence 2, Appl	671	32	44.4	286	2	US-09-624-670-58	Sequence 58, Appl
599	32	44.4	129	2	US-09-911-781-5	Sequence 5, Appl	672	32	44.4	289	2	US-09-145-828A-17	Sequence 17, Appl
600	32	44.4	130	2	US-10-400-902-5	Sequence 5, Appl	673	32	44.4	289	2	US-09-903-456-21	Sequence 21, Appl
601	32	44.4	130	2	US-09-270-767-31697	Sequence 31697, A	674	32	44.4	289	2	US-09-903-456-34	Sequence 34, Appl
602	32	44.4	130	2	US-09-270-767-46914	Sequence 46914, A	675	32	44.4	289	2	US-09-624-670-20	Sequence 20, Appl
603	32	44.4	141	2	US-09-328-352-6818	Sequence 6818, Ap	676	32	44.4	289	2	US-09-624-670-33	Sequence 33, Appl
604	32	44.4	145	2	US-09-270-767-43326	Sequence 43326, A	677	32	44.4	291	2	US-09-903-456-36	Sequence 36, Appl
605	32	44.4	153	2	US-09-270-767-36020	Sequence 36020, A	678	32	44.4	292	2	US-09-624-670-35	Sequence 35, Appl
606	32	44.4	153	2	US-09-270-767-51237	Sequence 51237, A	679	32	44.4	292	2	US-09-408-020-38	Sequence 38, Appl
607	32	44.4	159	1	US-08-653-402B-2	Sequence 2, Appl	680	32	44.4	293	2	US-09-408-020-72	Sequence 72, Appl
608	32	44.4	161	2	US-09-565-423-7	Sequence 7, Appl	681	32	44.4	293	2	US-09-095-758-9	Sequence 9, Appl
609	32	44.4	177	2	US-09-105-343A-7	Sequence 7, Appl	682	32	44.4	293	2	US-09-422-966-9	Sequence 9, Appl
610	32	44.4	178	2	US-09-145-828A-24	Sequence 24, Appl	683	32	44.4	293	2	US-09-145-828A-12	Sequence 12, Appl
611	32	44.4	178	2	US-09-903-456-26	Sequence 26, Appl	684	32	44.4	293	2	US-09-708-015A-9	Sequence 9, Appl

685	32	44.4	293	2	US-09-903-456-19	Sequence 19, Appl	758	32	44.4	384	1	US-08-675-650B-6	Sequence 6, Appl
686	32	44.4	293	2	US-09-624-670-18	Sequence 18, Appl	759	32	44.4	384	2	US-08-907-608-2	Sequence 2, Appl
687	32	44.4	300	1	US-08-661-052-4	Sequence 4, Appl	760	32	44.4	384	2	US-08-907-608-4	Sequence 4, Appl
688	32	44.4	300	2	US-09-188-082-4	Sequence 4, Appl	761	32	44.4	384	2	US-08-907-608-6	Sequence 6, Appl
689	32	44.4	300	2	US-09-364-088-4	Sequence 4, Appl	762	32	44.4	384	2	US-08-597-313D-7	Sequence 7, Appl
690	32	44.4	300	2	US-09-102-716-4	Sequence 4, Appl	763	32	44.4	384	2	US-09-059-769-10	Sequence 10, Appl
691	32	44.4	301	1	US-08-661-052-14	Sequence 14, Appl	764	32	44.4	384	2	US-09-354-211B-2	Sequence 2, Appl
692	32	44.4	301	2	US-09-188-082-14	Sequence 14, Appl	765	32	44.4	384	2	US-09-354-211B-6	Sequence 6, Appl
693	32	44.4	301	2	US-09-364-088-14	Sequence 14, Appl	766	32	44.4	384	2	US-09-354-211B-8	Sequence 8, Appl
694	32	44.4	301	2	US-09-102-716-14	Sequence 14, Appl	767	32	44.4	384	2	US-09-354-211B-10	Sequence 10, Appl
695	32	44.4	301	2	US-09-903-456-33	Sequence 33, Appl	768	32	44.4	384	2	US-09-354-211B-12	Sequence 12, Appl
696	32	44.4	301	2	US-09-624-670-32	Sequence 32, Appl	769	32	44.4	384	2	US-09-354-211B-14	Sequence 14, Appl
697	32	44.4	309	2	US-08-530-862B-8	Sequence 8, Appl	770	32	44.4	384	2	US-09-354-211B-16	Sequence 16, Appl
698	32	44.4	309	2	US-08-597-313D-8	Sequence 8, Appl	771	32	44.4	384	2	US-09-354-211B-18	Sequence 18, Appl
699	32	44.4	309	2	US-09-885-189-8	Sequence 8, Appl	772	32	44.4	384	2	US-09-128-602B-1	Sequence 1, Appl
700	32	44.4	313	2	US-09-902-540-9934	Sequence 9934, Ap	773	32	44.4	384	2	US-09-128-602B-2	Sequence 2, Appl
701	32	44.4	317	2	US-09-145-828A-7	Sequence 13, Appl	774	32	44.4	384	2	US-09-128-602B-4	Sequence 4, Appl
702	32	44.4	317	2	US-09-903-456-13	Sequence 13, Appl	775	32	44.4	384	2	US-09-128-602B-6	Sequence 6, Appl
703	32	44.4	317	2	US-09-624-670-12	Sequence 12, Appl	776	32	44.4	384	2	US-09-128-602B-8	Sequence 8, Appl
704	32	44.4	318	2	US-09-145-828A-19	Sequence 19, Appl	777	32	44.4	384	2	US-09-128-602B-10	Sequence 10, Appl
705	32	44.4	318	2	US-09-903-456-25	Sequence 25, Appl	778	32	44.4	384	2	US-09-128-602B-12	Sequence 12, Appl
706	32	44.4	318	2	US-09-624-670-24	Sequence 24, Appl	779	32	44.4	384	2	US-09-128-602B-14	Sequence 14, Appl
707	32	44.4	329	2	US-09-502-783A-9	Sequence 9, Appl	780	32	44.4	384	2	US-09-128-602B-16	Sequence 16, Appl
708	32	44.4	329	2	US-09-339-912A-9	Sequence 9, Appl	781	32	44.4	384	2	US-09-128-602B-18	Sequence 18, Appl
709	32	44.4	329	2	US-09-195-662A-9	Sequence 9, Appl	782	32	44.4	384	2	US-09-482-287-2	Sequence 2, Appl
710	32	44.4	333	2	US-09-463-702A-39	Sequence 39, Appl	783	32	44.4	384	2	US-09-482-287-4	Sequence 4, Appl
711	32	44.4	333	2	US-09-699-135-39	Sequence 39, Appl	784	32	44.4	384	2	US-09-482-287-6	Sequence 6, Appl
712	32	44.4	334	2	US-09-546-986A-8	Sequence 8, Appl	785	32	44.4	384	2	US-09-966-888-2	Sequence 2, Appl
713	32	44.4	334	2	US-09-524-730-8	Sequence 8, Appl	786	32	44.4	384	2	US-09-966-888-4	Sequence 4, Appl
714	32	44.4	335	2	US-09-821-687-11	Sequence 11, Appl	787	32	44.4	384	2	US-09-966-888-6	Sequence 6, Appl
715	32	44.4	339	2	US-09-543-681A-4731	Sequence 4731, Ap	788	32	44.4	384	2	US-09-995-297-2	Sequence 2, Appl
716	32	44.4	342	2	US-09-328-352-7250	Sequence 7250, Ap	789	32	44.4	384	2	US-09-995-297-4	Sequence 4, Appl
717	32	44.4	342	2	US-09-602-787A-380	Sequence 380, App	790	32	44.4	384	2	US-09-995-297-6	Sequence 6, Appl
718	32	44.4	344	2	US-08-466-343D-9	Sequence 9, Appl	791	32	44.4	384	2	US-09-995-297-8	Sequence 8, Appl
719	32	44.4	344	2	US-09-502-784A-9	Sequence 9, Appl	792	32	44.4	384	2	US-09-995-297-10	Sequence 10, Appl
720	32	44.4	347	1	US-08-461-244-3	Sequence 3, Appl	793	32	44.4	384	2	US-09-995-297-12	Sequence 12, Appl
721	32	44.4	350	2	US-09-270-767-43527	Sequence 43527, A	794	32	44.4	384	2	US-09-995-297-14	Sequence 14, Appl
722	32	44.4	352	2	US-09-203-958A-2	Sequence 2, Appl	795	32	44.4	384	2	US-09-995-297-16	Sequence 16, Appl
723	32	44.4	355	2	US-09-501-115-12	Sequence 12, Appl	796	32	44.4	384	2	US-09-995-297-18	Sequence 18, Appl
724	32	44.4	355	2	US-10-357-886-12	Sequence 12, Appl	797	32	44.4	384	2	US-09-697-379-4	Sequence 4, Appl
725	32	44.4	358	2	US-09-107-532A-5676	Sequence 5676, Ap	798	32	44.4	384	2	US-10-116-212A-4	Sequence 4, Appl
726	32	44.4	358	2	US-09-270-767-41449	Sequence 41449, A	799	32	44.4	384	2	US-08-885-169-7	Sequence 7, Appl
727	32	44.4	360	1	US-08-450-393A-4	Sequence 4, Appl	800	32	44.4	387	1	US-08-872-302-5	Sequence 5, Appl
728	32	44.4	360	2	US-08-446-669-4	Sequence 4, Appl	801	32	44.4	387	2	US-09-059-769-13	Sequence 13, Appl
729	32	44.4	360	2	US-09-045-583-50	Sequence 50, Appl	802	32	44.4	387	2	US-09-161-994A-17	Sequence 17, Appl
730	32	44.4	360	2	US-09-045-583-51	Sequence 51, Appl	803	32	44.4	387	2	US-09-638-937-5	Sequence 5, Appl
731	32	44.4	360	2	US-09-534-185-50	Sequence 50, Appl	804	32	44.4	387	2	US-08-602-010A-6	Sequence 6, Appl
732	32	44.4	360	2	US-08-833-752-7	Sequence 51, Appl	805	32	44.4	391	1	US-08-680-726A-6	Sequence 6, Appl
733	32	44.4	360	2	US-09-131-827A-2	Sequence 2, Appl	806	32	44.4	391	1	US-09-092-409-6	Sequence 6, Appl
734	32	44.4	360	2	US-09-131-827A-20	Sequence 20, Appl	807	32	44.4	391	1	US-08-559-303B-76	Sequence 76, Appl
735	32	44.4	360	2	US-09-668-097A-32	Sequence 32, Appl	808	32	44.4	393	2	US-09-175-828-76	Sequence 76, Appl
736	32	44.4	360	2	US-09-938-719-7	Sequence 7, Appl	809	32	44.4	393	2	US-09-753-143-76	Sequence 76, Appl
737	32	44.4	360	2	US-09-625-573-4	Sequence 4, Appl	810	32	44.4	415	2	US-10-172-527A-16	Sequence 16, Appl
738	32	44.4	360	2	US-09-939-226B-7	Sequence 7, Appl	811	32	44.4	420	2	US-09-799-978-42	Sequence 42, Appl
739	32	44.4	360	2	US-09-826-509-473	Sequence 473, App	812	32	44.4	421	2	US-09-198-452A-932	Sequence 932, App
740	32	44.4	360	2	US-10-089-787-2	Sequence 7, Appl	813	32	44.4	421	2	US-09-438-185A-869	Sequence 869, App
741	32	44.4	360	2	US-09-938-703B-7	Sequence 7, Appl	814	32	44.4	422	1	US-07-698-926A-2	Sequence 2, Appl
742	32	44.4	360	2	US-09-938-703B-7	Sequence 7, Appl	815	32	44.4	432	1	US-09-712-072C-2	Sequence 2, Appl
743	32	44.4	360	4	PCT-US95-00476-4	Sequence 4, Appl	816	32	44.4	432	1	US-09-612-402B-36	Sequence 36, Appl
744	32	44.4	370	1	US-08-668-097A-34	Sequence 34, Appl	817	32	44.4	432	1	US-09-542-520-36	Sequence 36, Appl
745	32	44.4	374	1	US-08-450-393A-2	Sequence 2, Appl	818	32	44.4	444	2	US-09-134-001C-4300	Sequence 4300, Ap
746	32	44.4	374	2	US-08-446-669-2	Sequence 2, Appl	819	32	44.4	462	2	US-09-252-991A-24194	Sequence 24194, A
747	32	44.4	374	2	US-10-039-659A-14	Sequence 14, Appl	820	32	44.4	471	2	US-09-673-814D-11	Sequence 11, Appl
748	32	44.4	374	2	US-09-625-573-2	Sequence 2, Appl	821	32	44.4	446	1	US-09-333-666-119	Sequence 11, Appl
749	32	44.4	374	2	PCT-US95-00476-2	Sequence 2, Appl	822	32	44.4	446	2	US-09-282-218A-19	Sequence 19, Appl
750	32	44.4	377	4	US-09-949-016-11221	Sequence 11221, A	823	32	44.4	455	2	US-09-612-402B-36	Sequence 36, Appl
751	32	44.4	379	2	US-09-133-962A-6	Sequence 6, Appl	824	32	44.4	458	2	US-09-542-520-36	Sequence 36, Appl
752	32	44.4	379	2	US-09-697-379-6	Sequence 6, Appl	825	32	44.4	462	2	US-09-252-991A-24194	Sequence 24194, A
753	32	44.4	382	2	US-10-116-212A-6	Sequence 6, Appl	826	32	44.4	471	2	US-09-673-814D-11	Sequence 11, Appl
754	32	44.4	382	2	US-09-492-709A-99	Sequence 299, App	827	32	44.4	476	2	US-09-673-814D-11	Sequence 11, Appl
755	32	44.4	383	2	US-08-530-862B-7	Sequence 7, Appl	828	32	44.4	476	2	US-09-673-814D-11	Sequence 11, Appl
756	32	44.4	384	1	US-08-675-650B-2	Sequence 2, Appl	829	32	44.4	476	2	US-09-673-814D-11	Sequence 11, Appl
757	32	44.4	384	1	US-08-675-650B-4	Sequence 4, Appl	830	32	44.4	476	2	US-09-673-814D-11	Sequence 11, Appl

831	32	44.4	478	2	US-09-134-001C-5065	Sequence 5065, Ap	904	32	44.4	1298	2	US-08-901-710-2	Sequence 2, Appli
832	32	44.4	485	2	US-09-291-023A-18	Sequence 18, Appl	905	32	44.4	1298	2	US-08-446-648-33	Sequence 33, Appl
833	32	44.4	485	2	US-09-381-687-1	Sequence 1, Appli	906	32	44.4	1298	2	US-09-982-610-33	Sequence 33, Appl
834	32	44.4	485	2	US-09-540-715A-18	Sequence 18, Appl	907	32	44.4	1298	4	US-09-169-079-2	Sequence 2, Appli
835	32	44.4	496	2	US-09-270-767-4392	Sequence 4392, A	908	32	44.4	1298	4	PCT-US95-04228-3	Sequence 33, Appl
836	32	44.4	498	2	US-09-107-532A-6991	Sequence 6991, Ap	909	32	44.4	1362	1	US-08-874-678-33	Sequence 33, Appl
837	32	44.4	501	2	US-09-465-519-2	Sequence 2, Appli	910	32	44.4	1362	2	US-08-643-889-33	Sequence 33, Appl
838	32	44.4	501	2	US-09-971-611-4	Sequence 4, Appli	911	32	44.4	1362	2	US-09-348-866-33	Sequence 33, Appl
839	32	44.4	501	2	US-10-136-272-2	Sequence 2, Appli	912	32	44.4	1363	1	US-10-105-901A-3	Sequence 33, Appl
840	32	44.4	501	2	US-10-136-272-2	Sequence 2, Appli	913	32	44.4	1363	1	US-08-340-011-4	Sequence 4, Appli
841	32	44.4	501	2	US-10-136-272-4	Sequence 4, Appli	914	32	44.4	1363	1	US-08-874-678-32	Sequence 32, Appl
842	32	44.4	505	2	US-09-612-402B-17	Sequence 17, Appl	915	32	44.4	1363	2	US-08-643-839-32	Sequence 32, Appl
843	32	44.4	505	2	US-09-542-520-17	Sequence 17, Appl	916	32	44.4	1363	2	US-08-901-710-4	Sequence 32, Appl
844	32	44.4	511	2	US-09-830-230A-586	Sequence 586, App	917	32	44.4	1363	2	US-09-348-886-32	Sequence 32, Appli
845	32	44.4	516	2	US-09-986-676A-2	Sequence 2, Appli	918	32	44.4	1363	2	US-09-375-248-2	Sequence 2, Appli
846	32	44.4	516	2	US-09-971-611-2	Sequence 2, Appli	919	32	44.4	1363	2	US-09-375-248-19	Sequence 19, Appl
847	32	44.4	528	2	US-09-830-230A-585	Sequence 585, App	920	32	44.4	1363	2	US-09-166-079-4	Sequence 4, Appli
848	32	44.4	530	2	US-09-328-352-7333	Sequence 7333, Ap	921	32	44.4	1363	2	US-10-105-901A-32	Sequence 32, Appl
849	32	44.4	536	2	US-09-270-767-44004	Sequence 44004, A	922	32	44.4	1368	1	US-08-874-678-34	Sequence 34, Appl
850	32	44.4	540	2	US-09-902-540-16745	Sequence 16745, A	923	32	44.4	1368	2	US-08-643-839-34	Sequence 34, Appl
851	32	44.4	549	2	US-09-252-991A-26327	Sequence 26327, A	924	32	44.4	1368	2	US-09-348-886-34	Sequence 34, Appl
852	32	44.4	553	1	US-08-661-052-16	Sequence 16, Appl	925	32	44.4	1368	2	US-10-105-901A-34	Sequence 34, Appl
853	32	44.4	553	2	US-09-188-082-16	Sequence 16, Appl	926	32	44.4	1531	2	US-09-976-594-203	Sequence 203, App
854	32	44.4	553	2	US-09-364-088-16	Sequence 16, Appl	927	32	44.4	3571	2	US-09-911-842A-2	Sequence 2, Appli
855	32	44.4	553	2	US-09-102-716-16	Sequence 16, Appl	928	31.5	43.8	57	2	US-10-006-937-6	Sequence 6, Appli
856	32	44.4	557	2	US-09-514-245-8	Sequence 8, Appli	929	31.5	43.8	119	2	US-08-767-128-10	Sequence 10, Appl
857	32	44.4	563	2	US-09-252-991A-26415	Sequence 26415, A	930	31.5	43.8	131	2	US-10-006-937-10	Sequence 10, Appl
858	32	44.4	599	2	US-09-328-352-7756	Sequence 7756, Ap	931	31.5	43.8	135	2	US-08-284-516C-36	Sequence 36, Appl
859	32	44.4	621	2	US-09-252-991A-26414	Sequence 26414, A	932	31.5	43.8	135	2	US-08-284-516C-40	Sequence 40, Appl
860	32	44.4	626	2	US-09-134-000C-4072	Sequence 4072, Ap	933	31.5	43.8	135	2	US-09-537-911A-36	Sequence 36, Appl
861	32	44.4	633	2	US-09-976-594-282	Sequence 282, App	934	31.5	43.8	138	2	US-09-537-911A-40	Sequence 40, Appl
862	32	44.4	633	2	US-09-821-687-10	Sequence 10, Appl	935	31.5	43.8	147	2	US-08-589-939-1	Sequence 1, Appli
863	32	44.4	640	2	US-09-252-991A-27542	Sequence 27542, A	936	31.5	43.8	147	2	US-09-069-628-16	Sequence 16, Appl
864	32	44.4	647	1	US-08-844-056-2	Sequence 2, Appli	937	31.5	43.8	239	2	US-09-270-767-43595	Sequence 43595, A
865	32	44.4	650	2	US-09-107-532A-5521	Sequence 5521, Ap	938	31.5	43.8	256	2	US-09-526-778A-2	Sequence 2, Appli
866	32	44.4	660	2	US-09-583-110-3241	Sequence 3241, Ap	939	31.5	43.8	258	2	US-09-526-778A-4	Sequence 4, Appli
867	32	44.4	666	2	US-09-107-433-3422	Sequence 3422, Ap	940	31.5	43.8	264	2	US-09-526-778A-78	Sequence 78, Appl
868	32	44.4	670	2	US-10-197-220-169	Sequence 169, App	941	31.5	43.8	276	2	US-09-134-000C-3606	Sequence 3606, Ap
869	32	44.4	702	2	US-10-188-066-2	Sequence 2, Appl	942	31.5	43.8	298	2	US-09-270-767-36798	Sequence 36798, A
870	32	44.4	741	2	US-09-328-352-5898	Sequence 5898, Ap	943	31.5	43.8	296	2	US-09-270-767-52015	Sequence 52015, A
871	32	44.4	765	2	US-09-248-796A-20068	Sequence 20068, A	944	31.5	43.8	305	2	US-09-500-569-2	Sequence 2, Appli
872	32	44.4	777	1	US-08-874-678-3	Sequence 3, Appli	945	31.5	43.8	305	2	US-09-971-823B-2	Sequence 2, Appli
873	32	44.4	777	2	US-08-643-839-3	Sequence 3, Appli	946	31.5	43.8	343	1	US-08-599-171A-28	Sequence 28, Appl
874	32	44.4	777	2	US-09-348-886-3	Sequence 3, Appli	947	31.5	43.8	343	1	US-08-646-590B-28	Sequence 28, Appl
875	32	44.4	777	2	US-10-105-901A-3	Sequence 3, Appli	948	31.5	43.8	343	2	US-09-069-226-28	Sequence 28, Appl
876	32	44.4	819	1	US-08-464-517-7	Sequence 7, Appli	949	31.5	43.8	343	2	US-09-412-184-28	Sequence 28, Appl
877	32	44.4	819	1	US-08-246-361A-7	Sequence 7, Appli	950	31.5	43.8	358	2	US-09-500-569-18	Sequence 18, Appl
878	32	44.4	819	4	US-08-463-772-7	Sequence 7, Appli	951	31.5	43.8	358	2	US-09-971-823B-18	Sequence 18, Appl
879	32	44.4	819	4	PCT-US93-05000-7	Sequence 7, Appli	952	31.5	43.8	364	1	US-08-204-288-2	Sequence 2, Appli
880	32	44.4	835	2	US-09-438-185A-728	Sequence 728, App	953	31.5	43.8	364	1	US-08-715-325-2	Sequence 5, Appli
881	32	44.4	982	2	US-09-556-877-176	Sequence 176, App	954	31.5	43.8	365	1	US-08-715-325-2	Sequence 2, Appli
882	32	44.4	982	2	US-09-620-412C-176	Sequence 176, App	955	31.5	43.8	365	2	US-09-500-569-4	Sequence 4, Appli
883	32	44.4	982	2	US-09-598-419-176	Sequence 176, App	956	31.5	43.8	365	2	US-09-971-823B-4	Sequence 4, Appli
884	32	44.4	984	2	US-09-612-402B-43	Sequence 43, Appl	957	31.5	43.8	365	2	US-09-947-027-6	Sequence 6, Appli
885	32	44.4	1006	2	US-09-556-877-190	Sequence 190, App	958	31.5	43.8	368	2	US-08-991-677-6	Sequence 6, Appli
886	32	44.4	1006	2	US-09-620-412C-190	Sequence 190, App	959	31.5	43.8	442	2	US-09-540-236-2820	Sequence 2820, App
887	32	44.4	1006	2	US-09-598-419-190	Sequence 190, App	960	31.5	43.8	474	2	US-09-248-796A-17534	Sequence 17534, A
888	32	44.4	1012	2	US-09-612-402B-2	Sequence 2, Appli	961	31.5	43.8	524	2	US-10-006-937-13	Sequence 13, Appl
889	32	44.4	1012	2	US-09-542-520-2	Sequence 2, Appli	962	31.5	43.8	543	2	US-10-006-937-12	Sequence 12, Appl
890	32	44.4	1013	2	US-09-612-402B-15	Sequence 15, Appl	963	31.5	43.8	617	2	US-09-107-443-4596	Sequence 4596, Ap
891	32	44.4	1013	2	US-09-612-402B-16	Sequence 16, Appl	964	31.5	43.8	655	2	US-09-298-727-2	Sequence 2, Appli
892	32	44.4	1013	2	US-09-542-520-15	Sequence 15, Appl	965	31.5	43.8	656	2	US-09-583-110-3258	Sequence 3258, Ap
893	32	44.4	1013	2	US-09-542-520-16	Sequence 16, Appl	966	31.5	43.8	658	2	US-09-583-110-4743	Sequence 4743, Ap
894	32	44.4	1062	2	US-09-487-558B-334	Sequence 234, App	967	31.5	43.8	659	2	US-09-107-433-4595	Sequence 4595, Ap
895	32	44.4	1166	2	US-09-248-796A-19646	Sequence 19646, A	968	31.5	43.8	1577	1	US-08-793-824-2	Sequence 2, Appli
896	32	44.4	1287	4	US-08-200-232-2	Sequence 2, Appli	969	31.5	43.8	2710	1	US-08-568-459A-12	Sequence 12, Appli
897	32	44.4	1287	4	PCT-US95-02219-2	Sequence 2, Appli	970	31.5	43.8	2710	1	US-08-487-886B-12	Sequence 12, Appl
898	32	44.4	1287	4	PCT-US95-02219A-2	Sequence 2, Appli	971	31.5	43.8	2710	2	US-09-210-288-12	Sequence 12, Appl
899	32	44.4	1296	2	US-08-470-260-3	Sequence 3, Appli	972	31.5	43.8	2710	2	US-10-153-273-12	Sequence 12, Appl
900	32	44.4	1296	2	US-08-471-491-3	Sequence 3, Appli	973	31.5	43.8	3060	1	US-08-487-826B-14	Sequence 14, Appl
901	32	44.4	1296	2	US-08-466-662-3	Sequence 3, Appli	974	31	43.1	12	1	US-08-208-886C-85	Sequence 85, Appl
902	32	44.4	1298	1	US-08-822-616-33	Sequence 33, Appli	975	31	43.1	12	1	US-08-704-744-87	Sequence 87, Appl
903	32	44.4	1298	1	US-08-340-011-2	Sequence 2, Appli	976	31	43.1	12	1	US-08-469-557-66	Sequence 66, Appl

977 31 43.1 12 1 US-08-290-793B-66 Sequence 66, Appl
978 31 43.1 20 2 US-09-962-756-768 Sequence 768, App
979 31 43.1 24 2 US-09-329-350-17 Sequence 17, Appl
980 31 43.1 24 2 US-08-841-636A-17 Sequence 17, Appl
981 31 43.1 24 6 5470825-4 Patent No. 5470825
982 31 43.1 25 1 US-08-245-853-4 Sequence 4, Appl1
983 31 43.1 25 1 US-08-573-675-4 Sequence 4, Appl1
984 31 43.1 36 1 US-08-053-131-84 Sequence 84, Appl1
985 31 43.1 36 1 US-08-645-641-84 Sequence 84, Appl1
986 31 43.1 36 1 US-07-853-408B-84 Sequence 84, Appl1
987 31 43.1 36 1 US-08-096-762-84 Sequence 84, Appl1
988 31 43.1 36 1 US-08-308-865-84 Sequence 84, Appl1
989 31 43.1 36 2 US-09-042-353-281 Sequence 281, App
990 31 43.1 36 2 US-08-758-417A-129 Sequence 129, App
991 31 43.1 36 4 PCT-US92-10983-84 Sequence 84, Appl
992 31 43.1 55 2 US-09-270-767-35314 Sequence 36314, A
993 31 43.1 55 2 US-08-468-011A-9 Sequence 51531, A
994 31 43.1 60 2 US-08-468-011A-9 Sequence 9, Appl1
995 31 43.1 60 2 US-09-236-468A-9 Sequence 21341, A
996 31 43.1 62 2 US-09-248-796A-21341 Sequence 21341, A
997 31 43.1 63 2 US-09-107-433-3438 Sequence 3438, Ap
998 31 43.1 64 2 US-09-134-000C-4532 Sequence 4532, Ap
999 31 43.1 68 2 US-09-248-796A-26745 Sequence 26745, A
1000 31 43.1 72 2 US-09-248-796A-23699 Sequence 23699, A

ALIGNMENTS

RESULT 1
US-08-974-899-12
Sequence 12, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Prestea, Leonard G.
APPLICANT: Jardiou, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-974-899-12
Query Match 100.0%; Score 72; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTYFPDY 12
Db 1 GIFYGTYFPDY 12

RESULT 2
US-09-795-798-12
Sequence 12, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Prestea, Leonard G.
APPLICANT: Jardiou, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-795-798-12
Query Match 100.0%; Score 72; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTYFPDY 12
Db 1 GIFYGTYFPDY 12
RESULT 3
US-09-027-449-50
Sequence 50, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Prestea, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-50

Query Match 100.0%; Score 72; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYTTFDY 12
DB 100 GIFYGTYTTFDY 111

RESULT 4
US-08-804-444A-50
Sequence 50, Application US/0880444A
Patent No. 6117980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-804-444A-50

Query Match 100.0%; Score 72; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYTTFDY 12
DB 100 GIFYGTYTTFDY 111

RESULT 5
US-09-026-985-50
Sequence 50, Application US/09026985
Patent No. 6133426

GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-026-985-50

Query Match 100.0%; Score 72; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYTTFDY 12
DB 100 GIFYGTYTTFDY 111

RESULT 6
US-09-121-952A-50
Sequence 50, Application US/09121952A
Patent No. 645835
GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokhi, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-50
Query Match 100.0%; Score 72; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTYFDY 12
DB 100 GIFYGTYFDY 111
RESULT 7
US-09-234-340A-50
Sequence 50, Application US/09234340A
Patent No. 6468532
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokhi, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-50
Query Match 100.0%; Score 72; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTYFDY 12
DB 100 GIFYGTYFDY 111
RESULT 8
US-09-355-014-50
Sequence 50, Application US/09355014
Patent No. 6870033
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokhi, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
FILING DATE: 21-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-355-014-50
SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Query Match 100.0%; Score 72; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFYGTTTFDY 12
Db 100 GIFYGTTTFDY 111

RESULT 9
US-08-974-899-4
Sequence 4, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 60/031971
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-4

Query Match 100.0%; Score 72; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFYGTTTFDY 12
Db 99 GIFYGTTTFDY 110

RESULT 10
US-08-974-899-5
Sequence 5, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 60/031971
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-5

Query Match 100.0%; Score 72; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFYGTTTFDY 12
Db 99 GIFYGTTTFDY 110

RESULT 11
US-08-974-899-24
Sequence 24, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/974,899
;; FILING DATE:
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/031971
;; FILING DATE: 11/27/96
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 40,378
;; REFERENCE/DOCKET NUMBER: P1014R1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1994
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 121 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-974-899-24

Query Match 100.0%; Score 72; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYFDY 12
|||
Db 99 GIFYGTYFDY 110

RESULT 12
US-09-795-798-4
; Sequence 4, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-795-798-4

Query Match 100.0%; Score 72; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYFDY 12
|||
Db 99 GIFYGTYFDY 110

RESULT 13
US-09-795-798-5
; Sequence 5, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-795-798-5

Query Match 100.0%; Score 72; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYFDY 12
|||
Db 99 GIFYGTYFDY 110

RESULT 14
US-09-795-798-24
; Sequence 24, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-795-798-24

Query Match 100.0%; Score 72; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYPDY 12
|||
Db 99 GIFYGTYPDY 110

RESULT 15
US-08-497-312-26
Sequence 26, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
TITLE OF INVENTION: antibody variable domains, compositions containing them.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE:
COUNTRY: CUBA
ZIP: 11600
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
TELECOMMUNICATION INFORMATION:

TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-497-312-26

Query Match 75.0%; Score 54; DB 1; Length 120;
Best Local Similarity 63.6%; Pred. No. 0.3;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYFYGTYPDY 12
:|:|:|:|
Db 99 VYYGSSYFDY 109

RESULT 16
US-08-497-312-28
Sequence 28, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
TITLE OF INVENTION: antibody variable domains, compositions containing them.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE:
COUNTRY: CUBA
ZIP: 11600
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497,312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 1PM04UT
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-497-312-28

Query Match 75.0%; Score 54; DB 1; Length 120;
Best Local Similarity 63.6%; Pred. No. 0.3;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYFYGTYPDY 12

Db 99 YYYGSSYFDY 109

RESULT 17
US-09-252-991A-20350

; Sequence 20350, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 20350

; LENGTH: 439

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20350

Query Match 63.9%; Score 46; DB 2; Length 439;

Best Local Similarity 72.7%; Pred. No. 19;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYFGTYTYPD 11

Db 214 GHFGTYTYPD 224

RESULT 18
US-10-092-246-10

; Sequence 10, Application US/10092246

; Patent No. 6501314

; GENERAL INFORMATION:

; APPLICANT: The Minister of National Defence, Government of Canada

; APPLICANT: Fulton, R E

; APPLICANT: Alvi, Azhar E

; APPLICANT: Nagata, Leslie

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC

; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)

; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10/092,246

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Mouse hybridoma cell line 1A4A1

US-10-092-246-10

Query Match 61.1%; Score 44; DB 2; Length 122;

Best Local Similarity 66.7%; Pred. No. 10;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTYTYPD 12

Db 103 YYGSSYFDY 111

RESULT 19
US-10-092-246-11

; Sequence 11, Application US/10092246

; Patent No. 6501314

; GENERAL INFORMATION:

; APPLICANT: The Minister of National Defence, Government of Canada

; APPLICANT: Fulton, R E

; APPLICANT: Alvi, Azhar E

; APPLICANT: Nagata, Leslie

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo

; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)

; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10/092,246

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Mouse hybridoma cell line 1A4A1

US-10-092-246-11

Query Match 61.1%; Score 44; DB 2; Length 122;

Best Local Similarity 66.7%; Pred. No. 10;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTYTYPD 12

Db 103 YYGSSYFDY 111

RESULT 20
US-10-096-246A-10

; Sequence 10, Application US/10096246A

; Patent No. 6818748

; GENERAL INFORMATION:

; APPLICANT: Fulton, R. Elaine

; APPLICANT: Nagata, Leslie

; APPLICANT: Alvi, Azhar E

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of

; TITLE OF INVENTION: Monoclonal scFv Antibody Against Venezuelan Equine Encephalitis

; TITLE OF INVENTION: Virus (VEE)

; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10/096,246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 10

; LENGTH: 122

; TYPE: PRT

; ORGANISM: mouse

US-10-096-246A-10

Query Match 61.1%; Score 44; DB 2; Length 122;

Best Local Similarity 66.7%; Pred. No. 10;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTYTYPD 12

Db 103 YYGSSYFDY 111

RESULT 21
US-10-096-246A-11

; Sequence 11, Application US/10096246A

; Patent No. 6818748

; GENERAL INFORMATION:

; APPLICANT: Fulton, R. Elaine

; APPLICANT: Nagata, Leslie

; APPLICANT: Alvi, Azhar E

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of

; TITLE OF INVENTION: Monoclonal scFv Antibody Against Venezuelan Equine Encephalitis

; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10/096,246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11

; LENGTH: 122

TYPE: PRT
ORGANISM: mouse
US-10-096-246A-11

Query Match
Best Local Similarity 61.1%; Score 44; DB 2; Length 122;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
:|||||
Db 103 YYGSSYFDY 111

RESULT 22
US-08-454-899G-15
Sequence 15, Application US/08454899G
Patent No. 6602503
GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.
APPLICANT: Carr, Frank J.
APPLICANT: Tempest, Philip R.
TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
FILE REFERENCE: 10274-007001
CURRENT APPLICATION NUMBER: US/08/454,899G
CURRENT FILING DATE: 1995-05-31
PRIOR APPLICATION NUMBER: US 08/004,798
PRIOR FILING DATE: 1993-01-12
PRIOR APPLICATION NUMBER: PCT/US94/00266
PRIOR FILING DATE: 1994-01-07
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 139
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: heavy chain variable region insert
US-08-454-899G-15

Query Match
Best Local Similarity 61.1%; Score 44; DB 2; Length 139;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
:|||||
Db 120 YYGSSYFDY 128

RESULT 23
US-08-428-257A-72
Sequence 72, Application US/08428257A
Patent No. 5885808
GENERAL INFORMATION:
APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A. A.
TITLE OF INVENTION: Compounds to target cells
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,257A
FILING DATE: 07/05/95
CLASSIFICATION: 514

INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-257A-72

Query Match
Best Local Similarity 61.1%; Score 44; DB 1; Length 269;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
:|||||
Db 123 YYGSSYFDY 131

RESULT 24
US-08-491-988-3
Sequence 3, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY NISSEN GOLDBERG KTEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-3

Query Match
Best Local Similarity 61.1%; Score 44; DB 1; Length 269;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
:|||||
Db 123 YYGSSYFDY 131

RESULT 25
US-08-491-988-9
Sequence 9, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENON A.
APPLICANT: SPOONER, ROBERT A.

APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-9

Query Match 61.1%; Score 44; DB 1; Length 402;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 FYGTTYFDY 12
:|::|
Db 123 YYGSSYFDY 131

RESULT 26
US-08-491-988-7
Sequence 7, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090

TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-7

Query Match 61.1%; Score 44; DB 1; Length 415;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 FYGTTYFDY 12
:|::|
Db 123 YYGSSYFDY 131

RESULT 27
US-08-491-988-5
Sequence 5, Application US/08491988
Patent No. 5973116
GENERAL INFORMATION:
APPLICANT: EPENETOS, AGAMENON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA
TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: MCAULAY NISSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-5

Query Match 61.1%; Score 44; DB 1; Length 435;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 FYGTTYFDY 12
:|::|
Db 123 YYGSSYFDY 131

RESULT 28
US-09-583-110-4749
Sequence 4749, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...236
SEQUENCE DESCRIPTION: SEQ ID NO: 3704
US-09-107-433-3704

Query Match 59.7%; Score 43; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFDY 12
| | | | | : | |
| | | | | : | |
Db 113 IPFYGTTHADY 123

RESULT 29
US-09-107-433-3704
; Sequence 3704, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION NUMBER: 60/085131
; APPLICATION DATA:
; APPLICATION NUMBER: 60/051553
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3704:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae

FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...236
SEQUENCE DESCRIPTION: SEQ ID NO: 3704
US-09-107-433-3704

Query Match 59.7%; Score 43; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFYGTTFDY 12
| | | | | : | |
| | | | | : | |
Db 115 IPFYGTTHADY 125

RESULT 30
US-08-678-194-8
; Sequence 8, Application US/08678194
; Patent No. 5922845
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,194
; FILING DATE: July 11, 1996
; PRIOR APPLICATION DATA: No. 5922845e
; APPLICATION NUMBER: US
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Beth A. Arnold
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-678-194-8

Query Match 58.3%; Score 42; DB 1; Length 142;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1 GIYFYGTTFDY 12
| | | | | : | |
| | | | | : | |
Db 118 GVIYGSYEAPPY 131

RESULT 31
US-08-890-011-8
; Sequence 8, Application US/08890011
; Patent No. 6193966
; GENERAL INFORMATION:

```

;
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
; TITLE OF INVENTION: Comprised of Anti-FC
; TITLE OF INVENTION: {SYMBOL 97 \f "Symbol"} Receptor Antibodies
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,011
; FILING DATE: July 9, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/678,194
; FILING DATE: July 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-064CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-890-011-8

Query Match      58.3%; Score 42; DB 2; Length 142;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy      1 GIFYGTTY--FDY 12
        |||:|||||
Db      118 GVTYGSSTYEAFFY 131

RESULT 32
US-09-262-724-8
; Sequence 8, Application US/09262724
; Patent No. 6303755
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
; TITLE OF INVENTION: Comprised of Anti-FC{SYMBOL 97 \f "Symbol"}
; Receptor Antibodies
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
```

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/262,724
; FILING DATE: 04-Mar-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,194
; FILING DATE: July 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Beth A. Arnold
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-262-724-8

Query Match      58.3%; Score 42; DB 2; Length 142;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

Qy      1 GIFYGTTY--FDY 12
        |||:|||||
Db      118 GVTYGSSTYEAFFY 131

RESULT 33
US-09-621-976-4012
; Sequence 4012, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4012
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17...-1
; US-09-621-976-4012

Query Match      58.3%; Score 42; DB 2; Length 142;
Best Local Similarity 63.6%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 GIFYGTTYFD 11
        |||
Db      20 GIFYSNKRLD 30

RESULT 34
US-09-203-958A-4
; Sequence 4, Application US/09203958A
; Patent No. 6682928
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: GOLDSTEIN, Joel
; APPLICANT: GRAZIANO, Robert
; APPLICANT: DEO, Yashwant M.
; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
```

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; TITLE OF INVENTION: BINDING COMPONENTS
; FILE REFERENCE: MXI-099CPA
; CURRENT APPLICATION NUMBER: US/09/203,958A
; CURRENT FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 60/067232
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-203-958A-4

Query Match      58.3%; Score 42; DB 2; Length 353;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 7; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY      1 GYFYGTYY--PDY 12
        ||:||||:|
DB      136 GYYYSYAPPY 149

RESULT 35
US-09-270-767-58255
; Sequence 58255, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58255
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58255

Query Match      57.6%; Score 41.5; DB 2; Length 26;
Best Local Similarity 72.7%; Pred. No. 5.1;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      1 GYFYGTYY 10
        ||:||||
DB      9 GYFYGTYY 19

RESULT 36
US-09-406-535-7
; Sequence 7, Application US/09406535
; Patent No. 6376653
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: T1e2 Antagonist Antibodies
; FILE REFERENCE: P50844
; CURRENT APPLICATION NUMBER: US/09/406,535
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,100
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:

```

```

; NAME/KEY: SITE
; LOCATION: (1)...(10)
; OTHER INFORMATION: heavy chain CDR 3
US-09-406-535-7

Query Match      54.2%; Score 39; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 FYGTTFDY 12
        ||:||||
DB      2 YGPFYFDY 10

RESULT 37
US-09-406-535-2
; Sequence 2, Application US/09406535
; Patent No. 6376653
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: T1e2 Antagonist Antibodies
; FILE REFERENCE: P50844
; CURRENT APPLICATION NUMBER: US/09/406,535
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,100
; EARLIER FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-406-535-2

Query Match      54.2%; Score 39; DB 2; Length 119;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 FYGTTFDY 12
        ||:||||
DB      100 YGPFYFDY 108

RESULT 38
US-10-014-012-214
; Sequence 214, Application US/10014012
; Patent No. 6919189
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: McWhiter, John
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: NESTED OLIGONUCLEOTIDES CONTAINING A HAIRPIN FOR NUCLEIC ACID
; FILE REFERENCE: 1087-35
; CURRENT APPLICATION NUMBER: US/10/014,012
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,669
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/323,400
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 214
; LENGTH: 121
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: cloned antibody
US-10-014-012-214

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Query Match 54.2%; Score 39; DB 2; Length 121;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IYFGTYFD 11
||:|||||:
Db 45 IYSGTTYN 54

RESULT 39
US-10-014-012-213
; Sequence 213, Application US/10014012
; Patent No. 6919189

; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: McWhirter, John
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: NESTED OLIGONUCLEOTIDES CONTAINING A HAIRPIN FOR NUCLEIC ACID
; TITLE OF INVENTION: AMPLIFICATION
; FILE REFERENCE: 1087-35
; CURRENT APPLICATION NUMBER: US/10/014,012
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,669
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/323,400
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 213
; LENGTH: 122
; TYPE: PRT

; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: cloned antibody
US-10-014-012-213

Query Match 54.2%; Score 39; DB 2; Length 122;
Best Local Similarity 60.0%; Pred. No. 61;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IYFGTYFD 11
||:|||||:
Db 48 IYSGTTYN 57

RESULT 40
US-08-860-174A-7
; Sequence 7, Application US/08860174A
; Patent No. 5989830

; GENERAL INFORMATION:
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelis Paul Erik
; APPLICANT: VERHOEIJEN, Martine Elisa
; APPLICANT: WILSON, Steve
; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; STREET: 9th Floor, East Tower
; CITY: WASHINGTON, D.C.
; STATE:
; COUNTRY: UNITED STATES
; ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,174A
; FILING DATE: June 16, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95307332.7
; FILING DATE: October 16, 1995
; APPLICATION NUMBER: PCT/EP/96/03605
; FILING DATE: August 14, 1996
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-860-174A-7

Query Match 54.2%; Score 39; DB 1; Length 142;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FYGTYFDY 12
:|||||
Db 123 YYGKGYFDY 131

RESULT 41
US-08-860-174A-12
; Sequence 12, Application US/08860174A
; Patent No. 5989830

; GENERAL INFORMATION:
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelis Paul Erik
; APPLICANT: VERHOEIJEN, Martine Elisa
; APPLICANT: WILSON, Steve
; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; STREET: 9th Floor, East Tower
; CITY: WASHINGTON, D.C.
; STATE:
; COUNTRY: UNITED STATES
; ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,174A
; FILING DATE: June 16, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95307332.7
; FILING DATE: October 16, 1995
; APPLICATION NUMBER: PCT/EP/96/03605
; FILING DATE: August 14, 1996
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-860-174A-12

Query Match 54.2%; Score 39; DB 1; Length 274;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FYGTYFDY 12
:|||||
Db 123 YYGKGYFDY 131

RESULT 42
US-08-860-174A-10
; Sequence 10, Application US/08860174A
; Patent No. 5989830
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelis Paul Erik
; APPLICANT: VERHOEIJEN, Martine Elisa
; APPLICANT: WILSON, Steve
; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
; TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; STREET: 9th Floor, East Tower
; CITY: WASHINGTON, D.C.
; STATE:
; COUNTRY: UNITED STATES
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,174A
; FILING DATE: June 16, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95307332.7
; FILING DATE: October 16, 1995
; APPLICATION NUMBER: PCT/EP/96/03605
; FILING DATE: August 14, 1996
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
US-08-860-174A-10

Query Match 54.2%; Score 39; DB 1; Length 282;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FYGTYFPDY 12
Db 123 YYGKGFDY 131

RESULT 43
US-09-540-236-3513
; Sequence 3513, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3513
; LENGTH: 486
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-3513

Query Match 54.2%; Score 39; DB 2; Length 486;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIFYGTYFPDY 12
Db 39 GIVCGMTVYDY 50

RESULT 44
US-09-514-245-2
; Sequence 2, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAUD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CAROLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-2

Query Match 54.2%; Score 39; DB 2; Length 545;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FYGTYFPDY 12
Db 237 FFGPQTFDY 245

RESULT 45
US-09-537-120-2
; Sequence 2, Application US/09537120
; Patent No. 6608018
; GENERAL INFORMATION:
; APPLICANT: No. 6608018ozymes A/S
; APPLICANT: Shinohara, Mari L.
; TITLE OF INVENTION: Polypeptides having branching enzyme activity and nucleic acids
; TITLE OF INVENTION: same
; FILE REFERENCE: 5860.200-US
; CURRENT APPLICATION NUMBER: US/09/537,120
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Rhodothermus obamensis
US-09-537-120-2

Query Match 54.2%; Score 39; DB 2; Length 621;
Best Local Similarity 54.5%; Pred. No. 3.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IYFGTYFPDY 12
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RESULT 46
US-09-563-222C-55
; Sequence 55, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-55

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Best Local Similarity 58.3% Pred. No. 12;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Db 1 GGYGYGYYYDY 12

RESULT 47
US-09-248-796A-21665
; Sequence 21665, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21665
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21665

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Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYFYGTTFDY 12
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RESULT 48
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; Sequence 14, Application US/08434000A
; Patent No. 6046037
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
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NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Filth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 1
APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-434-000A-14
US-08-434-000A-14
Query Match          52.8% Score 38; DB 2; Length 132;
Best Local Similarity 66.7% Pred. No. 94;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FYGTTFDY 12
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Db 113 YYCATYFDY 121

RESULT 49
US-09-312-157-14
; Sequence 14, Application US/09312157
; Patent No. 6303341
; GENERAL INFORMATION:
; APPLICANT: ANDREW C. HIATT, JULIAN
; APPLICANT: K.-C. MA, THOMAS LEHNER
; TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
; TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Filth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
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SOFTWARE: Word Perfect 5.1
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APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-351
SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
DESCRIPTION: Guy's 13 Gamma 1
US-09-312-157-14

Query Match 52.8%; Score 38; DB 2; Length 132;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
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Db 113 YYCATYFDY 121

RESULT 50
US-09-717-888-14
Sequence 14, Application US/09717888
Patent No. 6808709
GENERAL INFORMATION:
APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
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FILING DATE: 20-No. 6808709-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/367,395
FILING DATE: 30-Dec-94
ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
TELEX: 67-3510
SEQUENCE LISTING
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
DESCRIPTION: Guy's 13 Gamma 1
US-09-717-888-14

Query Match 52.8%; Score 38; DB 2; Length 132;
Best Local Similarity 66.7%; Pred. No. 94;
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Db 113 YYCATYFDY 121

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Wed Jan 18 11:47:39 2006

us-10-665-658-12.rapbm

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:50:44 ; Search time 58.6336 Seconds
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Title: US-10-665-658-12

Perfect score: 72

Sequence: 1 GIVFYGTYRFDY 12

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Post-processing: Minimum Match 0%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	72	100.0	121	4	US-10-727-737-4
7	72	100.0	121	4	US-10-727-737-5
8	72	100.0	121	4	US-10-727-737-17
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16	56	77.8	11	4	US-10-727-737-52
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19	54	75.0	255	5	US-10-511-794-21
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111	39	54.2	126	4	US-10-041-860-306	Sequence 306, App	184	39	54.2	594	5	US-10-732-923-23690	Sequence 23690, A
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122	39	54.2	309	3	US-09-777-789-36	Sequence 36, Appl	195	39	54.2	852	6	US-11-050-926-57	Sequence 57, Appl
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130	39	54.2	309	3	US-09-795-271-43	Sequence 43, Appl	203	39	54.2	1069	4	US-10-177-293-80	Sequence 80, Appl
131	39	54.2	309	3	US-09-974-149-20	Sequence 20, Appl	204	39	54.2	1069	6	US-11-050-926-55	Sequence 55, Appl
132	39	54.2	317	4	US-10-292-798-128	Sequence 128, App	205	39	54.2	1090	4	US-10-097-340-61	Sequence 61, Appl
133	39	54.2	318	3	US-09-886-055-389	Sequence 389, App	206	39	54.2	1091	6	US-11-050-926-61	Sequence 61, Appl
134	39	54.2	318	3	US-09-804-291-389	Sequence 389, App	207	39	54.2	1491	4	US-10-732-923-1740	Sequence 1740, Ap
135	39	54.2	318	4	US-10-017-161-152	Sequence 152, App	208	39	54.2	1741	4	US-10-437-963-126375	Sequence 126375, Sequence 52, Appl
136	39	54.2	318	4	US-10-292-798-130	Sequence 130, App	209	39	53.5	13	5	US-10-745-775-5	Sequence 52, Appl
137	39	54.2	318	4	US-10-343-650A-532	Sequence 532, App	210	39	53.5	13	5	US-10-745-775-52	Sequence 52, Appl
138	39	54.2	318	4	US-10-473-518-68	Sequence 68, Appl	211	39	53.5	13	5	US-10-745-775-54	Sequence 54, Appl
139	39	54.2	318	5	US-10-819-316-389	Sequence 389, App	212	39	53.5	13	5	US-10-745-775-64	Sequence 56, Appl
140	39	54.2	319	3	US-09-886-055-69	Sequence 69, Appl	213	39	53.5	13	5	US-10-745-775-68	Sequence 58, Appl
141	39	54.2	319	3	US-09-974-591-6	Sequence 6, Appl	214	39	53.5	13	5	US-10-745-775-62	Sequence 62, Appl
142	39	54.2	319	3	US-09-777-789-7	Sequence 7, Appl	215	39	53.5	16	4	US-10-169-351-11	Sequence 11, Appl
143	39	54.2	319	3	US-09-777-789-23	Sequence 23, Appl	216	39	53.5	118	5	US-10-938-353-111	Sequence 11, App
144	39	54.2	319	3	US-09-777-789-27	Sequence 27, Appl	217	39	53.5	120	5	US-10-745-775-1	Sequence 1, Appl
145	39	54.2	319	3	US-09-804-291-69	Sequence 69, Appl	218	39	53.5	120	5	US-10-783-710-1	Sequence 31, Appl
146	39	54.2	319	3	US-09-907-218-67	Sequence 67, Appl	219	39	53.5	125	4	US-10-169-351-31	Sequence 31, Appl
147	39	54.2	319	3	US-09-974-149-6	Sequence 6, Appl	220	39	53.5	125	4	US-10-169-351-102	Sequence 102, App
148	39	54.2	319	4	US-10-220-382-12	Sequence 12, Appl	221	39	53.5	252	4	US-10-169-351-49	Sequence 49, Appl
149	39	54.2	319	5	US-10-819-316-69	Sequence 69, Appl	222	39	53.5	276	3	US-09-855-254B-2	Sequence 2, Appl
150	39	54.2	320	3	US-09-886-055-385	Sequence 385, App	223	39	53.5	432	4	US-10-282-122A-60828	Sequence 60828, A
151	39	54.2	320	3	US-09-804-291-385	Sequence 385, App	224	39	53.5	447	5	US-10-745-775-16	Sequence 16, Appl
152	39	54.2	320	4	US-10-024-399-38	Sequence 38, Appl	225	39	52.8	11	5	US-10-996-316-197	Sequence 197, Appl
153	39	54.2	320	4	US-10-387-629-132	Sequence 132, App	226	39	52.8	18	3	US-09-563-222-55	Sequence 55, Appl
154	39	54.2	320	4	US-10-292-798-528	Sequence 528, App	227	39	52.8	18	4	US-10-783-960-55	Sequence 55, Appl
155	39	54.2	320	4	US-10-343-650A-540	Sequence 540, App	228	39	52.8	65	4	US-10-425-115-766030	Sequence 766030, Sequence 346030,
156	39	54.2	320	4	US-10-473-518-7	Sequence 7, Appl	229	39	52.8	85	4	US-10-425-115-774579	Sequence 774579, Sequence 10, Appl
157	39	54.2	320	5	US-10-819-316-385	Sequence 385, App	230	39	52.8	120	5	US-10-503-504-4	Sequence 10, Appl
158	39	54.2	347	3	US-09-886-055-361	Sequence 361, App	231	39	52.8	120	5	US-10-484-280-4	Sequence 10, Appl
159	39	54.2	347	3	US-09-804-291-361	Sequence 361, App	232	39	52.8	120	5	US-10-484-280-4	Sequence 16, Appl
160	39	54.2	347	4	US-10-017-161-150	Sequence 150, App	233	39	52.8	120	5	US-10-484-280-28	Sequence 28, Appl
161	39	54.2	347	4	US-10-343-650A-536	Sequence 536, App	234	39	52.8	132	5	US-09-982-107-14	Sequence 14, Appl
162	39	54.2	347	5	US-10-819-316-361	Sequence 361, App	235	39	52.8	132	5	US-10-781-989-14	Sequence 14, Appl
163	39	54.2	352	4	US-10-282-122A-58554	Sequence 58554, A	236	39	52.8	143	4	US-10-424-599-178877	Sequence 178877, A
164	39	54.2	451	4	US-10-679-620-78	Sequence 78, Appl	237	39	52.8	182	4	US-10-767-701-99993	Sequence 99993, A
165	39	54.2	451	6	US-11-132-143-78	Sequence 78, Appl	238	39	52.8	196	4	US-10-424-599-984643	Sequence 984643, A
166	39	54.2	480	4	US-10-282-122A-63032	Sequence 63032, A	239	39	52.8	199	5	US-10-474-792-374	Sequence 374, App
167	39	54.2	512	4	US-10-679-620-70	Sequence 70, Appl	240	39	52.8	243	4	US-10-335-977-8234	Sequence 8234, Ap
168	39	54.2	512	6	US-11-132-143-70	Sequence 70, Appl	241	39	52.8	243	4	US-10-335-977-8235	Sequence 8235, Ap
169	39	54.2	517	6	US-10-679-620-68	Sequence 68, Appl	242	39	52.8	280	4	US-10-156-761-9488	Sequence 9488, Ap
170	39	54.2	517	6	US-11-132-143-68	Sequence 68, Appl	243	39	52.8	280	4	US-10-156-761-9491	Sequence 9491, Ap
171	39	54.2	519	4	US-10-679-620-66	Sequence 66, Appl	244	39	52.8	289	5	US-10-774-355A-2196	Sequence 2196, Ap
172	39	54.2	519	6	US-11-132-143-66	Sequence 66, Appl	245	39	52.8	310	5	US-10-774-355A-1740	Sequence 1740, Ap
173	39	54.2	545	4	US-10-682-420-2	Sequence 2, Appl	246	39	52.8	314	5	US-10-774-355A-2372	Sequence 2372, Ap

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247	38	52.8	315	5	US-10-774-355A-1403	Sequence 1403, Ap	320	37	51.4	19	4	US-10-783-950-61	Sequence 61, Appl
248	38	52.8	315	5	US-10-774-355A-1422	Sequence 1422, Ap	321	37	51.4	21	5	US-10-751-826-125	Sequence 125, Appl
249	38	52.8	320	4	US-10-023-601-36	Sequence 36, Appl	322	37	51.4	26	4	US-10-153-159-62	Sequence 62, Appl
250	38	52.8	330	5	US-10-774-355A-2069	Sequence 2069, Ap	323	37	51.4	26	4	US-10-153-176-62	Sequence 62, Appl
251	38	52.8	335	4	US-10-425-115-246563	Sequence 246563, Sequence 246574,	324	37	51.4	26	4	US-10-443-134A-62	Sequence 267112, Sequence 267127,
252	38	52.8	335	4	US-10-425-115-246574	Sequence 246574, Sequence 40448, Ap	325	37	51.4	34	4	US-10-425-115-267772	Sequence 267772, Sequence 232507,
253	38	52.8	335	5	US-10-739-930-7695	Sequence 7695, Ap	326	37	51.4	59	4	US-10-424-599-232057	Sequence 232507, Sequence 298035,
254	38	52.8	355	4	US-10-425-114-40448	Sequence 40448, A	327	37	51.4	71	4	US-10-425-115-298035	Sequence 298035, Sequence 302978,
255	38	52.8	430	3	US-09-815-242-11250	Sequence 11250, A	328	37	51.4	102	5	US-10-425-115-302978	Sequence 302978, Sequence 58, Appl
256	38	52.8	430	4	US-10-282-122A-58538	Sequence 58538, A	329	37	51.4	108	4	US-10-078-958-20	Sequence 58, Appl
257	38	52.8	443	4	US-10-758-979-12	Sequence 12, Appl	330	37	51.4	117	4	US-10-379-392-58	Sequence 122, Appl
258	38	52.8	450	5	US-10-503-504-11	Sequence 11, Appl	331	37	51.4	117	4	US-10-379-392-122	Sequence 122, Appl
259	38	52.8	450	5	US-10-484-280-18	Sequence 18, Appl	332	37	51.4	117	4	US-10-379-392-124	Sequence 124, Appl
260	38	52.8	456	4	US-10-369-493-3815	Sequence 3815, Ap	333	37	51.4	117	4	US-10-379-392-130	Sequence 130, Appl
261	38	52.8	504	4	US-10-437-963-187452	Sequence 187452, A	334	37	51.4	117	4	US-10-425-115-299086	Sequence 299086, Sequence 116, Appl
262	38	52.8	522	5	US-10-732-923-23526	Sequence 23526, A	335	37	51.4	117	4	US-09-056-160B-114	Sequence 116, Appl
263	38	52.8	523	4	US-10-099-322-123	Sequence 123, App	336	37	51.4	118	3	US-09-056-160B-116	Sequence 116, Appl
264	38	52.8	523	4	US-10-044-564-123	Sequence 123, App	337	37	51.4	118	3	US-09-056-160B-118	Sequence 118, Appl
265	38	52.8	539	5	US-10-732-923-23519	Sequence 23519, A	338	37	51.4	118	3	US-10-234-671-112	Sequence 112, App
266	38	52.8	551	4	US-10-369-493-3309	Sequence 3309, Ap	339	37	51.4	118	4	US-10-234-671-114	Sequence 114, App
267	38	52.8	552	4	US-10-369-493-3219	Sequence 3219, Ap	340	37	51.4	118	4	US-10-234-671-116	Sequence 116, App
268	38	52.8	593	4	US-10-156-761-14765	Sequence 14765, A	341	37	51.4	118	5	US-10-683-043-11	Sequence 11, Appl
269	38	52.8	607	5	US-10-029-345A-150	Sequence 150, App	342	37	51.4	118	5	US-10-683-043-12	Sequence 12, Appl
270	38	52.8	631	4	US-10-029-345A-178	Sequence 178, Appl	343	37	51.4	118	5	US-10-683-043-13	Sequence 13, Appl
271	38	52.8	662	5	US-09-807-721-2	Sequence 2, Appl	344	37	51.4	118	5	US-10-974-591-112	Sequence 112, App
272	38	52.8	669	3	US-10-487-065-2	Sequence 177, App	345	37	51.4	118	5	US-10-974-591-114	Sequence 114, App
273	38	52.8	699	5	US-10-029-345A-177	Sequence 177, App	346	37	51.4	118	5	US-10-974-591-116	Sequence 116, App
274	38	52.8	703	5	US-10-480-988-2	Sequence 2, Appl	347	37	51.4	118	5	US-10-915-499-13	Sequence 13, Appl
275	38	52.8	747	5	US-10-029-345A-176	Sequence 176, Appl	348	37	51.4	121	5	US-10-153-159-3	Sequence 3, Appl
276	38	52.8	800	4	US-10-724-972A-7441	Sequence 7441, Ap	349	37	51.4	123	4	US-10-153-176-3	Sequence 3, Appl
277	38	52.8	806	5	US-10-029-345A-175	Sequence 175, App	350	37	51.4	123	4	US-10-443-134A-3	Sequence 3, Appl
278	38	52.8	805	4	US-09-817-514A-6	Sequence 6, Appl	351	37	51.4	123	4	US-10-723-434-56	Sequence 56, Appl
279	38	52.8	915	3	US-10-754-115-58	Sequence 58, Appl	352	37	51.4	123	4	US-10-723-434-103	Sequence 103, App
280	38	52.8	930	4	US-10-609-113-13	Sequence 13, Appl	353	37	51.4	126	4	US-10-041-860-27	Sequence 27, Appl
281	38	52.8	930	4	US-10-609-113-13	Sequence 13, Appl	354	37	51.4	126	4	US-10-041-860-214	Sequence 214, App
282	38	52.8	938	4	US-10-754-115-42	Sequence 42, Appl	355	37	51.4	126	4	US-10-041-860-249	Sequence 249, App
283	38	52.8	940	4	US-10-706-424-16	Sequence 16, Appl	356	37	51.4	126	4	US-10-041-860-313	Sequence 313, App
284	38	52.8	940	4	US-10-365-742-64	Sequence 64, Appl	357	37	51.4	126	4	US-10-665-383-34	Sequence 34, Appl
285	38	52.8	949	4	US-10-706-424-14	Sequence 14, Appl	358	37	51.4	126	4	US-10-424-599-275271	Sequence 275271, Sequence 34, Appl
286	38	52.8	949	4	US-10-754-115-64	Sequence 64, Appl	359	37	51.4	127	4	US-10-388-214A-34	Sequence 34, Appl
287	38	52.8	953	4	US-10-609-113-19	Sequence 19, Appl	360	37	51.4	135	4	US-09-187-693-57	Sequence 57, Appl
288	38	52.8	953	4	US-10-754-115-43	Sequence 43, Appl	361	37	51.4	149	3	US-11-021-795-57	Sequence 57, Appl
289	38	52.8	960	4	US-10-706-424-12	Sequence 12, Appl	362	37	51.4	177	4	US-10-282-122A-7533	Sequence 7533, A
290	38	52.8	960	4	US-10-754-115-47	Sequence 47, Appl	363	37	51.4	179	4	US-10-017-161-1510	Sequence 1510, Ap
291	38	52.8	962	4	US-10-754-115-51	Sequence 51, Appl	364	37	51.4	212	4	US-10-282-122A-72381	Sequence 72381, A
292	38	52.8	962	4	US-11-020-848-4	Sequence 4, Appl	365	37	51.4	224	4	US-10-379-392-126	Sequence 126, App
293	38	52.8	999	6	US-11-097-143-22665	Sequence 22665, A	366	37	51.4	224	4	US-10-379-392-148	Sequence 148, App
294	38	52.8	1016	4	US-10-753-901-16	Sequence 16, Appl	367	37	51.4	224	4	US-10-379-392-130	Sequence 130, App
295	38	52.8	1016	4	US-10-754-115-16	Sequence 16, Appl	368	37	51.4	224	4	US-10-379-392-148	Sequence 148, App
296	38	52.8	1043	4	US-10-262-794A-61	Sequence 61, Appl	369	37	51.4	224	4	US-10-379-392-156	Sequence 156, App
297	37.5	52.1	13	5	US-10-989-462-215	Sequence 215, App	370	37	51.4	224	4	US-10-379-392-158	Sequence 158, App
298	37.5	52.1	13	5	US-10-989-462-232	Sequence 232, App	371	37	51.4	224	4	US-09-880-748-1941	Sequence 1941, Ap
299	37.5	52.1	136	5	US-10-989-462-141	Sequence 141, App	372	37	51.4	237	3	US-10-293-418-1941	Sequence 1941, Ap
300	37.5	52.1	132	5	US-10-910-901-24	Sequence 24, Appl	373	37	51.4	243	4	US-10-689-921-2	Sequence 2, Appl
301	37.5	52.1	181	4	US-10-335-977-6845	Sequence 6845, Ap	374	37	51.4	294	4	US-10-369-499-19705	Sequence 19705, A
302	37.5	52.1	223	4	US-10-335-977-6846	Sequence 6846, Ap	375	37	51.4	294	4	US-10-774-355A-2009	Sequence 2009, Ap
303	37.5	52.1	266	5	US-10-989-462-160	Sequence 160, App	376	37	51.4	311	5	US-10-774-355A-1760	Sequence 1760, Ap
304	37.5	52.1	301	4	US-10-335-977-6847	Sequence 6847, Ap	377	37	51.4	315	5	US-10-774-355A-1761	Sequence 1761, Ap
305	37.5	52.1	341	3	US-09-895-913A-322	Sequence 322, App	378	37	51.4	315	5	US-10-282-122A-58528	Sequence 58528, A
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307	37.5	52.1	341	4	US-10-335-977-6848	Sequence 6848, Ap	380	37	51.4	355	4	US-10-282-122A-57837	Sequence 57837, A
308	37.5	52.1	341	5	US-10-953-901-572	Sequence 572, App	381	37	51.4	445	4	US-11-031-485-10	Sequence 10, Appl
309	37.5	52.1	341	5	US-10-953-901-574	Sequence 574, App	382	37	51.4	467	6	US-10-020-786-11	Sequence 11, Appl
310	37.5	52.1	341	5	US-09-056-160B-58	Sequence 58, Appl	383	37	51.4	476	4	US-10-697-995-9	Sequence 9, Appl
311	37	51.4	13	3	US-10-334-671-58	Sequence 58, Appl	384	37	51.4	476	4	US-11-071-291-11	Sequence 11, Appl
312	37	51.4	13	5	US-10-974-591-58	Sequence 58, Appl	385	37	51.4	476	6	US-10-424-599-275264	Sequence 275264, Sequence 126464,
313	37	51.4	14	3	US-09-056-160B-129	Sequence 129, App	386	37	51.4	484	4	US-10-437-964-165464	Sequence 24, Appl
314	37	51.4	14	4	US-10-334-671-127	Sequence 127, App	387	37	51.4	508	4	US-09-983-531A-24	Sequence 24, Appl
315	37	51.4	14	5	US-10-574-591-127	Sequence 127, App	388	37	51.4	523	3	US-10-732-923-22439	Sequence 22439, A
316	37	51.4	19	3	US-09-563-222-61	Sequence 61, Appl	389	37	51.4	529	5	US-11-097-143-7515	Sequence 7515, Ap
317	37	51.4	19	4	US-10-153-159-6	Sequence 6, Appl	390	37	51.4	530	5	US-10-732-923-22517	Sequence 22517, A
318	37	51.4	19	4	US-10-153-176-6	Sequence 6, Appl	391	37	51.4	538	4	US-10-369-493-13028	Sequence 13028, A
319	37	51.4	19	4	US-10-443-134A-6	Sequence 6, Appl	392	37	51.4				

393	37	51.4	542	4	US-10-369-493-10234	Sequence 10234, A	466	37	51.4	735	4	US-10-176-913-88	Sequence 88, Appl
394	37	51.4	546	4	US-10-156-761-12759	Sequence 12759, A	467	37	51.4	735	4	US-10-180-552-88	Sequence 88, Appl
395	37	51.4	546	4	US-10-369-493-1706	Sequence 1706, Ap	468	37	51.4	735	4	US-10-180-557-88	Sequence 88, Appl
396	37	51.4	564	4	US-10-369-493-2006	Sequence 2006, Ap	469	37	51.4	735	4	US-10-173-700-88	Sequence 88, Appl
397	37	51.4	564	5	US-10-732-923-22512	Sequence 22512, A	470	37	51.4	735	4	US-10-174-572-88	Sequence 88, Appl
398	37	51.4	564	5	US-10-732-923-22612	Sequence 22612, A	471	37	51.4	735	4	US-10-174-579-88	Sequence 88, Appl
399	37	51.4	567	4	US-10-369-493-1543	Sequence 1543, Ap	472	37	51.4	735	4	US-10-174-582-88	Sequence 88, Appl
400	37	51.4	567	4	US-10-369-493-22210	Sequence 22210, A	473	37	51.4	735	4	US-10-174-588-88	Sequence 88, Appl
401	37	51.4	567	5	US-10-732-923-23614	Sequence 23614, A	474	37	51.4	735	4	US-10-175-739-88	Sequence 88, Appl
402	37	51.4	567	5	US-10-732-923-23615	Sequence 23615, A	475	37	51.4	735	4	US-10-175-740-88	Sequence 88, Appl
403	37	51.4	597	4	US-10-369-493-12700	Sequence 12700, A	476	37	51.4	735	4	US-10-175-743-88	Sequence 88, Appl
404	37	51.4	610	4	US-10-424-599-173580	Sequence 173580, A	477	37	51.4	735	4	US-10-176-448-88	Sequence 88, Appl
405	37	51.4	613	4	US-10-120-145-5	Sequence 5, Appl1	478	37	51.4	735	4	US-10-176-442-88	Sequence 88, Appl
406	37	51.4	613	4	US-10-364-649-16	Sequence 16, Appl	479	37	51.4	735	4	US-10-176-747-88	Sequence 88, Appl
407	37	51.4	648	5	US-10-757-093-17	Sequence 17, Appl	480	37	51.4	735	4	US-10-176-750-88	Sequence 88, Appl
408	37	51.4	651	4	US-10-421-175-2	Sequence 2, Appl1	481	37	51.4	735	4	US-10-176-985-88	Sequence 88, Appl
409	37	51.4	651	4	US-10-757-093-16	Sequence 16, Appl	482	37	51.4	735	4	US-10-176-987-88	Sequence 88, Appl
410	37	51.4	651	5	US-10-757-093-18	Sequence 18, Appl	483	37	51.4	735	4	US-10-176-992-88	Sequence 88, Appl
411	37	51.4	651	5	US-10-745-237-238	Sequence 238, App	484	37	51.4	735	4	US-10-176-993-88	Sequence 88, Appl
412	37	51.4	667	5	US-10-764-428-7	Sequence 7, Appl1	485	37	51.4	735	4	US-10-184-658-88	Sequence 88, Appl
413	37	51.4	667	5	US-10-764-428-13	Sequence 13, Appl	486	37	51.4	735	4	US-10-176-991-88	Sequence 88, Appl
414	37	51.4	686	3	US-09-983-531A-12	Sequence 12, Appl	487	37	51.4	735	4	US-10-173-695-88	Sequence 88, Appl
415	37	51.4	708	4	US-10-282-122A-68824	Sequence 68824, A	488	37	51.4	735	4	US-10-173-697-88	Sequence 88, Appl
416	37	51.4	722	4	US-10-136-841-6	Sequence 6, Appl1	489	37	51.4	735	4	US-10-173-705-88	Sequence 88, Appl
417	37	51.4	722	4	US-10-272-531A-6	Sequence 6, Appl1	490	37	51.4	735	4	US-10-174-576-88	Sequence 88, Appl
418	37	51.4	722	4	US-10-272-483A-6	Sequence 6, Appl1	491	37	51.4	735	4	US-10-174-585-88	Sequence 88, Appl
419	37	51.4	725	3	US-09-978-295A-74	Sequence 74, Appl	492	37	51.4	735	4	US-10-174-586-88	Sequence 88, Appl
420	37	51.4	735	3	US-09-978-697-74	Sequence 74, Appl	493	37	51.4	735	4	US-10-175-747-88	Sequence 88, Appl
421	37	51.4	735	3	US-09-978-192A-74	Sequence 74, Appl	494	37	51.4	735	4	US-10-176-441-88	Sequence 88, Appl
422	37	51.4	735	3	US-09-999-832A-74	Sequence 74, Appl	495	37	51.4	735	4	US-10-176-445-88	Sequence 88, Appl
423	37	51.4	735	3	US-09-978-189-74	Sequence 74, Appl	496	37	51.4	735	4	US-10-176-447-88	Sequence 88, Appl
424	37	51.4	735	3	US-09-978-608A-74	Sequence 74, Appl	497	37	51.4	735	4	US-10-176-493-88	Sequence 88, Appl
425	37	51.4	735	3	US-09-978-585A-74	Sequence 74, Appl	498	37	51.4	735	4	US-10-176-756-88	Sequence 88, Appl
426	37	51.4	735	3	US-09-978-191A-74	Sequence 74, Appl	499	37	51.4	735	4	US-10-176-911-88	Sequence 88, Appl
427	37	51.4	735	3	US-09-978-403A-74	Sequence 74, Appl	500	37	51.4	735	4	US-10-176-919-88	Sequence 88, Appl
428	37	51.4	735	3	US-09-978-564A-74	Sequence 74, Appl	501	37	51.4	735	4	US-10-176-925-88	Sequence 88, Appl
429	37	51.4	735	3	US-09-999-833A-74	Sequence 74, Appl	502	37	51.4	735	4	US-10-176-978-88	Sequence 88, Appl
430	37	51.4	735	3	US-09-981-915A-74	Sequence 74, Appl	503	37	51.4	735	4	US-10-179-510-88	Sequence 88, Appl
431	37	51.4	735	3	US-09-978-824-74	Sequence 74, Appl	504	37	51.4	735	4	US-10-180-543-88	Sequence 88, Appl
432	37	51.4	735	3	US-09-918-585A-74	Sequence 74, Appl	505	37	51.4	735	4	US-10-180-544-88	Sequence 88, Appl
433	37	51.4	735	3	US-09-999-834A-74	Sequence 74, Appl	506	37	51.4	735	4	US-10-180-546-88	Sequence 88, Appl
434	37	51.4	735	3	US-09-978-423A-74	Sequence 74, Appl	507	37	51.4	735	4	US-10-180-547-88	Sequence 88, Appl
435	37	51.4	735	3	US-09-978-193A-74	Sequence 74, Appl	508	37	51.4	735	4	US-10-180-549-88	Sequence 88, Appl
436	37	51.4	735	3	US-09-999-830A-74	Sequence 74, Appl	509	37	51.4	735	4	US-10-180-555-88	Sequence 88, Appl
437	37	51.4	735	3	US-09-978-757A-74	Sequence 74, Appl	510	37	51.4	735	4	US-10-180-559-88	Sequence 88, Appl
438	37	51.4	735	3	US-09-978-187B-74	Sequence 74, Appl	511	37	51.4	735	4	US-10-181-000-88	Sequence 88, Appl
439	37	51.4	735	3	US-09-978-643A-74	Sequence 74, Appl	512	37	51.4	735	4	US-10-183-010-88	Sequence 88, Appl
440	37	51.4	735	3	US-09-978-375A-74	Sequence 74, Appl	513	37	51.4	735	4	US-10-183-012-88	Sequence 88, Appl
441	37	51.4	735	3	US-09-978-298A-74	Sequence 74, Appl	514	37	51.4	735	4	US-10-184-614-88	Sequence 88, Appl
442	37	51.4	735	3	US-09-978-188A-74	Sequence 74, Appl	515	37	51.4	735	4	US-10-184-623-88	Sequence 88, Appl
443	37	51.4	735	3	US-09-978-681A-74	Sequence 74, Appl	516	37	51.4	735	4	US-10-184-625-88	Sequence 88, Appl
444	37	51.4	735	3	US-09-978-194A-74	Sequence 74, Appl	517	37	51.4	735	4	US-10-184-637-88	Sequence 88, Appl
445	37	51.4	735	3	US-09-999-829A-74	Sequence 74, Appl	518	37	51.4	735	4	US-10-184-646-88	Sequence 88, Appl
446	37	51.4	735	3	US-09-978-299A-74	Sequence 74, Appl	519	37	51.4	735	4	US-10-184-647-88	Sequence 88, Appl
447	37	51.4	735	3	US-09-978-654A-74	Sequence 74, Appl	520	37	51.4	735	4	US-10-184-652-88	Sequence 88, Appl
448	37	51.4	735	3	US-09-978-665A-74	Sequence 74, Appl	521	37	51.4	735	4	US-10-187-594-88	Sequence 88, Appl
449	37	51.4	735	3	US-09-978-802A-74	Sequence 74, Appl	522	37	51.4	735	4	US-10-187-596-88	Sequence 88, Appl
450	37	51.4	735	3	US-09-999-831A-74	Sequence 74, Appl	523	37	51.4	735	4	US-10-187-745-88	Sequence 88, Appl
451	37	51.4	735	3	US-09-978-824-74	Sequence 74, Appl	524	37	51.4	735	4	US-10-187-885-88	Sequence 88, Appl
452	37	51.4	735	4	US-10-052-586-88	Sequence 88, Appl	525	37	51.4	735	4	US-10-187-886-88	Sequence 88, Appl
453	37	51.4	735	4	US-10-174-590-88	Sequence 88, Appl	526	37	51.4	735	4	US-10-199-444-88	Sequence 88, Appl
454	37	51.4	735	4	US-10-176-758-88	Sequence 88, Appl	527	37	51.4	735	4	US-10-196-756-88	Sequence 88, Appl
455	37	51.4	735	4	US-10-175-737-88	Sequence 88, Appl	528	37	51.4	735	4	US-10-176-751-88	Sequence 88, Appl
456	37	51.4	735	4	US-10-174-581-88	Sequence 88, Appl	529	37	51.4	735	4	US-10-176-760-88	Sequence 88, Appl
457	37	51.4	735	4	US-10-176-483-88	Sequence 88, Appl	530	37	51.4	735	4	US-10-176-990-88	Sequence 88, Appl
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460	37	51.4	735	4	US-10-176-915-88	Sequence 88, Appl	533	37	51.4	735	4	US-10-180-548-88	Sequence 88, Appl
461	37	51.4	735	4	US-10-173-706-88	Sequence 88, Appl	534	37	51.4	735	4	US-10-180-551-88	Sequence 88, Appl
462	37	51.4	735	4	US-10-175-738-88	Sequence 88, Appl	535	37	51.4	735	4	US-10-180-998-88	Sequence 88, Appl
463	37	51.4	735	4	US-10-175-752-88	Sequence 88, Appl	536	37	51.4	735	4	US-10-180-999-88	Sequence 88, Appl
464	37	51.4	735	4	US-10-176-482-88	Sequence 88, Appl	537	37	51.4	735	4	US-10-183-013-88	Sequence 88, Appl
465	37	51.4	735	4	US-10-176-757-88	Sequence 88, Appl	538	37	51.4	735	4	US-10-184-612-88	Sequence 88, Appl

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540	37	51.4	735	4	US-10-184-617-88	Sequence 88, Appl	613	37	51.4	735	4	US-10-179-514-88	Sequence 88, Appl
541	37	51.4	735	4	US-10-184-622-88	Sequence 88, Appl	614	37	51.4	735	4	US-10-179-522-88	Sequence 88, Appl
542	37	51.4	735	4	US-10-184-628-88	Sequence 88, Appl	615	37	51.4	735	4	US-10-180-556-88	Sequence 88, Appl
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546	37	51.4	735	4	US-10-184-632-88	Sequence 88, Appl	619	37	51.4	735	4	US-10-184-620-88	Sequence 88, Appl
547	37	51.4	735	4	US-10-184-636-88	Sequence 88, Appl	620	37	51.4	735	4	US-10-184-643-88	Sequence 88, Appl
548	37	51.4	735	4	US-10-184-640-88	Sequence 88, Appl	621	37	51.4	735	4	US-10-184-656-88	Sequence 88, Appl
549	37	51.4	735	4	US-10-184-650-88	Sequence 88, Appl	622	37	51.4	735	4	US-10-192-010-88	Sequence 88, Appl
550	37	51.4	735	4	US-10-184-651-88	Sequence 88, Appl	623	37	51.4	735	4	US-10-205-908-88	Sequence 88, Appl
551	37	51.4	735	4	US-10-187-588-88	Sequence 88, Appl	624	37	51.4	735	4	US-10-017-081A-74	Sequence 74, Appl
552	37	51.4	735	4	US-10-187-597-88	Sequence 88, Appl	625	37	51.4	735	4	US-10-184-619-88	Sequence 88, Appl
553	37	51.4	735	4	US-10-187-598-88	Sequence 88, Appl	626	37	51.4	735	4	US-10-187-599-88	Sequence 88, Appl
554	37	51.4	735	4	US-10-187-600-88	Sequence 88, Appl	627	37	51.4	735	4	US-10-187-750-88	Sequence 88, Appl
555	37	51.4	735	4	US-10-187-601-88	Sequence 88, Appl	628	37	51.4	735	4	US-10-188-780-88	Sequence 88, Appl
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561	37	51.4	735	4	US-10-187-747-88	Sequence 88, Appl	634	37	51.4	735	4	US-10-195-889-88	Sequence 88, Appl
562	37	51.4	735	4	US-10-187-751-88	Sequence 88, Appl	635	37	51.4	735	4	US-10-196-748-88	Sequence 88, Appl
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564	37	51.4	735	4	US-10-187-754-88	Sequence 88, Appl	637	37	51.4	735	4	US-10-197-699-88	Sequence 88, Appl
565	37	51.4	735	4	US-10-187-757-88	Sequence 88, Appl	638	37	51.4	735	4	US-10-197-700-88	Sequence 88, Appl
566	37	51.4	735	4	US-10-187-758-88	Sequence 88, Appl	639	37	51.4	735	4	US-10-197-705-88	Sequence 88, Appl
567	37	51.4	735	4	US-10-188-767-88	Sequence 88, Appl	640	37	51.4	735	4	US-10-197-708-88	Sequence 88, Appl
568	37	51.4	735	4	US-10-188-769-88	Sequence 88, Appl	641	37	51.4	735	4	US-10-198-764-88	Sequence 88, Appl
569	37	51.4	735	4	US-10-188-770-88	Sequence 88, Appl	642	37	51.4	735	4	US-10-198-765-88	Sequence 88, Appl
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572	37	51.4	735	4	US-10-194-361-88	Sequence 88, Appl	645	37	51.4	735	4	US-10-199-305-88	Sequence 88, Appl
573	37	51.4	735	4	US-10-194-423-88	Sequence 88, Appl	646	37	51.4	735	4	US-10-199-306-88	Sequence 88, Appl
574	37	51.4	735	4	US-10-195-897-88	Sequence 88, Appl	647	37	51.4	735	4	US-10-199-310-88	Sequence 88, Appl
575	37	51.4	735	4	US-10-195-901-88	Sequence 88, Appl	648	37	51.4	735	4	US-10-199-311-88	Sequence 88, Appl
576	37	51.4	735	4	US-10-195-902-88	Sequence 88, Appl	649	37	51.4	735	4	US-10-199-314-88	Sequence 88, Appl
577	37	51.4	735	4	US-10-196-743-88	Sequence 88, Appl	650	37	51.4	735	4	US-10-199-317-88	Sequence 88, Appl
578	37	51.4	735	4	US-10-196-760-88	Sequence 88, Appl	651	37	51.4	735	4	US-10-199-665-88	Sequence 88, Appl
579	37	51.4	735	4	US-10-173-708-88	Sequence 88, Appl	652	37	51.4	735	4	US-10-199-666-88	Sequence 88, Appl
580	37	51.4	735	4	US-10-176-479-88	Sequence 88, Appl	653	37	51.4	735	4	US-10-201-534-88	Sequence 88, Appl
581	37	51.4	735	4	US-10-176-748-88	Sequence 88, Appl	654	37	51.4	735	4	US-10-201-534-88	Sequence 88, Appl
582	37	51.4	735	4	US-10-176-916-88	Sequence 88, Appl	655	37	51.4	735	4	US-10-201-770-88	Sequence 88, Appl
583	37	51.4	735	4	US-10-179-507-88	Sequence 88, Appl	656	37	51.4	735	4	US-10-201-855-88	Sequence 88, Appl
584	37	51.4	735	4	US-10-179-516-88	Sequence 88, Appl	657	37	51.4	735	4	US-10-201-856-88	Sequence 88, Appl
585	37	51.4	735	4	US-10-179-519-88	Sequence 88, Appl	658	37	51.4	735	4	US-10-202-469-88	Sequence 88, Appl
586	37	51.4	735	4	US-10-179-525-88	Sequence 88, Appl	659	37	51.4	735	4	US-10-202-470-88	Sequence 88, Appl
587	37	51.4	735	4	US-10-180-540-88	Sequence 88, Appl	660	37	51.4	735	4	US-10-202-476-88	Sequence 88, Appl
588	37	51.4	735	4	US-10-180-545-88	Sequence 88, Appl	661	37	51.4	735	4	US-10-202-934-88	Sequence 88, Appl
589	37	51.4	735	4	US-10-183-006-88	Sequence 88, Appl	662	37	51.4	735	4	US-10-202-935-88	Sequence 88, Appl
590	37	51.4	735	4	US-10-183-008-88	Sequence 88, Appl	663	37	51.4	735	4	US-10-202-936-88	Sequence 88, Appl
591	37	51.4	735	4	US-10-183-017-88	Sequence 88, Appl	664	37	51.4	735	4	US-10-202-939-88	Sequence 88, Appl
592	37	51.4	735	4	US-10-183-019-88	Sequence 88, Appl	665	37	51.4	735	4	US-10-205-504-88	Sequence 88, Appl
593	37	51.4	735	4	US-10-184-618-88	Sequence 88, Appl	666	37	51.4	735	4	US-10-205-509-88	Sequence 88, Appl
594	37	51.4	735	4	US-10-184-625-88	Sequence 88, Appl	667	37	51.4	735	4	US-10-205-895-88	Sequence 88, Appl
595	37	51.4	735	4	US-10-184-626-88	Sequence 88, Appl	668	37	51.4	735	4	US-10-205-899-88	Sequence 88, Appl
596	37	51.4	735	4	US-10-184-627-88	Sequence 88, Appl	669	37	51.4	735	4	US-10-205-900-88	Sequence 88, Appl
597	37	51.4	735	4	US-10-184-645-88	Sequence 88, Appl	670	37	51.4	735	4	US-10-205-909-88	Sequence 88, Appl
598	37	51.4	735	4	US-10-184-654-88	Sequence 88, Appl	671	37	51.4	735	4	US-10-193-890-88	Sequence 88, Appl
599	37	51.4	735	4	US-10-184-655-88	Sequence 88, Appl	672	37	51.4	735	4	US-10-183-002-88	Sequence 88, Appl
600	37	51.4	735	4	US-10-188-774-88	Sequence 88, Appl	673	37	51.4	735	4	US-10-184-621-88	Sequence 88, Appl
601	37	51.4	735	4	US-10-188-775-88	Sequence 88, Appl	674	37	51.4	735	4	US-10-184-638-88	Sequence 88, Appl
602	37	51.4	735	4	US-10-194-462-88	Sequence 88, Appl	675	37	51.4	735	4	US-10-187-752-88	Sequence 88, Appl
603	37	51.4	735	4	US-10-196-745-88	Sequence 88, Appl	676	37	51.4	735	4	US-10-194-461-88	Sequence 88, Appl
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606	37	51.4	735	4	US-10-197-694-88	Sequence 88, Appl	679	37	51.4	735	4	US-10-197-694-88	Sequence 88, Appl
607	37	51.4	735	4	US-10-176-484-88	Sequence 88, Appl	680	37	51.4	735	4	US-10-197-697-88	Sequence 88, Appl
608	37	51.4	735	4	US-10-176-753-88	Sequence 88, Appl	681	37	51.4	735	4	US-10-197-707-88	Sequence 88, Appl
609	37	51.4	735	4	US-10-176-917-88	Sequence 88, Appl	682	37	51.4	735	4	US-10-199-303-88	Sequence 88, Appl
610	37	51.4	735	4	US-10-176-982-88	Sequence 88, Appl	683	37	51.4	735	4	US-10-199-308-88	Sequence 88, Appl
611	37	51.4	735	4	US-10-179-506-88	Sequence 88, Appl	684	37	51.4	735	4	US-10-199-318-88	Sequence 88, Appl

685	37	51.4	735	4	US-10-199-458-88	Sequence 88	Appl	758	37	51.4	735	4	US-10-192-012-88	Sequence 88	Appl
686	37	51.4	735	4	US-10-199-462-88	Sequence 88	Appl	759	37	51.4	735	4	US-10-192-014-88	Sequence 88	Appl
687	37	51.4	735	4	US-10-201-324-88	Sequence 88	Appl	760	37	51.4	735	4	US-10-192-016-88	Sequence 88	Appl
688	37	51.4	735	4	US-10-201-328-88	Sequence 88	Appl	761	37	51.4	735	4	US-10-194-362-88	Sequence 88	Appl
689	37	51.4	735	4	US-10-201-527-88	Sequence 88	Appl	762	37	51.4	735	4	US-10-194-364-88	Sequence 88	Appl
690	37	51.4	735	4	US-10-201-528-88	Sequence 88	Appl	763	37	51.4	735	4	US-10-194-395-88	Sequence 88	Appl
691	37	51.4	735	4	US-10-201-529-88	Sequence 88	Appl	764	37	51.4	735	4	US-10-194-424-88	Sequence 88	Appl
692	37	51.4	735	4	US-10-201-530-88	Sequence 88	Appl	765	37	51.4	735	4	US-10-194-458-88	Sequence 88	Appl
693	37	51.4	735	4	US-10-202-408-88	Sequence 88	Appl	766	37	51.4	735	4	US-10-194-459-88	Sequence 88	Appl
694	37	51.4	735	4	US-10-202-409-88	Sequence 88	Appl	767	37	51.4	735	4	US-10-194-488-88	Sequence 88	Appl
695	37	51.4	735	4	US-10-202-411-88	Sequence 88	Appl	768	37	51.4	735	4	US-10-195-886-88	Sequence 88	Appl
696	37	51.4	735	4	US-10-202-472-88	Sequence 88	Appl	769	37	51.4	735	4	US-10-195-891-88	Sequence 88	Appl
697	37	51.4	735	4	US-10-205-502-88	Sequence 88	Appl	770	37	51.4	735	4	US-10-196-746-88	Sequence 88	Appl
698	37	51.4	735	4	US-10-205-507-88	Sequence 88	Appl	771	37	51.4	735	4	US-10-196-752-88	Sequence 88	Appl
699	37	51.4	735	4	US-10-205-511-88	Sequence 88	Appl	772	37	51.4	735	4	US-10-196-753-88	Sequence 88	Appl
700	37	51.4	735	4	US-10-205-902-88	Sequence 88	Appl	773	37	51.4	735	4	US-10-196-761-88	Sequence 88	Appl
701	37	51.4	735	4	US-10-205-907-88	Sequence 88	Appl	774	37	51.4	735	4	US-10-197-692-88	Sequence 88	Appl
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703	37	51.4	735	4	US-10-176-484-88	Sequence 88	Appl	776	37	51.4	735	4	US-10-197-696-88	Sequence 88	Appl
704	37	51.4	735	4	US-10-194-456-88	Sequence 88	Appl	777	37	51.4	735	4	US-10-197-698-88	Sequence 88	Appl
705	37	51.4	735	4	US-10-196-758-88	Sequence 88	Appl	778	37	51.4	735	4	US-10-197-703-88	Sequence 88	Appl
706	37	51.4	735	4	US-10-198-770-88	Sequence 88	Appl	779	37	51.4	735	4	US-10-197-711-88	Sequence 88	Appl
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ALIGNMENTS

RESULT 1

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; Publication No. US20030207336A1

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; APPLICANT: Presta, Leonard G.

; Jardieu, Paula M.

; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

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; TELEPHONE: 650/225-1994

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-795-798-12

Query Match 100.0%; Score 72; DB 3; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GIVFYGTTFDY 12
Db 1 GIVFYGTTFDY 12

RESULT 2

US-09-726-258-50

; Sequence 50, Application US/09726258

; Publication No. US20030021790A1

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc., Hseil, Vanessa

; APPLICANT: Koumetsi, Iphigenia

; APPLICANT: Leong, Steven R.

; APPLICANT: Presta, Leonard G.

; APPLICANT: Shahrokhi, Zahra

; APPLICANT: Zapata, Gerardo A.

; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/726,258

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/234,182

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/094003

; FILING DATE: 24-JUL-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: P1085R4-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5530

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 50:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 116 amino acids

; TYPE: amino acid

; TOPOLOGY: Linear

US-09-726-258-50

Query Match 100.0%; Score 72; DB 3; Length 116;

Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIVFYGTTFDY 12

Db 100 GIVFYGTTFDY 111

RESULT 3

US-09-795-798-4

; Sequence 4, Application US/09795798

; Publication No. US20030207336A1

; GENERAL INFORMATION:

; APPLICANT: Presta, Leonard G.

Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-795-798-4
Query Match 100.0%; Score 72; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTYFDY 12
DB 99 GIFYGTYFDY 110
RESULT 4
US-09-795-798-5
Sequence 5, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-795-798-5
Query Match 100.0%; Score 72; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTYFDY 12
DB 99 GIFYGTYFDY 110
RESULT 5
US-09-795-798-24
Sequence 24, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-795-798-24
Query Match 100.0%; Score 72; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFYGTYFDY 12


```
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1994
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 121 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-727-737-17

Query Match      100.0%; Score 72; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GIFYGTTYFDY 12
Db      99 GIFYGTTYFDY 110

RESULT 9
US-10-877-532-6
/ Sequence 6, Application US/10877532
/ Publication No. US20050038231A1
/ GENERAL INFORMATION:
/ APPLICANT: FAHRNER, ROBERT L.
/ APPLICANT: LAVERDIERE, AMY
/ APPLICANT: MCDONALD, PAUL J.
/ APPLICANT: O'LEARY, RHONA M.
/ TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAPHY
/ FILE REFERENCE: P2015R1
/ CURRENT APPLICATION NUMBER: US/10/877,532
/ CURRENT FILING DATE: 2004-06-24
/ PRIOR APPLICATION NUMBER: US 60/490,500
/ PRIOR FILING DATE: 2003-07-28
/ NUMBER OF SEQ ID NOS: 8
/ SEQ ID NO 6
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-10-877-532-6

Query Match      100.0%; Score 72; DB 5; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GIFYGTTYFDY 12
Db      99 GIFYGTTYFDY 110

RESULT 10
US-10-423-299-4
/ Sequence 4, Application US/10423299
/ Publication No. US20030229212A1
/ GENERAL INFORMATION:
/ APPLICANT: FAHRNER, ROBERT
/ APPLICANT: FOLLMAN, DEBORAH
/ APPLICANT: LEBRETON, BENEDECITE
/ APPLICANT: VAN REIS, ROBERT
/ TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
/ FILE REFERENCE: 39766-0121A
/ CURRENT APPLICATION NUMBER: US/10/423,299
/ CURRENT FILING DATE: 2003-04-25
/ PRIOR APPLICATION NUMBER: US 60/375,953
/ PRIOR FILING DATE: 2002-04-26
/ NUMBER OF SEQ ID NOS: 4
/ SEQ ID NO 4
/ LENGTH: 451
/ TYPE: PRT
/ ORGANISM: Artificial sequence
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```
/
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized
US-10-423-299-4

Query Match      100.0%; Score 72; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GIFYGTTYFDY 12
Db      99 GIFYGTTYFDY 110

RESULT 11
US-10-727-737-45
/ Sequence 45, Application US/10727737
/ Publication No. US20040146507A1
/ GENERAL INFORMATION:
/ APPLICANT: Presta, Leonard G.
/ APPLICANT: Jardieu, Paula M.
/ TITLE OF INVENTION: Antibody Mutants
/ NUMBER OF SEQUENCES: 79
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/727,737
/ FILING DATE: 03-Dec-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/975,329B
/ FILING DATE: 20-Nov-1997
/ APPLICATION NUMBER: 60/031945
/ FILING DATE: 27-Nov-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P1064R1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1994
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-727-737-45

Query Match      90.3%; Score 65; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GIFYGTTYFD 11
Db      1 GIFYGTTYFD 11

RESULT 12
US-10-727-737-50
/ Sequence 50, Application US/10727737
/ Publication No. US20040146507A1
/ GENERAL INFORMATION:
/ APPLICANT: Presta, Leonard G.
```

Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-727-737-50
Query Match 83.3%; Score 60; DB 4; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.017; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;
Qy 1 GIFYGYTYFD 11
Db 1 GIFYGYTYFD 11
RESULT 13
US-10-727-737-51
Sequence 51, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-727-737-51
Query Match 83.3%; Score 60; DB 4; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.017; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;
Qy 1 GIFYGYTYFD 11
Db 1 GIFYGYTYFD 11
RESULT 14
US-10-727-737-48
Sequence 48, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-727-737-48

Query Match 77.8%; Score 56; DB 4; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIFYGTYTYPD 11
|||
1 GIFYGTYTYPD 11

RESULT 15

US-10-727-737-49
Sequence 49, Application US/10727737
Publication No. US20040146507A1

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Query Match 77.8%; Score 56; DB 4; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIFYGTYTYPD 11
|||
1 GIFYGTYTYPD 11

RESULT 16

US-10-727-737-52

Sequence 52, Application US/10727737
Publication No. US20040146507A1

GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-10-727-737-52

Query Match 77.8%; Score 56; DB 4; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIFYGTYTYPD 11
|||
1 GIFYGTYTYPD 11

RESULT 17

US-10-511-794-17

Sequence 17, Application US/10511794
Publication No. US20050158322A1

GENERAL INFORMATION:

APPLICANT: Center for Genetic Engineering and Biotechnology
TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
FILE REFERENCE: 976-20 PCT/US
CURRENT APPLICATION NUMBER: US/10/511,794
PRIOR FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/CU2003/000005
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: CU2002/0086
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17

LENGTH: 232

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: diabody

US-10-511-794-17

Query Match 75.0%; Score 54; DB 5; Length 232;
Best Local Similarity 63.6%; Pred. No. 2.8;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYFYGTTFYFDY 12
:|:|:|:|:|
DB 98 VYYGSSYFDY 108

RESULT 18

US-10-511-794-16
; Sequence 16, Application US/10511794
; Publication No. US20050158322A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
; TITLE OF INVENTION: ANTIGEN (CEA)
; FILE REFERENCE: 976-20 PCT/US
; CURRENT APPLICATION NUMBER: US/10/511,794
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/CU2003/000005
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: CU2002/0086
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv
US-10-511-794-16

Query Match 75.0%; Score 54; DB 5; Length 241;
Best Local Similarity 63.6%; Pred. No. 2.9;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYFYGTTFYFDY 12
:|:|:|:|:|
DB 98 VYYGSSYFDY 108

RESULT 19

US-10-511-794-21
; Sequence 21, Application US/10511794
; Publication No. US20050158322A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC
; FILE REFERENCE: 976-20 PCT/US
; CURRENT APPLICATION NUMBER: US/10/511,794
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/CU2003/000005
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: CU2002/0086
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: diabody MS
US-10-511-794-21

Query Match 75.0%; Score 54; DB 5; Length 255;
Best Local Similarity 63.6%; Pred. No. 3;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 IYFYGTTFYFDY 12
:|:|:|:|:|
DB 98 VYYGSSYFDY 108

RESULT 20
US-10-745-775-48
; Sequence 48, Application US/10745775
; Publication No. US20040237124A1
; GENERAL INFORMATION:
; APPLICANT: Pons, Jaume
; TITLE OF INVENTION: ANTI-NGF ANTIBODIES AND METHODS USING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514722001400
; CURRENT APPLICATION NUMBER: US/10/745,775
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/436,905
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: US 60/443,522
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/510,006
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-745-775-48

Query Match 70.1%; Score 50.5; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.54;
Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 GIFYGTTFYFDY 12
|:|:|:|:|:|
DB 1 GIFYGTTFYFDY 13

RESULT 21

US-10-727-737-46
; Sequence 46, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:

```

;
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-727-737-46
;
Query Match          65.3%; Score 47; DB 4; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTTYFD 11
   ||| ||| |||
Db 1 GIFYGTTYFD 11

RESULT 22
US-10-745-775-11
; Sequence 11, Application US/10745775
; Publication No. US20040237124A1
; GENERAL INFORMATION:
; APPLICANT: Pons, Jaume
; APPLICANT: Rosenthal, Arnon
; TITLE OF INVENTION: ANTI-NGF ANTIBODIES AND METHODS USING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514712001400
; CURRENT APPLICATION NUMBER: US/10/745,775
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/436,905
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: US 60/443,522
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/510,006
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-745-775-11
;
Query Match          64.6%; Score 46.5; DB 5; Length 13;
Best Local Similarity 69.2%; Pred. No. 2.1;
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 GIFYGTT-YFDY 12
   |::|||::|||
Db 1 GGYVGTSTYFDY 13

RESULT 23
US-10-727-737-47
; Sequence 47, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

```

```

;
; MEDIUM TYPE: 3.5 inch, 1.44 Mb Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-727-737-47
;
Query Match          63.9%; Score 46; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIFYGTTYFD 11
   ||| ||| |||
Db 1 GIFYGAAAFD 11

RESULT 24
US-10-745-775-47
; Sequence 47, Application US/10745775
; Publication No. US20040237124A1
; GENERAL INFORMATION:
; APPLICANT: Pons, Jaume
; APPLICANT: Rosenthal, Arnon
; TITLE OF INVENTION: ANTI-NGF ANTIBODIES AND METHODS USING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514712001400
; CURRENT APPLICATION NUMBER: US/10/745,775
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/436,905
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: US 60/443,522
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/510,006
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-745-775-47
;
Query Match          63.2%; Score 45.5; DB 5; Length 13;
Best Local Similarity 69.2%; Pred. No. 3;
Matches 9; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 GIFYGTT-YFDY 12
   |::|||::|||
Db 1 GGYVGTAVYFDY 13

```

RESULT 25
US-11-083-779-2
; Sequence 2, Application US/11083779
; Publication No. US20050227292A1
; GENERAL INFORMATION:
; APPLICANT: Malaysian Rubber Board
; APPLICANT: Sundarasan, Elumalai
; APPLICANT: Arif, Siti Arifa Mad
; APPLICANT: Yeang, Hoong Yeet
; TITLE OF INVENTION: AN ALLERGENIC PROTEIN COMPLEX OF NATURAL RUBBER LATEX
; FILE REFERENCE: SHP-PT086
; CURRENT APPLICATION NUMBER: US/11/083,779
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: PI20040947
; PRIOR FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Hevea brasiliensis
US-11-083-779-2

Query Match 62.5%; Score 45; DB 6; Length 366;
Best Local Similarity 87.5%; Pred. No. 97;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGTTTFDY 12
| | | | |
| : | : | : |
DB 59 YGTTTFDY 66

RESULT 26
US-10-745-775-46
; Sequence 46, Application US/10745775
; Publication No. US20040237124A1
; GENERAL INFORMATION:
; APPLICANT: Pons, Jaume
; APPLICANT: Rosenthal, Arnon
; TITLE OF INVENTION: ANTI-NGF ANTIBODIES AND METHODS USING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 514712001400
; CURRENT APPLICATION NUMBER: US/10/745,775
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: US 60/436,905
; PRIOR FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: US 60/443,522
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/510,006
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-745-775-46

Query Match 61.8%; Score 44.5; DB 5; Length 13;
Best Local Similarity 69.2%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 GIFYGTT-YFDY 12
| : | : | : |
| : | : | : |
DB 1 GGYYGTSYFDY 13

RESULT 27
US-10-996-316-196
; Sequence 196, Application US/10996316

; Publication No. US20050129690A1
; GENERAL INFORMATION:
; APPLICANT: Alexion Pharmaceuticals, Inc.
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; APPLICANT: Kretz-Rommel, Anke
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC
; TITLE OF INVENTION: LEUCEMIA CELLS AND USES THEREOF
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)
; CURRENT APPLICATION NUMBER: US/10/996,316
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 196
; LENGTH: 11
; TYPE: PRT
; ORGANISM: murine
US-10-996-316-196

Query Match 61.1%; Score 44; DB 5; Length 11;
Best Local Similarity 77.8%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 FYGTTTFDY 12
| | | | |
| : | : | : |
DB 3 FYGNPYFDY 11

RESULT 28
US-10-700-632-79
; Sequence 79, Application US/10700632
; Publication No. US20050118183A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-CD3 ANTIBODIES AND METHODS FOR TREATMENT OF ACUTE MYELOID
; TITLE OF INVENTION: LEUCEMIA USING THE SAME
; FILE REFERENCE: A8427
; CURRENT APPLICATION NUMBER: US/10/700,632
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,332
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-700-632-79

Query Match 61.1%; Score 44; DB 5; Length 118;
Best Local Similarity 66.7%; Pred. No. 4.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTTFDY 12
| : | : | : |
| : | : | : |
DB 100 YGSSYFDY 108

RESULT 29
US-10-351-748-24
; Sequence 24, Application US/10351748
; Publication No. US20040127688A1
; GENERAL INFORMATION:

```

; APPLICANT: Winter, Gregory Paul
; TITLE OF INVENTION: IMPROVEMENT IN OR RELATING TO ALTERED
; FILE REFERENCE: 7806-011-999 (CAM 107814-999010)
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 08/452,462
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 07/942,146
; PRIOR FILING DATE: 1992-09-08
; PRIOR APPLICATION NUMBER: 07/624,515
; PRIOR FILING DATE: 1990-12-07
; PRIOR APPLICATION NUMBER: 07/189,814
; PRIOR FILING DATE: 1988-05-03
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 120
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of VH domain of BI-8 antibody (Fig 2)
US-10-351-748-24

Query Match          61.1%; Score 44; DB 4; Length 120;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 FYGTYFDY 12
       :|:::|
Db      101 YYGSSYFDY 109

RESULT 30
US-10-351-748-24
; Sequence 24, Application US/10351748
; Publication No. US20040192897A2
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; TITLE OF INVENTION: IMPROVEMENT IN OR RELATING TO ALTERED
; FILE REFERENCE: 7806-011-999 (CAM 107814-999010)
; CURRENT APPLICATION NUMBER: US/10/351,748
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 08/452,462
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 07/942,146
; PRIOR FILING DATE: 1992-09-08
; PRIOR APPLICATION NUMBER: 07/624,515
; PRIOR FILING DATE: 1990-12-07
; PRIOR APPLICATION NUMBER: 07/189,814
; PRIOR FILING DATE: 1988-05-03
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 120
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of VH domain of BI-8 antibody (Fig 2)
US-10-351-748-24

Query Match          61.1%; Score 44; DB 4; Length 120;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 FYGTYFDY 12
       :|:::|
Db      101 YYGSSYFDY 109
```

```

; Sequence 71, Application US/10729441
; Publication No. US20040265307A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/729,441
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-729-441-71

Query Match          61.1%; Score 44; DB 5; Length 120;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 FYGTYFDY 12
       :|:::|
Db      101 YYGSSYFDY 109

RESULT 32
US-10-729-441-72
; Sequence 72, Application US/10729441
; Publication No. US20040265307A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/729,441
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-729-441-72

Query Match          61.1%; Score 44; DB 5; Length 120;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      4 FYGTYFDY 12
       :|:::|
Db      101 YYGSSYFDY 109

RESULT 33
US-10-895-135-57
; Sequence 57, Application US/10895135
; Publication No. US20050123549A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; APPLICANT: PAYNE, Gillian
; APPLICANT: CHUN, Philid
; APPLICANT: TAVARES, Daniel
; TITLE OF INVENTION: A CA6 ANTIGEN-SPECIFIC CYTOTOXIC CONJUGATE AND METHODS OF USING
; FILE REFERENCE: A8621
; CURRENT APPLICATION NUMBER: US/10/895,135
US-10-729-441-71
```

CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: 60/488,447
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57
LENGTH: 120
TYPE: PRT
ORGANISM: Mus musculus
US-10-895-135-57

Query Match 61.1%; Score 44; DB 5; Length 120;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
:|||||
Db 101 YYGSSYFDY 109

RESULT 34
US-10-897-406-71
Sequence 71, Application US/10897406
Publication No. US20050186203A1
GENERAL INFORMATION:
APPLICANT: Immunogen, Inc.
TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
FILE REFERENCE: A8338
CURRENT APPLICATION NUMBER: US/10/897,406
CURRENT FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: US/10/170,390
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic antibody structure
US-10-897-406-71

Query Match 61.1%; Score 44; DB 5; Length 120;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
:|||||
Db 101 YYGSSYFDY 109

RESULT 35
US-10-897-406-72
Sequence 72, Application US/10897406
Publication No. US20050186203A1
GENERAL INFORMATION:
APPLICANT: Immunogen, Inc.
TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
FILE REFERENCE: A8338
CURRENT APPLICATION NUMBER: US/10/897,406
CURRENT FILING DATE: 2004-07-23
PRIOR APPLICATION NUMBER: US/10/170,390
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn version 3.1
SEQ ID NO 72
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic antibody structure
US-10-897-406-72

Query Match 61.1%; Score 44; DB 5; Length 120;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
:|||||
Db 101 YYGSSYFDY 109

RESULT 36
US-10-096-246-10
Sequence 10, Application US/10096246
Publication No. US20030100060A1
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo-
TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 122
TYPE: PRT
ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-10

Query Match 61.1%; Score 44; DB 4; Length 122;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
:|||||
Db 103 YYGSSYFDY 111

RESULT 37
US-10-096-246-11
Sequence 11, Application US/10096246
Publication No. US20030100060A1
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Alvi, Azhar E
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/096,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 122
TYPE: PRT
ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-11

Query Match 61.1%; Score 44; DB 4; Length 122;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FYGTTYFDY 12
:|||||
Db 103 YYGSSYFDY 111

RESULT 38
US-10-428-662-15

```
; Sequence 15, Application US/10428662
; Publication No. US20030185819A1
; GENERAL INFORMATION:
; APPLICANT: Lobb, Roy R.
; APPLICANT: Carr, Frank J.
; APPLICANT: Tempest, Philip R.
; TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
; FILE REFERENCE: 10274-007001
; CURRENT APPLICATION NUMBER: US/10/428,662
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US/08/454,899G
; PRIOR FILING DATE: 1995-05-31
; PRIOR APPLICATION NUMBER: US 08/004,798
; PRIOR FILING DATE: 1993-01-12
; PRIOR APPLICATION NUMBER: PCT/US94/00266
; PRIOR FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: heavy chain variable region insert
US-10-428-662-15
```

```
Query Match      61.1%; Score 44; DB 4; Length 139;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 FYGTTYFDY 12
       :|::|||
Db      120 YGSSYFDY 128
```

```
RESULT 39
US-10-351-748-26
; Sequence 26, Application US/10351748
; Publication No. US20040127688A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; TITLE OF INVENTION: IMPROVEMENT IN OR RELATING TO ALTERED
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 7806-011-999 (CAM 107814-999010)
; CURRENT APPLICATION NUMBER: US/10/351,748
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 08/452,462
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 07/942,146
; PRIOR FILING DATE: 1992-09-08
; PRIOR APPLICATION NUMBER: 07/624,515
; PRIOR FILING DATE: 1990-12-07
; PRIOR APPLICATION NUMBER: 07/189,814
; PRIOR FILING DATE: 1988-05-03
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of HUVNP gene (Fig 3)
US-10-351-748-26
```

```
Query Match      61.1%; Score 44; DB 4; Length 140;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 FYGTTYFDY 12
       :|::|||
Db      121 YGSSYFDY 129
```

```
RESULT 40
US-10-351-748-26
; Sequence 26, Application US/10351748
; Publication No. US20040192897A2
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: IMPROVEMENT IN OR RELATING TO ALTERED
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 7806-011-999 (CAM 107814-999010)
; CURRENT APPLICATION NUMBER: US/10/351,748
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 08/452,462
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 07/942,146
; PRIOR FILING DATE: 1992-09-08
; PRIOR APPLICATION NUMBER: 07/624,515
; PRIOR FILING DATE: 1990-12-07
; PRIOR APPLICATION NUMBER: 07/189,814
; PRIOR FILING DATE: 1988-05-03
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of HUVNP gene (Fig 3)
US-10-351-748-26
```

```
Query Match      61.1%; Score 44; DB 4; Length 140;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      4 FYGTTYFDY 12
       :|::|||
Db      121 YGSSYFDY 129
```

```
RESULT 41
US-11-097-143-27654
; Sequence 27654, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27654
; LENGTH: 344
; TYPE: PRT
; ORGANISM: DROSOPHILA
```

US-11-097-143-27654

Query Match 61.1%; Score 44; DB 6; Length 344;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GIFYGTYF 10
||| ||| |||
Db 269 GIFYGTYF 278

RESULT 42

US-10-335-977-5897
; Sequence 5897, Application US/10335977
; Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESSES:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts

COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 5897:

SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Helicobacter pylori
FEATURE:

NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...33

SEQUENCE DESCRIPTION: SEQ ID NO: 5897:

US-10-335-977-5897

Query Match 59.7%; Score 43; DB 4; Length 33;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GIFYGTYF 10
||| ||| |||
Db 16 GIFYGTYF 25

RESULT 43

US-10-335-977-5899
; Sequence 5899, Application US/10335977

Publication No. US20040052799A1

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESSES:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts

COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 5899:

SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Helicobacter pylori
FEATURE:

NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...121

SEQUENCE DESCRIPTION: SEQ ID NO: 5899:

US-10-335-977-5899

Query Match 59.7%; Score 43; DB 4; Length 121;
Best Local Similarity 70.0%; Pred. No. 65;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GIFYGTYF 10
||| ||| |||
Db 7 GIFYGTYF 16

RESULT 44

US-10-472-928-4236
; Sequence 4236, Application US/10472928
; Publication No. US20050020813A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE: P026926WO
CURRENT APPLICATION NUMBER: US/10/472,928

PRIOR FILING DATE: 2003-09-26
CURRENT APPLICATION NUMBER: GB-0107658.7

PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979

SOFTWARE: SeqWin99, version 1.03
SEQ ID NO: 4236

LENGTH: 227


```

: TYPE: PR1
: ORGANISM: Streptococcus pneumoniae
: FEATURE:
: OTHER INFORMATION: L-ribulose 5-phosphate 4-epimerase Arad, putative
: OTHER INFORMATION: Cellular location: cytoplasm
: OTHER INFORMATION: Similar to strain K6 sequence 15503866 (e-135)
: US-10-472-928-4236

```

Query Match	59.7%	Score 43;	DB 5;	Length 227;
Best Local Similarity	72.7%;	Pred. No. 1.2e+02;		
Matches	8;	Conservative	1;	Mismatches 2;
			Indels	0;
			Gaps	0

```

QY      2  IYFYGTYYEDY  12
          | | | | | : | |
Db     106 IPFYGTTHADY  116

```

RESULT 45
US-10-282-122A-74190
; Sequence 74190, Application US/10282122A
; Publication No. US20040029129A1

? APPLICANT: Wang, Liangsu
 ? APPLICANT: Zamudio, Carlos
 ? APPLICANT: Malone, Cheryl
 ? APPLICANT: Haselbeck, Robert
 ? APPLICANT: Ohlsen, Kari
 ? APPLICANT: Zyskind, Judith
 ? APPLICANT: Wall, Daniel
 ? APPLICANT: Trawick, John
 ? APPLICANT: Carr, Grant
 ? APPLICANT: Yamamoto, Robert
 ? APPLICANT: Forsyth, R.
 ? APPLICANT: Xu, H.

```

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A

```

```

;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191, 078
;; PRIOR FILING DATE: 2000-03-21

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;
; PRIOR APPLICATION NUMBER: 60/206,848
;
; PRIOR FILING DATE: 2000-05-23
;
; PRIOR APPLICATION NUMBER: 60/207,727
;
; PRIOR FILING DATE: 2000-05-26
;

;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347

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; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23

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;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09

```

; PRIORITY APPLICATION NUMBER: 60/269,308
; PRIORITY FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM

```

```

; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74190

```

```

; LENGTH: 234
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae

```

US-10-282-122A-74190

Query Match 59.7% Score 43 DB 4 Length 234

Best Local Similarity	72.7%;	Pred. No. 1.2e+02;	2
Matches	8; Conservative	1; Mismatches	2; Indels 0; Gaps 0

QY 2 IYFYGTTFDY 12
| | | | | : | |

Db 113 IPFYGTTHADY 123

RESULT 46

US-10-282-122A-74354
; Sequence 74354, Application US/10282122A
; Publication No. US20040029129A1
CURRENTLY UNPUBLISHED

; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT:

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; APPLICANT: Ohlsen, Kari
; APPLICANT: zyskind, Judith
; APPLICANT: wall, Daniel
; APPLICANT:

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; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Esse

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;
; PRIOR APPLICATION NUMBER: 60/242,578
;
; PRIOR FILING DATE: 2000-10-23
;
; PRIOR APPLICATION NUMBER: 60/253,625

;
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22

;
; PRIOR APPLICATION NUMBER: 60/267,636
;
; PRIOR FILING DATE: 2001-02-09
;
; PRIOR APPLICATION NUMBER: 60/269,308
;
; PRIOR FILING DATE: 2001-02-16
;

```

; Remaining Prior Application data rem
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1

```

```

; SEQ ID NO 74354
; LENGTH: 234
; TYPE: PRT
;

```

ORGANISM: *Streptococcus pyogenes*
US-10-282-122A-74354

Query Match	59.7%	Score 43	DB 4	Length 234
Best Local Similarity	72.7%	Pred. No. 1.2e+02		
Matches	8	Conservative	1	Mismatches 2
				Indels 0
				Gaps 0

QY 2 IYFYGTYYFDY 12
|||
|||:
|||

RESULT 47
US-10-617-320-3704
; Sequence 3704, Application US/10617320

Publication No. US20050136404A1
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSIS

NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/617.320
; FILING DATE: 10-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107.433
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Atinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3704:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1..236
; SEQUENCE DESCRIPTION: SEQ ID NO: 3704:
US-10-617-320-3704

Query Match          59.7%; Score 43; DB 5; Length 236;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 IYFYGTTFDY 12
        | ||| : ||
Db      115 IPFYGTTHADY 125

RESULT 48
US-10-300-846-8
; Sequence 8, Application US/10300846
; Publication No. US2003020737A1
; GENERAL INFORMATION:
; APPLICANT: HAN, YI
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ECHEVERRI, FERNANDO
; APPLICANT: WANG, KUN
; TITLE OF INVENTION: OLFACTORY RECEPTORS FOR ISOVALERIC ACID AND RELATED
; TITLE OF INVENTION: MALODORANTS AND USE THEREOF IN ASSAYS FOR
; TITLE OF INVENTION: IDENTIFICATION OF BLOCKERS OF MALODOR
; FILE REFERENCE: 078003-0291924
; CURRENT APPLICATION NUMBER: US/10/300.846
; FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/348.371
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/809,291
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/341,872
; PRIOR FILING DATE: 2001-12-21

```

```

; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-300-846-8

Query Match          59.7%; Score 43; DB 4; Length 310;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 IYFYGTTFDY 12
        | ||| : ||
Db      249 IPFYGSTTFY 259

RESULT 49
US-10-774-355A-1835
; Sequence 1835, Application US/10774355A
; Publication No. US20050043513A1
; GENERAL INFORMATION:
; APPLICANT: Firestein, Stuart
; APPLICANT: Zhang, Ximin
; TITLE OF INVENTION: MOUSE OLFACTORY RECEPTOR GENE SUPERFAMILY
; FILE REFERENCE: A34570-PCT-USA-A 070050.2520
; CURRENT APPLICATION NUMBER: US/10/774.355A
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: PCT/US02/25556
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/311,159
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/339,694
; PRIOR FILING DATE: 2001-12-12
; NUMBER OF SEQ ID NOS: 2596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1835
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-774-355A-1835

Query Match          59.7%; Score 43; DB 5; Length 310;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 IYFYGTTFDY 12
        | ||| : ||
Db      249 IPFYGSTTFY 259

RESULT 50
US-10-282-122A-74381
; Sequence 74381, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
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; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
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; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
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; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patencin version 3.1
; SEQ ID NO 74381
; LENGTH: 389
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; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74381

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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171	32	44.4	1013	7	US-11-103-957-9	Sequence 9, Appl	244	31	43.1	255	7	US-11-054-515-857	Sequence 857, App

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246	31	43.1	256	7	US-11-054-515-1463	Sequence 1463, Ap	319	30	41.7	338	6	US-10-055-877-175	Sequence 175, App
247	31	43.1	257	7	US-11-054-515-1607	Sequence 1607, Ap	320	30	41.7	353	6	US-10-641-697-77	Sequence 77, Appl
248	31	43.1	297	6	US-10-858-730-115	Sequence 115, App	321	30	41.7	358	6	US-10-055-877-176	Sequence 176, App
249	31	43.1	297	6	US-10-858-730-116	Sequence 116, App	322	30	41.7	358	6	US-10-055-877-177	Sequence 177, App
250	31	43.1	297	6	US-11-037-243-79	Sequence 79, Appl	323	30	41.7	374	7	US-11-196-976-4	Sequence 4, Appl
251	31	43.1	483	6	US-10-517-939-242	Sequence 242, App	324	30	41.7	375	7	US-11-196-976-2	Sequence 2, Appl
252	31	43.1	564	6	US-10-793-626-1296	Sequence 1296, Ap	325	30	41.7	375	7	US-11-103-957-95	Sequence 95, Appl
253	31	43.1	754	6	US-11-074-176-202	Sequence 202, App	326	30	41.7	386	6	US-10-467-657-7076	Sequence 7076, Ap
254	31	43.1	839	7	US-11-076-431-2	Sequence 2, Appl	327	30	41.7	387	6	US-10-510-386-212	Sequence 212, App
255	31	43.1	839	7	US-11-076-431-4	Sequence 4, Appl	328	30	41.7	397	6	US-10-793-626-644	Sequence 644, App
256	31	43.1	839	7	US-11-076-431-6	Sequence 6, Appl	329	30	41.7	401	6	US-10-641-678-33	Sequence 33, Appl
257	31	43.1	839	7	US-11-076-431-8	Sequence 8, Appl	330	30	41.7	408	6	US-10-467-657-2848	Sequence 2848, Ap
258	31	43.1	839	7	US-11-005-216-2	Sequence 2, Appl	331	30	41.7	429	6	US-10-525-710-52	Sequence 52, Appl
259	31	43.1	859	7	US-11-000-463-423	Sequence 423, App	332	30	41.7	429	6	US-10-525-710-54	Sequence 54, Appl
260	31	43.1	859	7	US-11-000-463-895	Sequence 895, App	333	30	41.7	440	6	US-10-525-710-52	Sequence 52, Appl
261	31	43.1	859	7	US-10-467-657-5656	Sequence 5656, Ap	334	30	41.7	441	6	US-10-995-561-638	Sequence 638, App
262	31	43.1	929	6	US-10-467-962B-81	Sequence 81, Appl	335	30	41.7	441	6	US-10-995-561-639	Sequence 639, App
263	31	43.1	1001	6	US-11-054-515-3175	Sequence 3175, Ap	336	30	41.7	444	6	US-11-108-519-14	Sequence 14, Appl
264	30.5	42.4	10	7	US-11-054-515-3032	Sequence 3032, Ap	337	30	41.7	451	6	US-10-467-657-5472	Sequence 5472, Ap
265	30.5	42.4	118	7	US-11-061-848-16	Sequence 16, Appl	338	30	41.7	484	6	US-10-467-657-5472	Sequence 5472, Ap
266	30.5	42.4	118	7	US-10-673-037-9	Sequence 9, Appl	339	30	41.7	487	7	US-11-193-473-2	Sequence 2, Appl
267	30.5	42.4	119	6	US-10-473-037-9	Sequence 9, Appl	340	30	41.7	511	7	US-11-012-762-66	Sequence 66, Appl
268	30.5	42.4	124	7	US-11-096-046-2	Sequence 2, Appl	341	30	41.7	521	7	US-11-143-960-32	Sequence 32, Appl
269	30.5	42.4	124	7	US-11-054-515-1953	Sequence 1953, Ap	342	30	41.7	544	6	US-10-432-463-20	Sequence 20, Appl
270	30.5	42.4	252	7	US-11-054-515-1627	Sequence 1627, Ap	343	30	41.7	548	7	US-11-137-465-47	Sequence 47, Appl
271	30.5	42.4	344	6	US-10-995-561-525	Sequence 525, App	344	30	41.7	608	6	US-10-873-528-8	Sequence 8, Appl
272	30.5	42.4	344	6	US-10-995-561-525	Sequence 525, App	345	30	41.7	703	7	US-11-052-554A-97	Sequence 97, Appl
273	30.5	42.4	598	7	US-11-052-554A-263	Sequence 263, App	346	30	41.7	744	7	US-11-052-554A-94	Sequence 94, Appl
274	30.5	42.4	598	7	US-11-052-554A-264	Sequence 264, App	347	30	41.7	751	7	US-11-052-554A-109	Sequence 109, Appl
275	30.5	42.4	667	7	US-11-096-046-29	Sequence 29, Appl	348	30	41.7	795	7	US-11-109-157A-14	Sequence 14, Appl
276	30.5	42.4	13	7	US-11-033-039-258	Sequence 258, Appl	349	30	41.7	801	6	US-10-793-626-2020	Sequence 2020, Ap
277	30	41.7	16	6	US-10-649-229-18	Sequence 18, Appl	350	30	41.7	816	7	US-11-090-439-48	Sequence 48, Appl
278	30	41.7	17	7	US-11-054-515-2790	Sequence 2790, Ap	351	30	41.7	860	7	US-11-189-521-2	Sequence 2, Appl
279	30	41.7	19	7	US-11-054-515-2167	Sequence 2167, Ap	352	30	41.7	1045	7	US-11-113-428-54	Sequence 54, Appl
280	30	41.7	20	7	US-11-054-515-2961	Sequence 2961, Ap	353	30	41.7	1072	7	US-11-115-639-47	Sequence 47, Appl
281	30	41.7	20	7	US-11-108-519-2	Sequence 2, Appl	354	30	41.7	1208	7	US-11-115-639-46	Sequence 46, Appl
282	30	41.7	40	6	US-10-957-887B-285	Sequence 285, App	355	30	41.7	1208	7	US-11-115-639-47	Sequence 47, Appl
283	30	41.7	43	6	US-10-957-887B-285	Sequence 285, App	356	30	41.7	1208	7	US-11-115-639-46	Sequence 46, Appl
284	30	41.7	44	6	US-10-957-887B-209	Sequence 209, App	357	30	41.7	1208	7	US-11-115-639-46	Sequence 46, Appl
285	30	41.7	44	6	US-10-957-887B-251	Sequence 251, App	358	29.5	41.0	15	7	US-11-054-515-2134	Sequence 2134, Ap
286	30	41.7	116	6	US-10-467-657-480	Sequence 480, App	359	29.5	41.0	16	7	US-11-054-515-2179	Sequence 2179, Ap
287	30	41.7	118	7	US-11-136-559-8	Sequence 8, Appl	360	29.5	41.0	16	7	US-11-054-515-3034	Sequence 3034, Ap
288	30	41.7	118	7	US-11-136-559-16	Sequence 16, Appl	361	29.5	41.0	16	7	US-11-054-515-3034	Sequence 3034, Ap
289	30	41.7	129	6	US-11-064-174-143	Sequence 143, App	362	29.5	41.0	248	7	US-11-054-515-900	Sequence 900, App
290	30	41.7	157	6	US-10-467-657-5104	Sequence 5104, Ap	363	29.5	41.0	248	7	US-11-054-515-1104	Sequence 1104, Ap
291	30	41.7	161	6	US-10-769-744-2	Sequence 2, Appl	364	29.5	41.0	248	7	US-11-054-515-1472	Sequence 1472, Ap
292	30	41.7	162	7	US-11-033-039-246	Sequence 246, App	365	29.5	41.0	248	7	US-11-054-515-1717	Sequence 1717, Ap
293	30	41.7	203	6	US-10-980-388-79	Sequence 79, Appl	366	29.5	41.0	248	7	US-11-054-515-1718	Sequence 1718, Ap
294	30	41.7	227	6	US-10-467-657-5190	Sequence 5190, App	367	29.5	41.0	248	7	US-11-054-515-1719	Sequence 1719, Ap
295	30	41.7	227	6	US-10-884-730-329	Sequence 329, App	368	29.5	41.0	248	7	US-11-054-515-1721	Sequence 1721, Ap
296	30	41.7	247	7	US-11-054-515-1993	Sequence 1993, App	369	29.5	41.0	248	7	US-11-054-515-1728	Sequence 1728, Ap
297	30	41.7	247	7	US-11-054-515-1998	Sequence 1998, App	370	29.5	41.0	248	7	US-11-054-515-1732	Sequence 1732, Ap
298	30	41.7	249	7	US-11-054-515-1445	Sequence 1445, App	371	29.5	41.0	248	7	US-11-054-515-1732	Sequence 1732, Ap
299	30	41.7	249	7	US-11-054-515-1641	Sequence 1641, App	372	29.5	41.0	248	7	US-11-054-515-1733	Sequence 1733, Ap
300	30	41.7	250	7	US-11-054-515-1325	Sequence 1325, App	373	29.5	41.0	248	7	US-11-054-515-1734	Sequence 1734, Ap
301	30	41.7	252	7	US-11-054-515-1435	Sequence 1435, App	374	29.5	41.0	248	7	US-11-054-515-1737	Sequence 1737, Ap
302	30	41.7	252	7	US-11-054-515-1500	Sequence 1500, App	375	29.5	41.0	248	7	US-11-054-515-1741	Sequence 1741, Ap
303	30	41.7	252	7	US-11-054-515-1690	Sequence 1690, App	376	29.5	41.0	248	7	US-11-054-515-1871	Sequence 1871, Ap
304	30	41.7	252	7	US-11-054-515-1852	Sequence 1852, App	377	29.5	41.0	248	7	US-11-054-515-1876	Sequence 1876, Ap
305	30	41.7	255	7	US-11-054-515-841	Sequence 841, App	378	29.5	41.0	248	7	US-11-054-515-1877	Sequence 1877, Ap
306	30	41.7	255	7	US-11-054-515-1137	Sequence 1137, App	379	29.5	41.0	248	7	US-11-054-515-1879	Sequence 1879, Ap
307	30	41.7	255	7	US-11-054-515-1597	Sequence 1597, App	380	29.5	41.0	250	7	US-11-054-515-7	Sequence 7, Appl
308	30	41.7	263	7	US-11-102-883-36	Sequence 36, Appl	381	29.5	41.0	251	7	US-11-054-515-1562	Sequence 1562, App
309	30	41.7	265	6	US-10-793-626-174	Sequence 174, App	382	29.5	41.0	251	7	US-11-054-515-1586	Sequence 1586, App
310	30	41.7	266	6	US-10-884-730-326	Sequence 326, App	383	29.5	41.0	251	7	US-11-054-515-1736	Sequence 1736, App
311	30	41.7	266	6	US-10-884-730-328	Sequence 328, App	384	29.5	41.0	251	7	US-11-054-515-1738	Sequence 1738, App
312	30	41.7	266	6	US-10-884-730-330	Sequence 330, App	385	29.5	41.0	251	7	US-11-054-515-1869	Sequence 1869, App
313	30	41.7	269	6	US-10-793-626-880	Sequence 880, App	386	29.5	41.0	251	7	US-11-054-515-1870	Sequence 1870, App
314	30	41.7	274	7	US-11-102-883-34	Sequence 34, Appl	387	29.5	41.0	251	7	US-11-054-515-1872	Sequence 1872, App
315	30	41.7	290	6	US-10-793-626-3024	Sequence 3024, App	388	29.5	41.0	251	7	US-11-054-515-1878	Sequence 1878, App
316	30	41.7	290	6	US-10-793-626-3252	Sequence 3252, App	389	29.5	41.0	279	7	US-11-032-797-5	Sequence 5, Appl
317	30	41.7	313	6	US-10-793-626-3102	Sequence 3102, App	390	29.5	41.0	281	7	US-11-213-368-11	Sequence 11, Appl

391	29.5	41.0	281	7	US-11-213-368-12	Sequence 12, Appl	464	29	40.3	376	7	US-11-012-762-40	Sequence 40, Appl
392	29.5	41.0	325	7	US-11-074-176-368	Sequence 368, App	465	29	40.3	379	6	US-10-858-730-24	Sequence 24, Appl
393	29.5	41.0	359	7	US-11-105-172-2	Sequence 2, Appl1	466	29	40.3	379	6	US-10-858-730-281	Sequence 281, Appl
394	29.5	41.0	430	6	US-10-467-657-1622	Sequence 1622, Ap	467	29	40.3	379	6	US-10-858-730-285	Sequence 285, App
395	29.5	41.0	709	6	US-10-131-826A-202	Sequence 202, App	468	29	40.3	379	6	US-10-858-730-290	Sequence 290, App
396	29.5	41.0	709	6	US-10-519-238-3	Sequence 3, Appl1	469	29	40.3	382	7	US-11-012-762-52	Sequence 52, Appl
397	29	40.3	14	7	US-11-054-515-3109	Sequence 3109, Ap	470	29	40.3	387	7	US-11-137-465-57	Sequence 57, Appl
398	29	40.3	16	7	US-11-054-515-2280	Sequence 2280, Ap	471	29	40.3	388	6	US-10-467-657-58	Sequence 58, Appl
399	29	40.3	17	6	US-10-834-397-210	Sequence 210, Appl	472	29	40.3	388	6	US-10-467-657-1864	Sequence 1864, Ap
400	29	40.3	19	6	US-10-632-150-90	Sequence 90, Appl	473	29	40.3	416	6	US-10-793-626-1402	Sequence 2402, Ap
401	29	40.3	19	7	US-11-054-515-3036	Sequence 3036, Ap	474	29	40.3	432	6	US-10-793-626-780	Sequence 780, App
402	29	40.3	19	7	US-11-073-457-90	Sequence 90, Appl	475	29	40.3	448	6	US-10-873-628-42	Sequence 42, Appl
403	29	40.3	19	7	US-11-073-460-90	Sequence 90, Appl	476	29	40.3	463	6	US-10-793-626-350	Sequence 350, App
404	29	40.3	23	7	US-11-054-515-2132	Sequence 2132, Ap	477	29	40.3	470	7	US-11-186-284-123	Sequence 123, App
405	29	40.3	23	7	US-11-054-515-3076	Sequence 3076, Ap	478	29	40.3	473	6	US-10-793-626-50	Sequence 60, Appl
406	29	40.3	47	6	US-10-485-517-270	Sequence 270, App	479	29	40.3	480	7	US-11-080-991-76	Sequence 76, Appl
407	29	40.3	97	6	US-11-084-554-43	Sequence 43, Appl	480	29	40.3	482	6	US-10-995-561-860	Sequence 560, App
408	29	40.3	113	6	US-10-932-334-65	Sequence 65, Appl	481	29	40.3	504	7	US-11-055-822-136	Sequence 136, App
409	29	40.3	118	7	US-11-061-848-3	Sequence 3, Appl1	482	29	40.3	518	6	US-10-995-561-559	Sequence 559, App
410	29	40.3	118	7	US-11-061-848-4	Sequence 4, Appl1	483	29	40.3	518	6	US-10-821-234-1165	Sequence 1165, Ap
411	29	40.3	118	7	US-11-061-848-5	Sequence 5, Appl1	484	29	40.3	527	6	US-10-705-633-1	Sequence 1, Appl1
412	29	40.3	118	7	US-11-061-848-6	Sequence 6, Appl1	485	29	40.3	527	6	US-10-705-633-2	Sequence 2, Appl1
413	29	40.3	118	7	US-11-061-848-7	Sequence 7, Appl1	486	29	40.3	527	6	US-10-705-633-3	Sequence 3, Appl1
414	29	40.3	118	7	US-11-061-848-8	Sequence 8, Appl1	487	29	40.3	528	6	US-10-467-657-1042	Sequence 1042, Ap
415	29	40.3	118	7	US-11-061-848-9	Sequence 9, Appl1	488	29	40.3	553	6	US-10-453-372-1164	Sequence 1164, Ap
416	29	40.3	119	7	US-11-221-900-12	Sequence 12, Appl	489	29	40.3	562	6	US-10-995-561-561	Sequence 561, App
417	29	40.3	120	6	US-10-932-334-74	Sequence 74, Appl	490	29	40.3	577	6	US-11-124-368A-232	Sequence 232, App
418	29	40.3	121	7	US-11-107-028-35	Sequence 35, Appl	491	29	40.3	596	6	US-10-453-372-1162	Sequence 1162, Ap
419	29	40.3	121	7	US-11-107-028-37	Sequence 37, Appl	492	29	40.3	596	6	US-10-453-372-1172	Sequence 1172, Ap
420	29	40.3	121	7	US-11-107-028-38	Sequence 38, Appl	493	29	40.3	604	6	US-10-453-372-1160	Sequence 1160, Ap
421	29	40.3	123	6	US-10-793-626-430	Sequence 430, App	494	29	40.3	612	6	US-10-453-372-1166	Sequence 1166, Ap
422	29	40.3	124	6	US-10-771-257-22	Sequence 22, Appl	495	29	40.3	604	6	US-10-453-372-1156	Sequence 1156, Ap
423	29	40.3	124	7	US-11-127-677-22	Sequence 22, Appl	496	29	40.3	657	7	US-11-179-977-1	Sequence 1, Appl1
424	29	40.3	127	6	US-10-793-626-1184	Sequence 1184, Ap	497	29	40.3	657	7	US-11-052-554A-113	Sequence 113, App
425	29	40.3	182	7	US-11-074-176-218	Sequence 218, App	498	29	40.3	668	7	US-11-052-554A-104	Sequence 104, App
426	29	40.3	183	7	US-11-069-642-125	Sequence 125, App	499	29	40.3	686	6	US-10-821-224-1027	Sequence 1027, Ap
427	29	40.3	225	6	US-10-793-626-1594	Sequence 1594, Ap	500	29	40.3	690	6	US-10-131-826A-306	Sequence 306, App
428	29	40.3	234	7	US-11-102-240-14	Sequence 14, Appl	501	29	40.3	698	6	US-10-793-626-2388	Sequence 2388, Ap
429	29	40.3	236	7	US-11-221-900-2	Sequence 2, Appl1	502	29	40.3	708	7	US-11-174-150-35	Sequence 25, Appl
430	29	40.3	247	6	US-10-519-238-1	Sequence 1, Appl1	503	29	40.3	721	7	US-11-060-920-5	Sequence 5, Appl1
431	29	40.3	250	7	US-11-054-515-933	Sequence 933, App	504	29	40.3	736	7	US-11-174-150-26	Sequence 26, Appl
432	29	40.3	250	7	US-11-054-515-1797	Sequence 1797, Ap	505	29	40.3	736	7	US-11-078-189-8	Sequence 8, Appl1
433	29	40.3	251	6	US-10-519-238-6	Sequence 6, Appl1	506	29	40.3	736	7	US-11-113-837-20	Sequence 20, Appl
434	29	40.3	251	7	US-11-054-515-195	Sequence 195, App	507	29	40.3	760	7	US-11-186-284-55	Sequence 35, Appl
435	29	40.3	251	7	US-11-054-515-1538	Sequence 1538, Ap	508	29	40.3	900	7	US-11-144-987-10	Sequence 10, Appl
436	29	40.3	253	6	US-10-793-626-928	Sequence 928, App	509	29	40.3	902	7	US-11-144-987-12	Sequence 12, Appl
437	29	40.3	253	6	US-10-793-626-1196	Sequence 1196, Ap	510	29	40.3	902	7	US-11-144-987-14	Sequence 14, Appl
438	29	40.3	253	7	US-11-054-515-1964	Sequence 1964, Ap	511	29	40.3	910	7	US-11-144-987-2	Sequence 2, Appl
439	29	40.3	254	7	US-11-054-515-1673	Sequence 1673, Ap	512	29	40.3	910	7	US-11-144-987-22	Sequence 22, Appl
440	29	40.3	255	7	US-11-054-515-4	Sequence 4, Appl1	513	29	40.3	917	7	US-11-144-987-24	Sequence 24, Appl
441	29	40.3	255	7	US-11-054-515-1054	Sequence 1054, Ap	514	29	40.3	917	7	US-11-144-987-26	Sequence 26, Appl
442	29	40.3	255	7	US-11-054-515-1056	Sequence 1056, Ap	515	29	40.3	934	6	US-10-453-372-1158	Sequence 1158, Ap
443	29	40.3	255	7	US-11-054-515-1065	Sequence 1065, Ap	516	29	40.3	964	7	US-11-137-465-88	Sequence 58, Appl
444	29	40.3	255	7	US-11-054-515-1786	Sequence 1786, Ap	517	29	40.3	965	7	US-11-113-424-4	Sequence 2, Appl1
445	29	40.3	258	7	US-11-054-515-1773	Sequence 1773, Ap	518	29	40.3	965	7	US-11-117-047-51	Sequence 51, Appl
446	29	40.3	272	7	US-11-046-456-23	Sequence 23, Appl	519	29	40.3	1092	6	US-10-821-234-999	Sequence 999, App
447	29	40.3	291	6	US-11-046-644-23	Sequence 23, Appl	520	29	40.3	1734	7	US-11-192-967-6	Sequence 6, Appl1
448	29	40.3	292	6	US-10-527-500-43	Sequence 43, Appl	521	29	40.3	1734	7	US-11-193-715-6	Sequence 6, Appl1
449	29	40.3	293	6	US-10-527-500-77	Sequence 77, Appl	522	29	40.3	2333	6	US-10-453-372-170	Sequence 170, App
450	29	40.3	303	6	US-10-770-726-52	Sequence 52, Appl	523	29	40.3	2480	6	US-10-995-561-825	Sequence 825, App
451	29	40.3	319	7	US-11-055-822-458	Sequence 458, App	524	29	40.3	2662	6	US-10-453-372-114	Sequence 114, App
452	29	40.3	319	7	US-11-055-822-876	Sequence 876, App	525	29	40.3	2723	6	US-10-453-372-148	Sequence 148, App
453	29	40.3	327	6	US-10-632-150-58	Sequence 58, App	526	29	40.3	2733	6	US-10-453-372-136	Sequence 136, App
454	29	40.3	327	7	US-11-073-457-58	Sequence 58, Appl	527	29	40.3	2733	6	US-10-453-372-142	Sequence 142, App
455	29	40.3	327	7	US-11-073-460-58	Sequence 58, Appl	528	29	40.3	2733	6	US-10-453-372-146	Sequence 146, App
456	29	40.3	348	6	US-10-878-556A-111	Sequence 111, App	529	29	40.3	2733	6	US-10-453-372-150	Sequence 150, App
457	29	40.3	364	7	US-11-012-762-38	Sequence 38, Appl	530	29	40.3	2733	6	US-10-453-372-154	Sequence 154, App
458	29	40.3	376	7	US-11-012-762-10	Sequence 10, Appl	531	29	40.3	2765	6	US-10-453-372-116	Sequence 116, App
459	29	40.3	376	7	US-11-012-762-16	Sequence 16, Appl	532	29	40.3	3116	6	US-10-995-561-826	Sequence 826, App
460	29	40.3	376	7	US-11-012-762-18	Sequence 18, Appl	533	29	40.3	4495	6	US-10-453-372-1002	Sequence 1002, Ap
461	29	40.3	376	7	US-11-012-762-20	Sequence 20, Appl	534	29	40.3	7102	7	US-11-143-980-48	Sequence 48, Appl
462	29	40.3	376	7	US-11-012-762-22	Sequence 22, Appl	535	29	39.6	15	7	US-11-054-515-2850	Sequence 2850, Ap
463	29	40.3	376	7	US-11-012-762-24	Sequence 24, Appl	536	29	39.6	117	7	US-11-149-943-81	Sequence 81, Appl

537	28.5	39.6	119	6	US-10-473-037-49	Sequence 49, Appl	610	28	38.9	256	6	US-10-467-657-7902	Sequence 7902, Ap
538	28.5	39.6	125	7	US-11-064-174-8	Sequence 8, Appl1	611	28	38.9	257	6	US-10-467-657-1118	Sequence 5118, Ap
539	28.5	39.6	125	7	US-11-064-174-20	Sequence 20, Appl	612	28	38.9	257	6	US-10-519-238-4	Sequence 4, Appl1
540	28.5	39.6	125	7	US-11-064-174-21	Sequence 21, Appl	613	28	38.9	257	7	US-11-102-240-94	Sequence 94, Appl
541	28.5	39.6	125	7	US-11-064-174-22	Sequence 22, Appl	614	28	38.9	260	7	US-11-054-515-1458	Sequence 1458, Ap
542	28.5	39.6	125	7	US-11-064-174-23	Sequence 23, Appl	615	28	38.9	268	6	US-10-995-561-718	Sequence 718, Appl
543	28.5	39.6	138	6	US-10-473-037-1	Sequence 1, Appl1	616	28	38.9	276	7	US-11-112-882-86	Sequence 86, Appl
544	28.5	39.6	138	6	US-11-054-515-924	Sequence 924, Appl	617	28	38.9	277	6	US-10-055-877-336	Sequence 236, Appl
545	28.5	39.6	247	7	US-11-054-515-2091	Sequence 2091, Ap	618	28	38.9	294	7	US-11-112-882-85	Sequence 85, Appl1
546	28.5	39.6	248	7	US-10-793-626-196	Sequence 196, App	619	28	38.9	295	7	US-11-067-121-2	Sequence 11, Appl
547	28.5	39.6	417	6	US-10-517-939-216	Sequence 276, App	620	28	38.9	299	6	US-10-793-626-1192	Sequence 1192, Ap
548	28.5	39.6	466	6	US-10-517-939-216	Sequence 276, App	621	28	38.9	299	6	US-10-793-626-1768	Sequence 1768, Ap
549	28.5	39.6	575	6	US-10-467-657-1456	Sequence 1456, Ap	622	28	38.9	304	7	US-11-112-882-3	Sequence 3, Appl1
550	28.5	39.6	579	6	US-10-528-673-2	Sequence 2, Appl1	623	28	38.9	306	7	US-11-017-550-35	Sequence 35, Appl1
551	28.5	39.6	1101	6	US-10-878-556A-107	Sequence 107, Appl	624	28	38.9	306	7	US-11-017-550-39	Sequence 39, Appl1
552	28.5	39.6	1237	7	US-11-052-554A-95	Sequence 95, Appl	625	28	38.9	306	7	US-11-017-550-42	Sequence 42, Appl1
553	28	38.9	8	7	US-11-127-677-128	Sequence 128, App	626	28	38.9	306	7	US-11-017-550-47	Sequence 47, Appl1
554	28	38.9	8	7	US-11-096-046-23	Sequence 23, Appl1	627	28	38.9	306	7	US-11-017-550-63	Sequence 63, Appl1
555	28	38.9	10	6	US-10-473-037-5	Sequence 5, Appl1	628	28	38.9	306	7	US-11-017-550-64	Sequence 64, Appl1
556	28	38.9	11	6	US-10-649-229-15	Sequence 15, Appl1	629	28	38.9	309	7	US-11-109-156-24	Sequence 24, Appl1
557	28	38.9	15	7	US-11-128-440-62	Sequence 62, Appl1	630	28	38.9	309	7	US-11-109-156-24	Sequence 24, Appl1
558	28	38.9	16	7	US-11-054-515-2129	Sequence 2129, Ap	631	28	38.9	314	6	US-10-995-793-74	Sequence 74, Appl1
559	28	38.9	17	7	US-11-054-515-2847	Sequence 2847, Ap	632	28	38.9	317	6	US-10-131-826A-524	Sequence 524, App
560	28	38.9	17	7	US-11-054-515-2876	Sequence 2876, Ap	633	28	38.9	317	7	US-11-102-240-116	Sequence 116, App
561	28	38.9	19	7	US-11-054-515-3145	Sequence 3145, Ap	634	28	38.9	317	7	US-11-196-618-2	Sequence 2, Appl1
562	28	38.9	21	7	US-11-149-943-32	Sequence 32, Appl1	635	28	38.9	317	7	US-11-196-618-4	Sequence 4, Appl1
563	28	38.9	24	7	US-11-054-515-2926	Sequence 2926, Ap	636	28	38.9	320	7	US-11-112-882-76	Sequence 76, Appl1
564	28	38.9	61	6	US-10-997-201A-9	Sequence 9, Appl1	637	28	38.9	324	7	US-11-196-618-16	Sequence 16, Appl1
565	28	38.9	64	6	US-10-467-657-8933	Sequence 8933, Ap	638	28	38.9	324	7	US-11-196-618-18	Sequence 18, Appl1
566	28	38.9	97	7	US-11-054-669-29	Sequence 29, Appl1	639	28	38.9	353	7	US-11-012-762-50	Sequence 50, Appl1
567	28	38.9	97	7	US-11-054-669-31	Sequence 31, Appl1	640	28	38.9	353	7	US-11-089-551A-4	Sequence 4, Appl1
568	28	38.9	97	7	US-11-084-554-41	Sequence 41, Appl1	641	28	38.9	355	6	US-10-995-561-720	Sequence 720, App
569	28	38.9	112	7	US-11-125-837-25	Sequence 25, Appl1	642	28	38.9	359	7	US-11-012-762-58	Sequence 58, Appl1
570	28	38.9	112	7	US-11-125-837-34	Sequence 34, Appl1	643	28	38.9	365	6	US-10-453-372-560	Sequence 560, App
571	28	38.9	116	7	US-11-054-669-101	Sequence 101, App	644	28	38.9	367	7	US-11-012-762-36	Sequence 36, Appl1
572	28	38.9	117	7	US-11-127-903-44	Sequence 44, Appl1	645	28	38.9	367	7	US-11-012-762-60	Sequence 60, Appl1
573	28	38.9	118	6	US-10-648-816-9	Sequence 9, Appl1	646	28	38.9	367	7	US-11-117-169-4	Sequence 12, Appl1
574	28	38.9	118	6	US-10-648-816-10	Sequence 10, Appl1	647	28	38.9	367	7	US-11-117-169-12	Sequence 12, Appl1
575	28	38.9	118	6	US-10-648-816-14	Sequence 14, Appl1	648	28	38.9	368	7	US-11-129-143-62	Sequence 62, Appl1
576	28	38.9	119	6	US-10-834-397-26	Sequence 26, Appl1	649	28	38.9	387	6	US-10-485-517-132	Sequence 132, App
577	28	38.9	124	7	US-11-096-046-4	Sequence 4, Appl1	650	28	38.9	393	7	US-11-111-239-11	Sequence 11, Appl1
578	28	38.9	125	6	US-10-771-257-49	Sequence 49, Appl1	651	28	38.9	395	6	US-10-453-372-554	Sequence 54, App
579	28	38.9	125	7	US-11-127-677-47	Sequence 47, Appl1	652	28	38.9	400	7	US-11-117-169-2	Sequence 2, Appl1
580	28	38.9	129	7	US-11-056-186-2	Sequence 2, Appl1	653	28	38.9	400	7	US-11-117-169-4	Sequence 4, Appl1
581	28	38.9	131	6	US-11-125-837-19	Sequence 19, Appl1	654	28	38.9	406	6	US-10-878-556A-11	Sequence 11, Appl1
582	28	38.9	151	6	US-10-793-626-2696	Sequence 2696, Ap	655	28	38.9	411	6	US-10-821-234-1386	Sequence 1386, Ap
583	28	38.9	172	6	US-10-485-517-134	Sequence 134, App	656	28	38.9	411	6	US-10-878-556A-140	Sequence 140, App
584	28	38.9	196	6	US-10-793-626-778	Sequence 778, App	657	28	38.9	412	6	US-10-485-517-285	Sequence 285, Appl
585	28	38.9	196	6	US-10-467-657-1158	Sequence 1158, Ap	658	28	38.9	421	6	US-10-467-657-3348	Sequence 3348, Ap
586	28	38.9	216	6	US-10-873-528-123	Sequence 123, App	659	28	38.9	423	6	US-10-453-372-558	Sequence 558, App
587	28	38.9	217	6	US-10-821-234-1568	Sequence 1568, Ap	660	28	38.9	423	7	US-11-047-383-11	Sequence 11, Appl1
588	28	38.9	217	7	US-11-080-991-58	Sequence 58, Appl1	661	28	38.9	424	7	US-11-138-643-13	Sequence 13, Appl1
589	28	38.9	219	7	US-11-206-746-2	Sequence 2, Appl1	662	28	38.9	424	7	US-11-047-383-10	Sequence 10, Appl1
590	28	38.9	219	7	US-11-052-554A-114	Sequence 114, App	663	28	38.9	425	6	US-10-453-372-552	Sequence 52, App
591	28	38.9	237	6	US-10-467-657-970	Sequence 970, App	664	28	38.9	425	6	US-11-096-276-2	Sequence 2, Appl1
592	28	38.9	238	6	US-10-927-641-68	Sequence 68, Appl1	665	28	38.9	426	6	US-10-453-372-556	Sequence 56, App
593	28	38.9	247	7	US-11-054-515-1137	Sequence 1137, Ap	666	28	38.9	426	6	US-11-047-383-13	Sequence 13, Appl1
594	28	38.9	247	7	US-11-054-515-1137	Sequence 1137, Ap	667	28	38.9	429	7	US-10-510-386-14	Sequence 14, Appl1
595	28	38.9	250	7	US-11-054-515-1335	Sequence 1335, Ap	668	28	38.9	469	6	US-10-510-386-14	Sequence 14, Appl1
596	28	38.9	251	7	US-11-054-515-947	Sequence 947, App	669	28	38.9	472	7	US-11-086-283-2	Sequence 2, Appl1
597	28	38.9	251	7	US-11-054-515-1332	Sequence 1332, Ap	670	28	38.9	483	7	US-11-184-574-4	Sequence 4, Appl1
598	28	38.9	251	7	US-11-054-515-1840	Sequence 1840, Ap	671	28	38.9	484	7	US-11-147-725-2	Sequence 2, Appl1
599	28	38.9	251	7	US-11-054-515-1921	Sequence 1921, Ap	672	28	38.9	485	6	US-10-630-203-2	Sequence 2, Appl1
600	28	38.9	252	7	US-11-054-515-956	Sequence 956, App	673	28	38.9	485	6	US-10-630-203-4	Sequence 4, Appl1
601	28	38.9	252	7	US-11-054-515-1311	Sequence 1311, App	674	28	38.9	485	7	US-11-103-037-1	Sequence 1, Appl1
602	28	38.9	253	7	US-11-054-515-1431	Sequence 1431, App	675	28	38.9	485	7	US-11-103-037-2	Sequence 2, Appl1
603	28	38.9	253	7	US-11-054-515-1449	Sequence 1449, App	676	28	38.9	505	6	US-10-793-626-2808	Sequence 2808, Ap
604	28	38.9	253	7	US-11-054-515-1814	Sequence 1814, Ap	677	28	38.9	505	6	US-10-467-657-2440	Sequence 2440, Ap
605	28	38.9	254	7	US-11-054-515-3244	Sequence 3244, Ap	678	28	38.9	552	6	US-10-131-826A-196	Sequence 196, App
606	28	38.9	254	7	US-11-054-515-838	Sequence 838, App	679	28	38.9	559	6	US-10-873-528-158	Sequence 158, App
607	28	38.9	254	7	US-11-054-515-870	Sequence 870, App	680	28	38.9	620	7	US-11-055-822-460	Sequence 460, App
608	28	38.9	254	7	US-11-054-515-1287	Sequence 1287, Ap	681	28	38.9	620	7	US-11-055-822-702	Sequence 702, App
609	28	38.9	254	7	US-11-054-515-1288	Sequence 1288, Ap	682	28	38.9	623	6	US-10-467-657-6260	Sequence 6260, App

683	28	38.9	635	6	US-10-821-234-1673	Sequence 1673, Ap	756	27	37.5	114	7	US-11-051-453-2	Sequence 2, Appl
684	28	38.9	644	6	US-10-467-657-5958	Sequence 5958, Ap	757	27	37.5	117	7	US-11-012-353-72	Sequence 72, Appl
685	28	38.9	666	7	US-11-096-046-27	Sequence 27, Appl	758	27	37.5	118	7	US-11-097-812-69	Sequence 69, Appl
686	28	38.9	667	7	US-11-096-046-25	Sequence 25, Appl	759	27	37.5	133	7	US-11-051-453-51	Sequence 51, Appl
687	28	38.9	667	7	US-11-096-046-28	Sequence 28, Appl	760	27	37.5	153	7	US-11-194-246-141	Sequence 141, Appl
688	28	38.9	667	7	US-11-096-046-30	Sequence 30, Appl	761	27	37.5	166	7	US-11-128-900-75	Sequence 75, Appl
689	28	38.9	695	6	US-10-467-657-4004	Sequence 4004, Ap	762	27	37.5	169	6	US-10-965-694-25	Sequence 25, Appl
690	28	38.9	695	6	US-11-167-856-2	Sequence 2, Appl	763	27	37.5	175	6	US-10-467-657-1384	Sequence 1384, Ap
691	28	38.9	695	7	US-11-096-046-26	Sequence 26, Appl	764	27	37.5	187	6	US-10-485-517-192	Sequence 292, Ap
692	28	38.9	701	6	US-10-793-626-710	Sequence 710, App	765	27	37.5	188	6	US-10-467-657-3332	Sequence 3332, Ap
693	28	38.9	703	7	US-11-124-215-17	Sequence 17, Appl	766	27	37.5	203	7	US-11-038-284-21	Sequence 21, Appl
694	28	38.9	703	7	US-11-172-145-12	Sequence 12, Appl	767	27	37.5	206	6	US-10-467-657-1004	Sequence 304, Ap
695	28	38.9	703	7	US-11-172-145-21	Sequence 21, Appl	768	27	37.5	211	7	US-11-052-554A-301	Sequence 301, App
696	28	38.9	703	7	US-11-172-145-22	Sequence 22, Appl	769	27	37.5	225	6	US-10-485-517-143	Sequence 143, App
697	28	38.9	737	6	US-10-055-877-156	Sequence 156, App	770	27	37.5	230	7	US-11-055-822-890	Sequence 890, App
698	28	38.9	786	7	US-11-070-627-9	Sequence 9, Appl	771	27	37.5	242	7	US-11-212-443-82	Sequence 82, Appl
699	28	38.9	934	7	US-11-108-864-19	Sequence 19, Appl	772	27	37.5	242	7	US-11-212-443-84	Sequence 84, Appl
700	28	38.9	934	7	US-11-052-554A-10	Sequence 10, Appl	773	27	37.5	243	7	US-11-054-515-995	Sequence 95, App
701	28	38.9	961	7	US-11-113-424-35	Sequence 35, Appl	774	27	37.5	248	7	US-11-054-515-1617	Sequence 1617, Ap
702	28	38.9	972	7	US-11-124-215-1	Sequence 1, Appl	775	27	37.5	248	7	US-11-054-515-1778	Sequence 1778, Ap
703	28	38.9	972	7	US-11-172-145-2	Sequence 2, Appl	776	27	37.5	249	6	US-10-793-626-3298	Sequence 3298, Ap
704	28	38.9	972	7	US-11-120-422-10	Sequence 10, Appl	777	27	37.5	250	7	US-11-054-515-883	Sequence 883, App
705	28	38.9	1052	6	US-10-467-657-3392	Sequence 3392, Ap	778	27	37.5	250	7	US-11-054-515-1461	Sequence 1461, Ap
706	28	38.9	1125	6	US-10-821-234-1444	Sequence 1444, Ap	779	27	37.5	250	7	US-11-054-515-1977	Sequence 1977, Ap
707	28	38.9	1125	6	US-10-485-517-127	Sequence 127, App	780	27	37.5	251	6	US-10-131-826A-266	Sequence 266, App
708	28	38.9	1436	6	US-10-453-372-1094	Sequence 1094, Ap	781	27	37.5	251	7	US-11-135-855-46	Sequence 46, Appl
709	28	38.9	1593	6	US-10-453-372-1092	Sequence 1092, Ap	782	27	37.5	252	7	US-11-054-515-1772	Sequence 1772, Ap
710	28	38.9	1613	7	US-11-108-528-84	Sequence 84, Appl	783	27	37.5	253	7	US-11-054-515-966	Sequence 966, App
711	28	38.9	1680	6	US-10-517-939-362	Sequence 362, App	784	27	37.5	253	7	US-11-054-515-1199	Sequence 1199, App
712	28	38.9	1767	7	US-11-052-554A-372	Sequence 372, App	785	27	37.5	254	7	US-11-054-515-1578	Sequence 1578, Ap
713	28	38.9	1804	6	US-10-513-786-2	Sequence 2, Appl	786	27	37.5	257	7	US-11-054-515-1579	Sequence 1579, Ap
714	28	38.9	1873	7	US-11-126-313-29	Sequence 29, Appl	787	27	37.5	258	6	US-10-467-657-8130	Sequence 4130, Ap
715	28	38.9	1892	7	US-11-075-185-6	Sequence 6, Appl	788	27	37.5	259	6	US-10-512-184-31	Sequence 31, Appl
716	28	38.9	2214	7	US-11-080-991-94	Sequence 94, Appl	789	27	37.5	259	6	US-10-512-184-33	Sequence 33, Appl
717	28	38.9	2591	6	US-10-453-372-718	Sequence 718, App	790	27	37.5	261	6	US-10-512-184-35	Sequence 35, Appl
718	28	38.9	2602	6	US-10-453-372-716	Sequence 716, App	791	27	37.5	263	6	US-10-793-626-204	Sequence 204, App
719	28	38.9	2617	6	US-10-453-372-666	Sequence 666, App	792	27	37.5	263	6	US-10-873-528-119	Sequence 119, App
720	28	38.9	2617	6	US-10-453-372-732	Sequence 732, App	793	27	37.5	272	6	US-10-467-657-9017	Sequence 9017, Ap
721	28	38.9	2617	6	US-10-453-372-734	Sequence 734, App	794	27	37.5	274	7	US-11-132-142-1	Sequence 1, Appl
722	28	38.9	2617	6	US-10-453-372-736	Sequence 736, App	795	27	37.5	282	6	US-10-517-939-446	Sequence 346, App
723	28	38.9	2617	6	US-10-453-372-738	Sequence 738, App	796	27	37.5	287	7	US-11-174-150-30	Sequence 30, Appl
724	28	38.9	2617	6	US-10-453-372-740	Sequence 740, App	797	27	37.5	289	7	US-11-052-554A-75	Sequence 75, Appl
725	28	38.9	2617	6	US-10-453-372-742	Sequence 742, App	798	27	37.5	302	7	US-11-182-592-6	Sequence 6, Appl
726	28	38.9	2617	6	US-10-453-372-744	Sequence 744, App	799	27	37.5	307	6	US-10-055-877-62	Sequence 62, Appl
727	28	38.9	2617	6	US-10-453-372-746	Sequence 746, App	800	27	37.5	307	6	US-10-055-877-332	Sequence 233, App
728	28	38.9	2617	6	US-10-453-372-748	Sequence 748, App	801	27	37.5	308	6	US-10-055-877-333	Sequence 233, App
729	28	38.9	2617	6	US-10-453-372-750	Sequence 750, App	802	27	37.5	310	6	US-10-512-340-47	Sequence 47, Appl
730	28	38.9	3073	7	US-11-143-980-50	Sequence 50, Appl	803	27	37.5	313	6	US-10-512-184-72	Sequence 72, Appl
731	28	38.9	3507	7	US-11-075-185-7	Sequence 7, Appl	804	27	37.5	313	6	US-10-055-877-234	Sequence 234, App
732	28	38.9	3655	7	US-11-075-185-5	Sequence 5, Appl	805	27	37.5	317	6	US-10-497-135-8	Sequence 8, Appl
733	28	38.9	3704	6	US-10-513-786-1	Sequence 1, Appl	806	27	37.5	318	6	US-10-497-135-7	Sequence 7, Appl
734	28	38.9	4128	6	US-10-770-726-77	Sequence 77, Appl	807	27	37.5	322	6	US-10-524-647-18	Sequence 18, Appl
735	27.5	38.2	208	6	US-10-510-386-172	Sequence 172, App	808	27	37.5	325	6	US-10-821-234-1261	Sequence 1261, Ap
736	27.5	38.2	739	7	US-11-078-189-12	Sequence 12, Appl	809	27	37.5	329	6	US-10-512-184-68	Sequence 68, Appl
737	27.5	38.2	758	7	US-11-052-554A-262	Sequence 262, App	810	27	37.5	329	6	US-10-512-184-70	Sequence 70, Appl
738	27.5	38.2	2197	7	US-11-075-185-8	Sequence 8, Appl	811	27	37.5	331	6	US-10-793-626-3256	Sequence 3256, Ap
739	27	37.5	12	7	US-11-089-266-9	Sequence 9, Appl	812	27	37.5	335	6	US-10-821-234-957	Sequence 957, App
740	27	37.5	15	7	US-11-054-515-2745	Sequence 2745, Ap	813	27	37.5	345	6	US-10-467-657-7598	Sequence 7598, App
741	27	37.5	16	7	US-11-054-515-2189	Sequence 2189, Ap	814	27	37.5	346	6	US-10-525-710-46	Sequence 46, App
742	27	37.5	22	7	US-11-054-515-2189	Sequence 8160, Ap	815	27	37.5	347	6	US-10-467-657-5824	Sequence 5824, Ap
743	27	37.5	30	6	US-10-467-657-8160	Sequence 8160, Ap	816	27	37.5	350	6	US-10-467-657-824	Sequence 824, Ap
744	27	37.5	37	6	US-10-467-657-1382	Sequence 1382, Ap	817	27	37.5	350	6	US-10-467-657-8735	Sequence 8735, App
745	27	37.5	59	6	US-10-467-657-4882	Sequence 4882, Ap	818	27	37.5	353	4	US-10-873-528-1332	Sequence 1332, App
746	27	37.5	69	7	US-11-051-481-50	Sequence 50, Appl	819	27	37.5	353	7	US-11-182-592-4	Sequence 4, Appl
747	27	37.5	79	6	US-10-770-726-58	Sequence 58, Appl	820	27	37.5	362	7	US-11-012-762-30	Sequence 30, Appl
748	27	37.5	82	6	US-10-467-657-1218	Sequence 1218, Ap	821	27	37.5	362	7	US-11-012-762-32	Sequence 32, Appl
749	27	37.5	91	7	US-11-051-481-49	Sequence 49, Appl	822	27	37.5	369	6	US-10-793-626-772	Sequence 672, App
750	27	37.5	105	7	US-11-105-268-30	Sequence 30, Appl	823	27	37.5	374	6	US-11-060-008-14	Sequence 14, Appl
751	27	37.5	107	7	US-11-105-268-16	Sequence 16, Appl	824	27	37.5	381	6	US-10-641-678-74	Sequence 74, Appl
752	27	37.5	107	7	US-11-105-268-18	Sequence 18, Appl	825	27	37.5	382	7	US-11-052-554A-37	Sequence 37, Appl
753	27	37.5	107	7	US-11-105-268-25	Sequence 25, Appl	826	27	37.5	390	7	US-11-194-246-288	Sequence 288, App
754	27	37.5	107	7	US-11-105-268-28	Sequence 28, Appl	827	27	37.5	415	6	US-10-627-633-2	Sequence 2, Appl
755	27	37.5	107	7	US-11-105-268-32	Sequence 32, Appl	828	27	37.5	416	6	US-10-641-678-73	Sequence 73, Appl

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832	27	37.5	433	6	US-10-641-678-34	Sequence 34, Appl	905	27	37.5	767	7	US-11-043-693-2	Sequence 22, Appl
833	27	37.5	438	6	US-10-641-678-49	Sequence 19, Appl	906	27	37.5	780	7	US-11-089-551A-22	Sequence 54, Appl
834	27	37.5	438	6	US-11-067-121-19	Sequence 19, Appl	907	27	37.5	787	6	US-10-517-939-54	Sequence 1117, Ap
835	27	37.5	447	6	US-10-641-678-58	Sequence 58, Appl	908	27	37.5	806	7	US-11-108-112-1117	Sequence 1118, Ap
836	27	37.5	449	6	US-10-641-678-38	Sequence 38, Appl	909	27	37.5	812	7	US-11-120-308-126	Sequence 126, App
837	27	37.5	451	6	US-10-641-678-56	Sequence 56, Appl	910	27	37.5	840	7	US-11-120-308-134	Sequence 134, App
838	27	37.5	451	6	US-10-641-678-57	Sequence 57, Appl	911	27	37.5	850	7	US-11-037-243-108	Sequence 108, App
839	27	37.5	452	6	US-10-641-678-50	Sequence 50, Appl	912	27	37.5	993	7	US-11-137-465-16	Sequence 36, Appl
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841	27	37.5	454	7	US-11-074-176-142	Sequence 142, App	914	27	37.5	1029	6	US-10-821-234-908	Sequence 908, App
842	27	37.5	456	6	US-10-641-678-51	Sequence 51, Appl	915	27	37.5	1127	6	US-10-858-730-13	Sequence 13, Appl
843	27	37.5	464	7	US-11-128-900-2	Sequence 2, Appl	916	27	37.5	1287	7	US-11-037-243-72	Sequence 72, Appl
844	27	37.5	464	7	US-11-128-900-66	Sequence 66, Appl	917	27	37.5	1306	6	US-10-995-561-905	Sequence 905, Appl
845	27	37.5	483	6	US-10-630-203-8	Sequence 8, Appl	918	27	37.5	1356	6	US-10-995-561-904	Sequence 904, App
846	27	37.5	483	6	US-10-630-203-30	Sequence 30, Appl	919	27	37.5	1356	6	US-10-995-561-906	Sequence 906, App
847	27	37.5	484	7	US-11-052-554A-177	Sequence 177, App	920	27	37.5	1410	6	US-10-821-234-1050	Sequence 1050, Ap
848	27	37.5	486	7	US-10-641-678-28	Sequence 28, App	921	27	37.5	1412	6	US-10-793-626-2052	Sequence 2052, Ap
849	27	37.5	488	7	US-11-055-822-850	Sequence 850, App	922	27	37.5	1633	7	US-11-108-528-86	Sequence 86, Appl
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851	27	37.5	495	6	US-10-641-678-93	Sequence 93, Appl	924	27	37.5	2004	6	US-10-467-657-84	Sequence 84, Appl
852	27	37.5	497	6	US-10-641-678-2	Sequence 2, Appl	925	27	37.5	2004	6	US-10-467-657-84	Sequence 84, Appl
853	27	37.5	497	6	US-10-641-678-8	Sequence 8, Appl	926	27	37.5	2004	6	US-10-821-234-1262	Sequence 1262, Ap
854	27	37.5	497	6	US-10-641-678-10	Sequence 10, Appl	927	27	37.5	2004	6	US-10-821-234-1262	Sequence 1262, Ap
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862	27	37.5	497	6	US-10-641-678-30	Sequence 30, Appl	935	27	37.5	2004	6	US-10-821-234-1262	Sequence 1262, Ap
863	27	37.5	497	6	US-10-641-678-33	Sequence 33, Appl	936	27	37.5	2004	6	US-10-821-234-1262	Sequence 1262, Ap
864	27	37.5	497	6	US-10-641-678-39	Sequence 39, Appl	937	27	37.5	2004	6	US-10-821-234-1262	Sequence 1262, Ap
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866	27	37.5	497	6	US-10-641-678-43	Sequence 43, Appl	939	27	37.5	2004	6	US-10-821-234-1262	Sequence 1262, Ap
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873	27	37.5	497	6	US-10-641-678-55	Sequence 55, Appl	946	27	37.5	2004	6	US-10-821-234-1262	Sequence 1262, Ap
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875	27	37.5	497	6	US-10-641-678-57	Sequence 57, Appl	948	27	37.5	2004	6	US-10-821-234-1262	Sequence 1262, Ap
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879	27	37.5	497	6	US-10-641-678-61	Sequence 61, Appl	952	27	37.5	2004	6	US-10-821-234-1262	Sequence 1262, Ap
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976 26 36.1 21 7 US-11-054-515-3010 Sequence 3010, Ap
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984 26 36.1 59 7 US-11-051-481-42 Sequence 42, Appl
985 26 36.1 63 6 US-10-467-657-822 Sequence 822, App
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997 26 36.1 99 7 US-11-084-554-55 Sequence 55, Appl
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999 26 36.1 100 7 US-11-054-669-76 Sequence 76, Appl
1000 26 36.1 100 7 US-11-084-554-103 Sequence 103, App

ALIGNMENTS

RESULT 1
US-10-665-658-12
Sequence 12, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-665-658-12

Query Match 100.0%; Score 72; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GIVFYGTTFDY 12

RESULT 2
US-10-665-658-4
Sequence 4, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-665-658-4

Query Match 100.0%; Score 72; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 99 GIVFYGTTFDY 110

RESULT 3
US-10-665-658-5
Sequence 5, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-665-658-5
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Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 99 GIFYGTYFDY 110
RESULT 4
US-10-665-658-24
Sequence 24, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-665-658-24

Query Match 100.0%; Score 72; DB 6; Length 121;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYFDY 12
DB 99 GIFYGTYFDY 110

RESULT 5
US-11-107-028-50
Sequence 50, Application US/11107028
Publication No. US20050276803A1
GENERAL INFORMATION:
APPLICANT: CHAN, ANDREW C.
APPLICANT: GONG, QIAN
APPLICANT: MARTIN, FLAVIUS
TITLE OF INVENTION: Method for Augmenting B Cell Depletion
FILE REFERENCE: P2112R1
CURRENT APPLICATION NUMBER: US/11/107,028
FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/563,263
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 50
LENGTH: 121
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-107-028-50

Query Match 100.0%; Score 72; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFYGTYFDY 12
DB 99 GIFYGTYFDY 110

Db 99 GIFYGTYFDY 110

RESULT 6

US-11-107-028-52
; Sequence 52, Application US/1107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 52
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-107-028-52

Query Match 100.0%; Score 72; DB 7; Length 121;
Best Local Similarity 100.0%; Pred. No. 7,1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFYGTYFDY 12
Db 99 GIFYGTYFDY 110

RESULT 7

US-10-665-658-51
; Sequence 51, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462

TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-665-658-51

Query Match 90.3%; Score 65; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9,1e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFYGTYFD 11
Db 1 GIFYGTYFD 11

RESULT 8

US-10-665-658-56
; Sequence 56, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-665-658-56

Query Match 83.3%; Score 60; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIFYGTYFD 11
Db 1 GIFYGTYFD 11

FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-665-658-55

Query Match 77.8%; Score 56; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIFYGTYFPD 11
Db 1 GIFYGTYFPD 11

RESULT 12
US-10-665-658-58
Sequence 58, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-665-658-58

Query Match 77.8%; Score 56; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0022;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIFYGTYFPD 11
Db 1 GIFYGTYFPD 11

RESULT 13
US-10-665-658-52
Sequence 52, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-665-658-52

Query Match 65.3%; Score 47; DB 6; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GIFYGTYFPD 11
Db 1 GIFYGTYFPD 11

RESULT 14
US-10-665-658-53
; Sequence 53, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-665-658-53
Query Match 63.9%; Score 46; DB 6; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.074;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GYFGTTFD 11
DB 1 GYFGAAAFD 11
RESULT 15
US-10-932-334-71
; Sequence 71, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14

; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-71
Query Match 61.1%; Score 44; DB 6; Length 120;
Best Local Similarity 66.7%; Pred. No. 1.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 FYGTFDFY 12
DB 101 YGSSYDFY 109
RESULT 16
US-10-932-334-72
; Sequence 72, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-72
Query Match 61.1%; Score 44; DB 6; Length 120;
Best Local Similarity 66.7%; Pred. No. 1.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 4 FYGTFDFY 12
DB 101 YGSSYDFY 109
RESULT 17
US-10-932-334-73
; Sequence 73, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: Immunogen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 224
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-224

Query Match 54.2%; Score 39; DB 6; Length 319;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IYFYGTTFDY 12
DB 250 IYFYGTTFDY 260

RESULT 21
US-11-102-201-1
Sequence 1, Application US/11102201
Publication No. US2005025594A1
GENERAL INFORMATION:
APPLICANT: SHELTON, David L.
APPLICANT: MANTYH, Patrick W.
TITLE OF INVENTION: METHODS FOR TREATING BONE CANCER PAIN BY
TITLE OF INVENTION: ADMINISTERING A NERVE GROWTH FACTOR ANTAGONIST
FILE REFERENCE: 51471-20021.00
CURRENT APPLICATION NUMBER: US/11/102,201
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: US 60/620,654
PRIOR FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: US 60/560,781
PRIOR FILING DATE: 2004-04-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-11-102-201-1

Query Match 53.5%; Score 38.5; DB 7; Length 120;
Best Local Similarity 61.5%; Pred. No. 9.5;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 GIFYGTT-YFDY 12
DB 98 GIFYGTT-YFDY 110

RESULT 22
US-10-524-198-2

Sequence 2, Application US/10524198
Publication No. US20050255125A1
GENERAL INFORMATION:
APPLICANT: AKZO Nobel N.V.
TITLE OF INVENTION: Novel mastitis vaccine
FILE REFERENCE: 2002.013
CURRENT APPLICATION NUMBER: US/10/524,198
CURRENT FILING DATE: 2005-02-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 200
TYPE: PRT
ORGANISM: Streptococcus uberis
US-10-524-198-2

Query Match 52.8%; Score 38; DB 6; Length 200;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YFYGTTFDY 12
DB 118 YFYGTTFDY 127

RESULT 23
US-10-647-956A-6
Sequence 6, Application US/10647956A
Publication No. US20050251878A1
GENERAL INFORMATION:
APPLICANT: French-Constant, Richard
APPLICANT: Bowen, David
APPLICANT: Rochelleau, Thomas
APPLICANT: Waterfield, Nicholas
TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
FILE REFERENCE: 61645
CURRENT APPLICATION NUMBER: US/10/647,956A
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817,514
PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/191806
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 915
TYPE: PRT
ORGANISM: Photorhabdus luminescens
US-10-647-956A-6

Query Match 52.8%; Score 38; DB 6; Length 915;
Best Local Similarity 50.0%; Pred. No. 74;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIFYGTTFY 10
DB 617 GIFYGTTFY 626

RESULT 24
US-10-648-816-11
Sequence 11, Application US/10648816
Publication No. US20050244405A1
GENERAL INFORMATION:
APPLICANT: Van Bruggen, Nicholas
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
TITLE OF INVENTION: And Uses Thereof
FILE REFERENCE: P1717D1
CURRENT APPLICATION NUMBER: US/10/648,816
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US/09/718,694
PRIOR FILING DATE: 2000-11-21

PRIOR APPLICATION NUMBER: US 09/218,481
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 11
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-648-816-11

Query Match 51.4%; Score 37; DB 6; Length 118;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 3 YFYGTT--YFD 11
|:|:|:|:|
Db 101 YYGTSHWYFD 111

RESULT 25
US-10-648-816-12
Sequence 12, Application US/10648816
Publication No. US20050244405A1
GENERAL INFORMATION:
APPLICANT: Van Bruggen, Nicholas
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
FILE REFERENCE: P171701
CURRENT APPLICATION NUMBER: US/10/648,816
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US/09/718,694
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 09/218,481
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 12
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-648-816-12

Query Match 51.4%; Score 37; DB 6; Length 118;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 3 YFYGTT--YFD 11
|:|:|:|:|
Db 101 YYGTSHWYFD 111

RESULT 26
US-10-648-816-13
Sequence 13, Application US/10648816
Publication No. US20050244405A1
GENERAL INFORMATION:
APPLICANT: Van Bruggen, Nicholas
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
FILE REFERENCE: P171701
CURRENT APPLICATION NUMBER: US/10/648,816
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US/09/718,694
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 09/218,481
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 13
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
US-10-648-816-13

Query Match 51.4%; Score 37; DB 6; Length 118;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 3 YFYGTT--YFD 11
|:|:|:|:|
Db 101 YYGTSHWYFD 111

RESULT 27
US-11-054-515-1941
Sequence 1941, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23p3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1941
LENGTH: 237
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1941

Query Match 51.4%; Score 37; DB 7; Length 237;
Best Local Similarity 45.5%; Pred. No. 30;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 YFYGTTTFYD 12
|:|:|:|:|
Db 93 YFCASTRYYD 103

RESULT 28
US-10-821-234-1480
Sequence 1480, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes Version 1.0

SEQ ID NO 1480
LENGTH: 651
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1480

Query Match
Best Local Similarity 51.4%; Score 37; DB 6; Length 651;
Pred. No. 77;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YFYGTYFDY 12
|||
Db 199 YFYQNTYFDY 208

RESULT 29
US-10-981-267-6
Sequence 6, Application US/10981267
Publication No. US20050281805A1
GENERAL INFORMATION:
APPLICANT: Lebowitz, Jonathan H
APPLICANT: Beverly, Stephen
APPLICANT: Sly, William S.
TITLE OF INVENTION: TARGETED THERAPEUTIC PROTEINS
FILE REFERENCE: SYM-009CP
CURRENT APPLICATION NUMBER: US/10/981,267
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/384,452
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/516,990
PRIOR FILING DATE: 2003-11-03
PRIOR APPLICATION NUMBER: PCT/US03/17211
PRIOR FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: US 10/272,531
PRIOR FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 60/445,734
PRIOR FILING DATE: 2003-02-06
PRIOR APPLICATION NUMBER: US 60/386,019
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: US 60/408,816
PRIOR FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 722
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-981-267-6

Query Match
Best Local Similarity 51.4%; Score 37; DB 6; Length 722;
Pred. No. 85;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 YFYGTYFDY 12
|||
Db 200 YFYQNTYFDY 209

RESULT 30
US-11-186-284-2
Sequence 2, Application US/11186284
Publication No. US20050286493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPW01-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 909
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-186-284-2

Query Match
Best Local Similarity 51.4%; Score 37; DB 7; Length 909;
Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIFYGTT 8
|||
Db 308 GIFYGTT 315

RESULT 31
US-10-821-234-1040
Sequence 1040, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes Version 1.0
SEQ ID NO 1040
LENGTH: 913
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1040

Query Match
Best Local Similarity 51.4%; Score 37; DB 6; Length 913;
Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIFYGTT 8
|||
Db 312 GIFYGTT 319

RESULT 32
US-11-054-515-2207
Sequence 2207, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10

```

; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2207
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2207

Query Match      50.0%; Score 36; DB 7; Length 12;
Best Local Similarity 85.7%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 GTTYFDY 12
Db      6 GTTYFDY 12

RESULT 33
US-11-054-515-1899
; Sequence 1899, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```

US-11-054-515-1899

Query Match      50.0%; Score 36; DB 7; Length 247;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 GTTYFDY 12
Db      104 GTTYFDY 110

RESULT 34
US-11-186-284-107
; Sequence 107, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-107

Query Match      50.0%; Score 36; DB 7; Length 417;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 YGTYFDY 12
Db      203 YGTGYFY 210

RESULT 35
US-11-012-353-75
; Sequence 75, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUM, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT APPLICATION NUMBER: US/11/012,353
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
```

```

; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 75
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-75
```

```

Query Match          49.3%; Score 35.5; DB 7; Length 117;
Best Local Similarity 42.9%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;
```

```
QY      2 IYF---YGTTFYFDY 12
      :|:|:|:|:|
Db      93 VYYCARYGRVFFDY 106
```

```

RESULT 36
US-11-012-353-79
; Sequence 79, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-79
```

```

Query Match          49.3%; Score 35.5; DB 7; Length 117;
Best Local Similarity 42.9%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;
```

```
QY      2 IYF---YGTTFYFDY 12
      :|:|:|:|:|
Db      93 VYYCARYGRVFFDY 106
```

RESULT 37

```

US-11-012-353-83
; Sequence 83, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 83
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-83
```

```

Query Match          49.3%; Score 35.5; DB 7; Length 117;
Best Local Similarity 42.9%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;
```

```
QY      2 IYF---YGTTFYFDY 12
      :|:|:|:|:|
Db      93 VYYCARYGRVFFDY 106
```

```

RESULT 38
US-11-012-353-162
; Sequence 162, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
; APPLICANT: GOETTSCH, LILIANE
; APPLICANT: CORVAIA, NATHALIE
; APPLICANT: DUFLOS, ALAIN
; APPLICANT: HAEUW, JEAN-FRANCOIS
; APPLICANT: LEGER, OLIVIER
; APPLICANT: BECK, ALAIN
; TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
; TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
; FILE REFERENCE: 017753-198
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 10/735,916
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: FR 0308538
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/FR03/00178
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: FR 0205753
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: FR 0200653
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: FR 0200654
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 162
```

```
SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 162
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-012-353-162
```

```
Query Match          49.3%; Score 35.5; DB 7; Length 117;
Best Local Similarity 42.9%; Pred. No. 27;
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;
```

```
QY      2 IYF---YGTTFDY 12
       :|:|:|:|
Db      93 VYTCARYGRVFPDY 106
```

```
RESULT 39
US-11-012-353-77
; Sequence 77, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
```

```
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT FILING DATE: 2004-12-16
PRIOR FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 77
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-11-012-353-77
```

```
Query Match          49.3%; Score 35.5; DB 7; Length 135;
Best Local Similarity 42.9%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;
```

```
QY      2 IYF---YGTTFDY 12
       :|:|:|:|
Db     111 VYTCARYGRVFPDY 124
```

```
RESULT 40
US-11-012-353-81
; Sequence 81, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
```

```
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
```

```
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 81
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-11-012-353-81
```

```
Query Match          49.3%; Score 35.5; DB 7; Length 135;
Best Local Similarity 42.9%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;
```

```
QY      2 IYF---YGTTFDY 12
       :|:|:|:|
Db     111 VYTCARYGRVFPDY 124
```

```
RESULT 41
US-11-012-353-85
; Sequence 85, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
```

```
APPLICANT: GOETSCH, LILIANE
APPLICANT: CORVAIA, NATHALIE
APPLICANT: DUFLOS, ALAIN
APPLICANT: HAEUW, JEAN-FRANCOIS
APPLICANT: LEGER, OLIVIER
APPLICANT: BECK, ALAIN
TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
TITLE OF INVENTION: RECEPTORS ANTIBODIES AND USES THEREOF
FILE REFERENCE: 017753-198
CURRENT APPLICATION NUMBER: US/11/012,353
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 10/735,916
PRIOR FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: FR 0308538
PRIOR FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: PCT/FR03/00178
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: FR 0205753
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: FR 0200653
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: FR 0200654
PRIOR FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 162
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 85
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-11-012-353-85
```

```
Query Match          49.3%; Score 35.5; DB 7; Length 135;
Best Local Similarity 42.9%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;
```


QY 2 IYF---YGTTFDY 12
:|:|:|
Db 111 VYTCARYGTVFDY 124

RESULT 42
US-10-873-427A-4
; Sequence 4, Application US/10873427A
; Publication No. US20050281914A1
; GENERAL INFORMATION:
; APPLICANT: STEELE, JAMES L.
; APPLICANT: BROADBENT, JEFFREY R.
; APPLICANT: SRIDHAR, VIDYA R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEP02
; TITLE OF INVENTION: AND PEP03
; FILE REFERENCE: WARF:009US
; CURRENT APPLICATION NUMBER: US/10/873,427A
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/452,257
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Lactobacillus helveticus
US-10-873-427A-4

Query Match 49.3%; Score 35.5; DB 6; Length 643;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 GIFYGTYF 10
|:|:|:|
Db 338 GYV-YGTYF 346

RESULT 43
US-10-873-427A-2
; Sequence 2, Application US/10873427A
; Publication No. US20050281914A1
; GENERAL INFORMATION:
; APPLICANT: STEELE, JAMES L.
; APPLICANT: BROADBENT, JEFFREY R.
; APPLICANT: SRIDHAR, VIDYA R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEP02
; TITLE OF INVENTION: AND PEP03
; FILE REFERENCE: WARF:009US
; CURRENT APPLICATION NUMBER: US/10/873,427A
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/452,257
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 647
; TYPE: PRT
; ORGANISM: Lactobacillus helveticus
US-10-873-427A-2

Query Match 49.3%; Score 35.5; DB 6; Length 647;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 GIFYGTYF 10
|:|:|:|
Db 340 GYV-YGTYF 348

RESULT 44
US-11-054-515-3043
; Sequence 3043, Application US/11054515
; Publication No. US2005025532A1

; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bvys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3043
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3043

Query Match 48.6%; Score 35; DB 7; Length 21;
Best Local Similarity 58.3%; Pred. No. 6.5;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GIFYGTYFDY 12
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Db 10 GYVPGDGYFDY 21

RESULT 45
US-11-149-943-40
; Sequence 40, Application US/11149943
; Publication No. US20060003412A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Aaron Keith
; APPLICANT: Desjarlais, John R.
; TITLE OF INVENTION: PROTEIN ENGINEERING WITH ANALOGOUS CONTACT ENVIRONMENTS
; FILE REFERENCE: 185833/US/3
; CURRENT APPLICATION NUMBER: US/11/149,943
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/602,566
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: US 11/008,647
; PRIOR FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-149-943-40

Query Match 48.6%; Score 35; DB 7; Length 21;
Best Local Similarity 50.0%; Pred. No. 6.5;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 IYFGTYFD 11
|:|:|:|
Db 2 IYSGSTYFN 11

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RESULT 46
US-11-149-943-42
; Sequence 42, Application US/11149943
; Publication No. US20060003412A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Aaron Keith
; APPLICANT: Desjarlais, John R.
; TITLE OF INVENTION: PROTEIN ENGINEERING WITH ANALOGOUS CONTACT ENVIRONMENTS
; FILE REFERENCE: 185633/US/3
; CURRENT APPLICATION NUMBER: US/11/149,943
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/602,566
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: US 11/008,647
; PRIOR FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-149-943-42

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Query Match	48.6%	Score 35;	DB 7;	Length 21;
Best Local Similarity	50.0%	Pred. No. 6.5;		
Matches	5;	Conservative	4;	Mismatches 1; Indels 0; Gaps 0

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QY      2 IYFYGTTFYFD  11
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db      2 IYYSGSTYYN  11
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RESULT 47
US-11-149-943-43
; Sequence 43, Application US/11149943
; Publication No. US20060003412A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Aaron Keith
; APPLICANT: Desjarlais, John R.
; TITLE OF INVENTION: PROTEIN ENGINEERING WITH ANALOGOUS CONTACT ENVIRONMENTS
; FILE REFERENCE: 185833/US/3
; CURRENT APPLICATION NUMBER: US/11/149,943
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/602,566
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: US 11/008,647
; PRIOR FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43
; LENGTH: 21
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-149-943-43

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Query Match Similarity	48.6%	Score 35;	DB 7;	Length 21;
Best Local Similarity	50.0%	Pred No. 6.5;		
Matches	5;	Conservative	4;	Mismatches 1; Indels 0; Gaps 0
OY	2	IYFGTYFD	11	
Db	2	IYSGSYVN	11	

RESULT 48
US-11-149-943-45
; Sequence 45, Application US/11149943
; Publication No. US20060003412A1
; GENERAL INFORMATION:
; APPLICANT: Chamberlain, Aaron Keith
; APPLICANT: Desjarlais, John R.

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/ TITLE OF INVENTION: PROTEIN ENGINEERING WITH ANMLOGOUS CONTACT ENVIRONMENTS
/ FILE REFERENCE: 185633/US/3
/ CURRENT APPLICATION NUMBER: US/11/149,943
/ CURRENT FILING DATE: 2005-06-09
/ PRIOR APPLICATION NUMBER: US 60/602,566
/ PRIOR FILING DATE: 2004-08-17
/ PRIOR APPLICATION NUMBER: US 11/008,647
/ PRIOR FILING DATE: 2004-12-08
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 45
/ LENGTH: 21
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-149-943-45

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Query Match	48.6%	Score 35;	DB 7;	Length 21;
Best Local Similarity	50.0%	Pred. No. 6.5;		
Matches	5;	Conservative	4;	Mismatches 1;
				Indels 0;
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QY 2 IYFYGTTFYFD 11
||:|:|:|:|:
Db 2 IYSGSTYYN 11

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RESULT 49
US-11-128-900-85
; Sequence 85, Application US/11128900
; Publication No. US2005028716A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN B.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: AIX-FFM1 DIV3
; CURRENT APPLICATION NUMBER: US/11/128, 900
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 6613647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 76
; TYPE: PR1
; ORGANISM: Homo sapiens
US-11-128-900-85

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Query Match	48.6%	Score 35;	DB 7;	Length 76;
Best Local Similarity	50.0%	Pred. No. 21;		
Matches	5;	Conservative	4;	Mismatches
			1;	Indels
			0;	Gaps
			0;	
QY	2	IYFYGTTFD	11	
		: : : :		
Db	30	IYSGSTIYN	39	

RESULT 50
US-10-821-234-949
; Sequence 949, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stöche-Crain, Birgit

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; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 949
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-949

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Query Match      48.6%; Score 35; DB 6; Length 80;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GIFYGTTYFDY 12
Db      45 GNYGYGGYADY 56

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Search completed: January 17, 2006, 12:13:33
 Job time : 5 secs

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99	38	74.5	108	3	AAW82345	Human con	172	37	72.5	95	2	AAW72062	AAW72062	OF7K.9 VK
100	38	74.5	108	5	ABP61191	Human ant	173	37	72.5	95	2	AAW72063	AAW72063	OF7K.19 V
101	38	74.5	108	8	ADG38991	Human con	174	37	72.5	95	2	AAW72060	AAW72060	OF7K.16 V
102	38	74.5	108	8	ADR03366	Human sub	175	37	72.5	95	2	AAW72061	AAW72061	OF7K.11 V
103	38	74.5	108	8	ADP79572	Human Kap	176	37	72.5	95	2	AAW72059	AAW72059	OF7K.3 VK
104	38	74.5	109	5	AAU74544	Human sub	177	37	72.5	95	6	ABO27153	ABO27153	Human ger
105	38	74.5	109	7	ADP11403	Human sub	178	37	72.5	95	7	ADP10195	ADP10195	Antibody
106	38	74.5	109	8	ADP11415	Adf11415 2D8 anti-	179	37	72.5	95	7	ADP10093	ADP10093	VEGF anti
107	38	74.5	109	8	ADM38453	Adf138453 CD11a lig	180	37	72.5	95	7	ADP09988	ADP09988	Antibody
108	38	74.5	109	9	AEK38745	Nea38745 Human VL	181	37	72.5	95	7	ADJ80273	ADJ80273	Kappa ge
109	38	74.5	110	5	AAE28149	Human con	182	37	72.5	95	8	ADU08742	ADU08742	Human ant
110	38	74.5	111	5	ADY34023	Ady34023 Anti-Tie	183	37	72.5	95	8	ADU86536	ADU86536	Immunoglo
111	38	74.5	111	9	ADY34009	Ady34009 Anti-Tie	184	37	72.5	95	9	ADY75447	ADY75447	Human ger
112	38	74.5	125	6	ABG71755	Abg71755 Variable	185	37	72.5	95	9	AEA53928	AEA53928	Novel hum
113	38	74.5	125	9	ADY58503	Ady58503 Consensus	186	37	72.5	95	9	ABE13648	ABE13648	Novel hum
114	38	74.5	126	2	AAV17492	AAV17492 Consensus	187	37	72.5	96	7	ADP64828	ADP64828	MBK-4-L
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116	38	74.5	126	2	AAV08703	AAV08703 Human lig	189	37	72.5	100	5	AAE23989	AAE23989	Human MOG
117	38	74.5	126	2	AAV08701	AAV08701 Human con	190	37	72.5	101	9	ABE01068	ABE01068	Human lig
118	38	74.5	126	3	AAV83645	AAV83645 Conserved	191	37	72.5	102	9	ADY33953	ADY33953	Anti-Tie
119	38	74.5	126	5	ABE04943	ABE04943 Human CD2	192	37	72.5	102	9	ADY33961	ADY33961	Anti-Tie
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121	38	74.5	126	6	ABG71656	Abg71656 Consensus	194	37	72.5	104	9	ADZ42035	ADZ42035	Ig L chai
122	38	74.5	126	6	ABG71769	Abg71769 Variable	195	37	72.5	105	5	ABG76534	ABG76534	HCV El an
123	38	74.5	126	7	ADP00054	ADP00054 Human con	196	37	72.5	106	8	ADJ22136	ADJ22136	Anti-plat
124	38	74.5	128	5	ABE04947	ABE04947 CD28 synt	197	37	72.5	106	9	ADM07075	ADM07075	Anti-Peaa
125	38	74.5	130	5	AAU10776	AAU10776 Light cha	198	37	72.5	107	2	AAW58493	AAW58493	Human lam
126	38	74.5	131	6	ABG71753	Abg71753 Antibody	199	37	72.5	107	2	AAW58493	AAW58493	Human Kap
127	38	74.5	132	6	AAU10775	AAU10775 Light cha	200	37	72.5	107	3	AAV71472	AAV71472	Mouse mon
128	38	74.5	133	6	ABG71752	Abg71752 Antibody	201	37	72.5	107	3	AAV71238	AAV71238	Humanised
129	38	74.5	133	6	ADP11439	Adf11439 9H7 anti-	202	37	72.5	107	4	AAE80988	AAE80988	Human ant
130	38	74.5	133	7	ADP11427	Adf11427 2D8 anti-	203	37	72.5	107	4	AAE85350	AAE85350	Antibody
131	38	74.5	135	7	ADP64780	Adp64780 Hu-A8-1 c	204	37	72.5	107	4	AAE66414	AAE66414	Human Fab
132	38	74.5	247	9	ADY21472	Ady21472 Mature fo	205	37	72.5	107	5	AAE28871	AAE28871	Human KDR
133	37	72.5	11	4	AAE85368	AAE85368 Antibody	206	37	72.5	107	5	ABB07235	ABB07235	Anti-IL-4
134	37	72.5	11	4	AAE66416	AAE66416 Human Fab	207	37	72.5	107	6	ABJ26764	ABJ26764	VEGF bind
135	37	72.5	11	5	AAE28850	AAE28850 Human KDR	208	37	72.5	107	6	ABR54917	ABR54917	Light cha
136	37	72.5	11	5	AAU76330	AAU76330 Human ant	209	37	72.5	107	6	ABR54916	ABR54916	Light cha
137	37	72.5	11	6	ABJ26743	Abj26743 VEGF bind	210	37	72.5	107	7	ADD024419	ADD024419	Human lig
138	37	72.5	11	7	ADD24394	Add24394 Human IgG	211	37	72.5	107	7	ADD80796	ADD80796	Human glo
139	37	72.5	11	7	ADD69238	Add69238 Human lig	212	37	72.5	107	8	ADJ01155	ADJ01155	Human Kap
140	37	72.5	11	7	ADD69235	Add69235 Human lig	213	37	72.5	107	8	ADJ22109	ADJ22109	Anti-plat
141	37	72.5	11	7	ADD69235	Add69235 Human lig	214	37	72.5	107	8	ADJ22135	ADJ22135	Anti-plat
142	37	72.5	11	7	ADD80771	Add80771 Human var	215	37	72.5	107	8	ADJ22134	ADJ22134	Anti-plat
143	37	72.5	11	7	ADD89874	Add89874 Human ant	216	37	72.5	107	8	ADK18272	ADK18272	KDR bindi
144	37	72.5	11	8	ADH89419	Adh89419 Human tra	217	37	72.5	107	8	ADU86569	ADU86569	Immunoglo
145	37	72.5	11	8	ADH89428	Adh89428 Human tra	218	37	72.5	107	9	ADY34076	ADY34076	Anti-Tie
146	37	72.5	11	8	ADK18247	Adk18247 KDR bindi	219	37	72.5	107	9	ADY26776	ADY26776	Anti-NGF
147	37	72.5	11	8	ADM41605	Adm41605 Interleuk	220	37	72.5	107	9	ADY93871	ADY93871	Anti-SARS
148	37	72.5	11	8	ADS88073	Ads88073 Human CD2	221	37	72.5	107	9	ADY93864	ADY93864	Anti-SARS
149	37	72.5	11	8	ADS88067	Ads88067 Human CD2	222	37	72.5	107	9	AEA08940	AEA08940	Antibody
150	37	72.5	11	8	ADS88079	Ads88079 Human CD2	223	37	72.5	107	9	AEA40471	AEA40471	Anti-VEGF
151	37	72.5	11	8	ADS19239	Adsl9239 Light cha	224	37	72.5	107	9	ABE19292	ABE19292	IgG kappa
152	37	72.5	11	8	ADG64649	Adg64649 Human ant	225	37	72.5	107	9	ABE19293	ABE19293	IgG kappa
153	37	72.5	11	8	ADG52384	Adg52384 Fab targe	226	37	72.5	107	9	ABE17724	ABE17724	Anti-PcTV
154	37	72.5	11	8	ADG52432	Adg52432 Fab targe	227	37	72.5	108	2	AAW04333	AAW04333	Light cha
155	37	72.5	11	8	ADM07069	Adm07069 Anti-Peaa	228	37	72.5	108	4	AAE69212	AAE69212	Human ant
156	37	72.5	11	9	ADM07085	Adm07085 Anti-Peaa	229	37	72.5	108	4	AAE69213	AAE69213	Human ant
157	37	72.5	11	9	ADM04907	Adm04907 PAPP-A im	230	37	72.5	108	5	AAW51173	AAW51173	Human Vg/
158	37	72.5	11	9	ADY26813	Ady26813 Human ant	231	37	72.5	108	5	AAW51173	AAW51173	Human Vg/
159	37	72.5	11	9	ADY93860	Ady93860 Anti-SARS	232	37	72.5	108	6	AAU76334	AAU76334	Human ant
160	37	72.5	11	9	AEA53685	Aea53685 Novel hum	233	37	72.5	108	6	ADH89224	ADH89224	Human ant
161	37	72.5	11	9	AEA53694	Aea53694 Novel hum	234	37	72.5	108	7	ADD69214	ADD69214	Human ant
162	37	72.5	11	9	AEA53692	Aea53692 Novel hum	235	37	72.5	108	7	ADD69213	ADD69213	Human ant
163	37	72.5	11	9	AEA45811	Aea45811 Apolipoptr	236	37	72.5	108	7	ADD69213	ADD69213	Human ant
164	37	72.5	11	9	AEA40606	Aea40606 Anti-VEGF	237	37	72.5	108	7	ADU73533	ADU73533	Human ger
165	37	72.5	11	9	ABE01024	ABE01024 Human IP1	238	37	72.5	108	7	ADU73534	ADU73534	Erythropo
166	37	72.5	11	9	ABE01029	ABE01029 Human IP1	239	37	72.5	108	8	ADJ22138	ADJ22138	Anti-plat
167	37	72.5	11	9	ABE28757	ABE28757 Human CDR	240	37	72.5	108	8	ADJ22138	ADJ22138	Anti-plat
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170	37	72.5	94	7	ADC64830	ADC64830 HBBK-4-L	243	37	72.5	108	9	ADM08866	ADM08866	IGF-IR an

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245	37	72.5	108	9	AE801057	Human	IP1	Ae801057	318	37	72.5	236	5	ABG63490	Human	alb	Abg63490
246	37	72.5	108	9	AE801062	Human	IP1	Ae801062	319	37	72.5	236	7	AD664781	Hu-A12-1		Ad664781
247	37	72.5	109	4	AA662756	Human	HIV	Aa662756	320	37	72.5	236	7	AD664783	Hu-D4-2	C	Ad664783
248	37	72.5	109	4	AA662756	Human	Fab	Aa662756	321	37	72.5	236	7	AD664784	Hu-D4-3--		Ad664784
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251	37	72.5	110	9	ADX02205	SARS	coro	Adx02205	324	37	72.5	236	8	ADL76755	Albumin	F	Adl76755
252	37	72.5	110	9	ADX02049	SARS	coro	Adx02049	325	37	72.5	240	7	AD664792	Hu-B-E3	C	Ad664792
253	37	72.5	111	9	ADY33989	Anti-Tie		Ady33989	326	37	72.5	241	7	AD664791	Hu-B-A5	C	Ad664791
254	37	72.5	111	9	ADY33989	Anti-Tie		Ady33989	327	37	72.5	241	7	AD664787	Hu-A-D2	C	Ad664787
255	37	72.5	115	2	AA386648	Human	V-k	Aa386648	328	37	72.5	241	7	AD664786	Hu-A-B7	C	Ad664786
256	37	72.5	115	2	AA662928	Human	V-k	Aa662928	329	37	72.5	241	7	AD664788	Hu-A-E5	C	Ad664788
257	37	72.5	115	2	AA662928	Human	V-k	Aa662928	330	37	72.5	241	7	AD664789	Hu-A-G7	C	Ad664789
258	37	72.5	115	2	AA662928	Human	DNA	Aa662928	331	37	72.5	241	7	AD664789	Hu-A-G7	C	Ad664789
259	37	72.5	115	2	AA662928	Human	DNA	Aa662928	332	37	72.5	247	8	ADH34575	scFv	SC02	Adh34575
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261	37	72.5	119	8	AD039453	Human	AB1	Ad039453	334	37	72.5	248	9	ADX01838	SARS	coro	Adx01838
262	37	72.5	119	9	AEA53873	Novel	hum	Aea53873	335	37	72.5	251	5	ADP45038	Human	Bly	Adp45038
263	37	72.5	119	9	AEA53873	Novel	hum	Aea53873	336	37	72.5	251	5	ADP45038	Human	Bly	Adp45038
264	37	72.5	119	9	AEA53873	Novel	hum	Aea53873	337	37	72.5	251	9	ADG95865	Single	ch	Adg95865
265	37	72.5	120	2	AAW03946	Novel	hum	Aaw03946	338	37	72.5	252	9	ADX01956	SARS	coro	Adx01956
266	37	72.5	122	6	ABJ36934	Anti-CD40		Abj36934	339	37	72.5	634	6	ABB82300	SARS	coro	Abb82300
267	37	72.5	125	6	ABJ36934	Anti-CD40		Abj36934	340	37	72.5	11	4	AAU08345	Drosophi		Aau08345
268	37	72.5	126	6	ABJ36934	Anti-CD40		Abj36934	341	37	72.5	11	4	AAU08345	Drosophi		Aau08345
269	37	72.5	127	8	AD588053	Human	CD2	Ad588053	342	37	72.5	11	5	AAO17647	Human	FAP	Aao17647
270	37	72.5	127	8	AD588053	Human	CD2	Ad588053	343	37	72.5	11	5	AAO17647	Human	FAP	Aao17647
271	37	72.5	127	8	AD588053	Human	CD2	Ad588053	344	37	72.5	11	7	ADW04827	Human	FAP	Adw04827
272	37	72.5	127	8	AD588053	Human	CD2	Ad588053	345	37	72.5	11	9	ADW04827	Human	FAP	Adw04827
273	37	72.5	128	6	AD588053	Human	CD2	Ad588053	346	37	72.5	11	9	ADW04827	Human	FAP	Adw04827
274	37	72.5	128	8	ADW41547	Anti-inte		Adw41547	347	37	72.5	11	9	ADW41547	Anti-inte		Adw41547
275	37	72.5	128	8	ADW41547	Anti-inte		Adw41547	348	37	72.5	11	9	ADW41547	Anti-inte		Adw41547
276	37	72.5	129	5	AA551174	Human	rec	Aa551174	349	37	72.5	102	9	ADY33949	Human	ant	Ady33949
277	37	72.5	129	5	AA551174	Human	rec	Aa551174	350	37	72.5	102	9	ADY33949	Human	ant	Ady33949
278	37	72.5	129	6	ABJ36924	Anti-CD40		Abj36924	351	37	72.5	107	4	AA693657	Human	ant	Aa693657
279	37	72.5	129	6	ABJ36924	Anti-CD40		Abj36924	352	37	72.5	107	6	ABG75339	Human	ant	Abg75339
280	37	72.5	130	7	AD089877	Human	ant	Ad089877	353	37	72.5	107	6	ABG75339	Human	ant	Abg75339
281	37	72.5	130	8	AD089877	Human	ant	Ad089877	354	37	72.5	107	6	ABG75339	Human	ant	Abg75339
282	37	72.5	130	8	AD089877	Human	ant	Ad089877	355	37	72.5	107	6	ABG75339	Human	ant	Abg75339
283	37	72.5	130	8	AD089877	Human	ant	Ad089877	356	37	72.5	107	6	ABG75339	Human	ant	Abg75339
284	37	72.5	131	5	ABP62212	Human	imm	Abp62212	357	37	72.5	107	6	ABG75339	Human	ant	Abg75339
285	37	72.5	131	5	ABP62212	Human	imm	Abp62212	358	37	72.5	107	6	ABG75339	Human	ant	Abg75339
286	37	72.5	131	7	ADJ73531	Erythro		Adj73531	359	37	72.5	108	4	AA693659	Human	ant	Aa693659
287	37	72.5	133	5	ABP62213	Human	imm	Abp62213	360	37	72.5	108	4	AA693659	Human	ant	Aa693659
288	37	72.5	133	5	ABP62213	Human	imm	Abp62213	361	37	72.5	108	6	ABO27476	Anti-Rh(D		Ab027476
289	37	72.5	133	5	ABP62213	Human	imm	Abp62213	362	37	72.5	108	7	ADL91354	VL chain		Adl91354
290	37	72.5	139	6	AAE35896	Human	CD2	Aae35896	363	37	72.5	108	8	ADP96647	Human	ant	Adp96647
291	37	72.5	139	6	AAE35896	Human	CD2	Aae35896	364	37	72.5	108	8	ADP96647	Human	ant	Adp96647
292	37	72.5	142	6	AAE35897	Human	6.1	Aae35897	365	37	72.5	108	8	ADP96647	Human	ant	Adp96647
293	37	72.5	146	3	AAE35897	Human	6.1	Aae35897	366	37	72.5	108	8	ADP96647	Human	ant	Adp96647
294	37	72.5	146	3	AAE35897	Human	6.1	Aae35897	367	37	72.5	108	8	ADP96647	Human	ant	Adp96647
295	37	72.5	156	6	AAE35897	Human	6.1	Aae35897	368	37	72.5	108	8	ADP96647	Human	ant	Adp96647
296	37	72.5	156	6	AAE35897	Human	6.1	Aae35897	369	37	72.5	108	8	ADP96647	Human	ant	Adp96647
297	37	72.5	214	2	AAE35897	Human	6.1	Aae35897	370	37	72.5	108	8	ADP96647	Human	ant	Adp96647
298	37	72.5	214	2	AAE35897	Human	6.1	Aae35897	371	37	72.5	108	8	ADP96647	Human	ant	Adp96647
299	37	72.5	214	2	AAE35897	Human	6.1	Aae35897	372	37	72.5	108	8	ADP96647	Human	ant	Adp96647
300	37	72.5	215	7	ADFL1435	16E1	anti	Adfl1435	373	37	72.5	108	8	ADP96647	Human	ant	Adp96647
301	37	72.5	215	7	ADFL1435	16E1	anti	Adfl1435	374	37	72.5	108	8	ADP96647	Human	ant	Adp96647
302	37	72.5	224	4	AA899339	Human	gen	Aa899339	375	37	72.5	109	8	ADP96647	Human	ant	Adp96647
303	37	72.5	224	4	AA899339	Human	gen	Aa899339	376	37	72.5	109	8	ADP96647	Human	ant	Adp96647
304	37	72.5	224	4	AA899339	Human	int	Aa899339	377	37	72.5	109	8	ADP96647	Human	ant	Adp96647
305	37	72.5	224	4	AA899339	Human	int	Aa899339	378	37	72.5	109	8	ADP96647	Human	ant	Adp96647
306	37	72.5	224	4	AA899339	Human	int	Aa899339	379	37	72.5	109	8	ADP96647	Human	ant	Adp96647
307	37	72.5	224	4	AA899339	Human	int	Aa899339	380	37	72.5	109	8	ADP96647	Human	ant	Adp96647
308	37	72.5	224	4	AA899339	Human	int	Aa899339	381	37	72.5	109	8	ADP96647	Human	ant	Adp96647
309	37	72.5	224	4	AA899339	Human	int	Aa899339	382	37	72.5	109	8	ADP96647	Human	ant	Adp96647
310	37	72.5	224	4	AA899339	Human	int	Aa899339	383	37	72.5	109	8	ADP96647	Human	ant	Adp96647
311	37	72.5	224	4	AA899339	Human	int	Aa899339	384	37	72.5	109	8	ADP96647	Human	ant	Adp96647
312	37	72.5	224	4	AA899339	Human	int	Aa899339	385	37	72.5	109	8	ADP96647	Human	ant	Adp96647
313	37	72.5	224	4	AA899339	Human	int	Aa899339	386	37	72.5	109	8	ADP96647	Human	ant	Adp96647
314	37	72.5	224	4	AA899339	Human	int	Aa899339	387	37	72.5	109	8	ADP96647	Human	ant	Adp96647
315	37	72.5	224	4	AA899339	Human	int	Aa899339	388	37	72.5	109	8	ADP96647	Human	ant	Adp96647
316	37	72.5	225	8	ADW41573	Anti-inte		Adw41573	389	37	72.5	128	2	AA693659	Human	ant	Aa693659

390	36	70.6	128	2	AAW03721	AAW03721	Anti-huma	463	35	68.6	95	9	AEA53925	AEA53925	Novel hum
391	36	70.6	129	2	AAR65018	AAR65018	93KA9 ant	464	35	68.6	95	9	AEA53916	AEA53916	Novel hum
392	36	70.6	171	2	AAW03725	AAW03725	Humanised	465	35	68.6	95	9	AEA53973	AEA53973	Novel hum
393	36	70.6	215	4	AAU08378	AAU08378	Anti-OPCb	466	35	68.6	95	9	AEB13574	AEB13574	Human var
394	36	70.6	236	4	AAV96297	AAV96297	Human IGF	467	35	68.6	95	9	AEB13616	AEB13616	Human var
395	36	70.6	242	8	ADQ75289	ADQ75289	Immunoglo	468	35	68.6	95	9	AEB13618	AEB13618	Human var
396	36	70.6	244	8	ADQ75290	ADQ75290	Immunoglo	469	35	68.6	95	9	AEB13627	AEB13627	Human var
397	36	70.6	248	4	AAQ78409	AAQ78409	Amtno aci	470	35	68.6	95	9	AEB13623	AEB13623	Human var
398	36	70.6	253	5	AAO14057	AAO14057	Anti-PAPA	471	35	68.6	95	9	AEB13563	AEB13563	Human var
399	36	70.6	255	5	AAO14054	AAO14054	Anti-PAPA	472	35	68.6	95	9	AEB13570	AEB13570	Human var
400	36	70.6	256	5	ABP45016	ABP45016	Human Bly	473	35	68.6	95	9	AEB13565	AEB13565	Human var
401	36	70.6	256	7	ADG95843	ADG95843	Single ch	474	35	68.6	96	7	ADK18905	ADK18905	Anti-huma
402	36	70.6	256	7	AEA24172	AEA24172	Anti-HAaH	475	35	68.6	96	7	ADK18903	ADK18903	Anti-huma
403	36	70.6	260	5	AAO14055	AAO14055	Anti-PAPA	476	35	68.6	96	7	AEA53958	AEA53958	Novel hum
404	36	70.6	260	5	AAO14056	AAO14056	Anti-PAPA	477	35	68.6	102	5	ABB07183	ABB07183	Novel hum
405	36	70.6	262	5	AAO14058	AAO14058	Anti-PAPA	478	35	68.6	102	6	AAE38330	AAE38330	Human ant
406	35	68.6	11	6	AAO31090	AAO31090	Human A2-	479	35	68.6	102	8	AD126682	AD126682	Human ant
407	35	68.6	11	7	ABO33863	ABO33863	Anti-GPI-	480	35	68.6	102	8	ADY33969	ADY33969	Anti-T1e
408	35	68.6	11	8	ADP47051	ADP47051	Murine 1i	481	35	68.6	104	6	ABR41821	ABR41821	Light cha
409	35	68.6	11	9	ADY21319	ADY21319	Human ant	482	35	68.6	104	7	ABO33828	ABO33828	Human ant
410	35	68.6	11	9	ADM04803	ADM04803	PAP-A im	483	35	68.6	104	9	AD235774	AD235774	Anti-gliu
411	35	68.6	11	9	ADY98290	ADY98290	Human ant	484	35	68.6	107	2	ABR54303	ABR54303	Anti-HIV
412	35	68.6	11	9	ADZ35809	ADZ35809	Anti-gliu	485	35	68.6	107	2	ABR54305	ABR54305	Anti-HIV
413	35	68.6	11	9	AEA38787	AEA38787	Human ger	486	35	68.6	107	2	ABR52041	ABR52041	Light cha
414	35	68.6	11	9	AEA53695	AEA53695	Novel hum	487	35	68.6	107	2	AAW01261	AAW01261	VL region
415	35	68.6	11	9	AEA53524	AEA53524	Novel hum	488	35	68.6	107	2	AAW01263	AAW01263	VL region
416	35	68.6	11	9	AEA46173	AEA46173	Novel hum	489	35	68.6	107	3	AAV98222	AAV98222	Anti-gp12
417	35	68.6	11	9	AEA44922	AEA44922	Apoliopor	490	35	68.6	107	3	AAV98224	AAV98224	Anti-gp12
418	35	68.6	11	9	AEA45595	AEA45595	Apoliopor	491	35	68.6	107	3	AAV95113	AAV95113	Anti-gp12
419	35	68.6	11	9	AEA45026	AEA45026	Apoliopor	492	35	68.6	107	3	AAV95115	AAV95115	Anti-gp12
420	35	68.6	11	9	AEA5197	AEA5197	Apoliopor	493	35	68.6	107	6	ABJ18721	ABJ18721	Anti-huma
421	35	68.6	12	6	ABJ18733	ABJ18733	Anti-body	494	35	68.6	107	7	ADK18800	ADK18800	Anti-huma
422	35	68.6	12	6	ABJ18711	ABJ18711	Anti-body	495	35	68.6	107	7	ADK18910	ADK18910	Anti-huma
423	35	68.6	12	6	ABJ18703	ABJ18703	Anti-body	496	35	68.6	107	7	ADK18799	ADK18799	Anti-huma
424	35	68.6	12	6	ABJ18709	ABJ18709	Anti-body	497	35	68.6	107	7	ADK18833	ADK18833	Anti-huma
425	35	68.6	12	6	ABJ18705	ABJ18705	Anti-body	498	35	68.6	107	7	ADK18608	ADK18608	Anti-huma
426	35	68.6	12	6	AAV02503	AAV02503	Clome sel	499	35	68.6	107	7	ADK18610	ADK18610	Anti-huma
427	35	68.6	88	3	AAV56659	AAV56659	Partial p	500	35	68.6	107	7	ADK18834	ADK18834	Anti-huma
428	35	68.6	88	3	AAV56652	AAV56652	Partial p	501	35	68.6	107	7	ADP03946	ADP03946	Murine-ex
429	35	68.6	88	3	ABO27134	ABO27134	Human ger	502	35	68.6	107	8	AD122108	AD122108	Anti-plat
430	35	68.6	95	6	ABO27128	ABO27128	Human ger	503	35	68.6	107	8	AD125438	AD125438	Human mab
431	35	68.6	95	6	ABO27136	ABO27136	Human ger	504	35	68.6	107	8	AD125434	AD125434	Human mab
432	35	68.6	95	6	ADC99834	ADC99834	Germline	505	35	68.6	107	8	ADP22358	ADP22358	Human ant
433	35	68.6	95	7	ADDO5438	ADDO5438	Anti-MUC1	506	35	68.6	107	8	ADP22400	ADP22400	Human ant
434	35	68.6	95	7	ADP10163	ADP10163	Anti-body	507	35	68.6	107	9	ADV21317	ADV21317	Human ant
435	35	68.6	95	7	ADP10174	ADP10174	Anti-body	508	35	68.6	107	9	ADX98405	ADX98405	Human ant
436	35	68.6	95	7	ADP09956	ADP09956	Anti-body	509	35	68.6	107	9	AEA45102	AEA45102	Apoliopor
437	35	68.6	95	7	ADP09967	ADP09967	Anti-body	510	35	68.6	107	9	AEA62455	AEA62455	Mouse 1B3
438	35	68.6	95	7	ADP10165	ADP10165	Anti-body	511	35	68.6	108	2	AAK54320	AAK54320	Anti-HIV
439	35	68.6	95	7	ADP10061	ADP10061	VEGF anti	512	35	68.6	108	2	AAW01288	AAW01288	VL region
440	35	68.6	95	7	ADP10072	ADP10072	VEGF anti	513	35	68.6	108	2	AAW15524	AAW15524	Anti-TGF
441	35	68.6	95	7	ADP10068	ADP10068	VEGF anti	514	35	68.6	108	3	AAV98249	AAV98249	Anti-gp12
442	35	68.6	95	7	ADP10170	ADP10170	Anti-body	515	35	68.6	108	3	AAV95140	AAV95140	Anti-gp12
443	35	68.6	95	7	ADP09958	ADP09958	Anti-body	516	35	68.6	108	4	AAH62757	AAH62757	Human HIV
444	35	68.6	95	7	ADP09963	ADP09963	Anti-body	517	35	68.6	108	4	AAH62951	AAH62951	Amtno aci
445	35	68.6	95	7	ADP10063	ADP10063	VEGF anti	518	35	68.6	108	6	ABJ18679	ABJ18679	Anti-huma
446	35	68.6	95	7	ADP099876	ADP099876	Anti-MUC1	519	35	68.6	108	7	ADK18904	ADK18904	Anti-huma
447	35	68.6	95	7	ADK188585	ADK188585	Anti-huma	520	35	68.6	108	8	ADP46983	ADP46983	Human var
448	35	68.6	95	7	ADK18909	ADK18909	Anti-huma	521	35	68.6	108	8	ADP46980	ADP46980	Human var
449	35	68.6	95	7	ADK18921	ADK18921	Anti-huma	522	35	68.6	108	8	ADP46982	ADP46982	Murine 1i
450	35	68.6	95	7	ADK18911	ADK18911	Anti-huma	523	35	68.6	108	8	ADP46984	ADP46984	Murine 1i
451	35	68.6	95	7	ADJ80248	ADJ80248	Vkappa ge	524	35	68.6	108	8	ADW04801	ADW04801	PAP-A im
452	35	68.6	95	7	ADJ80256	ADJ80256	Vkappa ge	525	35	68.6	108	9	ADX01787	ADX01787	SARS coro
453	35	68.6	95	7	ADJ80254	ADJ80254	Vkappa ge	526	35	68.6	108	9	AEA45222	AEA45222	Apoliopor
454	35	68.6	95	7	ADJ80245	ADJ80245	Vkappa ge	527	35	68.6	108	9	AEA44962	AEA44962	Apoliopor
455	35	68.6	95	8	ADDO7317	ADDO7317	Human ant	528	35	68.6	109	2	AAK30764	AAK30764	Consensus
456	35	68.6	95	8	ADDO7323	ADDO7323	Human ant	529	35	68.6	109	2	AAK47041	AAK47041	Sequence
457	35	68.6	95	8	ADDO7335	ADDO7335	Human ant	530	35	68.6	109	2	AAW27543	AAW27543	Human Ab
458	35	68.6	95	8	ADDO7314	ADDO7314	Human ant	531	35	68.6	109	6	ADA89110	ADA89110	MS-Pro-28
459	35	68.6	95	9	ADY75419	ADY75419	Human ger	532	35	68.6	109	6	ADA90110	ADA90110	Anti-Abet
460	35	68.6	95	9	ADY75428	ADY75428	Human ger	533	35	68.6	109	6	AAO31075	AAO31075	Human ant
461	35	68.6	95	9	ADY75422	ADY75422	Human ger	534	35	68.6	109	6	ADG74361	ADG74361	MSPro 11g
462	35	68.6	95	9	ADY75430	ADY75430	Human ger	535	35	68.6	109	7			

536	35	68.6	109	7	ADL91338	Adl91338	VL chain	609	34	66.7	11	9	ADY26817	Ady26817	Human ant
537	35	68.6	109	8	ADY6365	Ady6365	Intracell	610	34	66.7	11	9	ADY26807	Ady26807	Human ant
538	35	68.6	109	8	ADY66958	Ady66958	Human imm	611	34	66.7	11	9	ADY26807	Ady26807	Human ant
539	35	68.6	110	6	ABR40155	Abt40155	Humanised	612	34	66.7	11	9	ABR53528	ABR53528	Novel hum
540	35	68.6	110	6	ABR40155	Abt40155	Humanised	613	34	66.7	11	9	ABR53804	ABR53804	Novel hum
541	35	68.6	110	8	ADG64756	Adg64756	Humanised	614	34	66.7	11	9	ABR53696	ABR53696	Novel hum
542	35	68.6	110	8	ADG64754	Adg64754	Humanised	615	34	66.7	11	9	ABR53686	ABR53686	Novel hum
543	35	68.6	111	2	AAR61097	Aar61097	Human can	616	34	66.7	11	9	ABR45023	ABR45023	Novel hum
544	35	68.6	113	7	ADD28266	Add28266	Human het	617	34	66.7	11	9	ABR45191	ABR45191	Novel hum
545	35	68.6	113	7	ADD28266	Add28266	Human het	618	34	66.7	11	9	ABR45191	ABR45191	Novel hum
546	35	68.6	113	7	ADD28266	Add28266	Human het	619	34	66.7	11	9	ABR45190	ABR45190	Novel hum
547	35	68.6	119	9	AEA33957	Aea33957	Novel hum	620	34	66.7	11	9	ABR45194	ABR45194	Novel hum
548	35	68.6	119	9	AEA33326	Aea33326	Novel hum	621	34	66.7	11	9	ABR45194	ABR45194	Novel hum
549	35	68.6	120	9	AEA33282	Aea33282	Novel hum	622	34	66.7	11	9	ABR45194	ABR45194	Novel hum
550	35	68.6	120	9	AEA33282	Aea33282	Novel hum	623	34	66.7	11	9	ABR45194	ABR45194	Novel hum
551	35	68.6	122	5	ABP62202	Abp62202	Human imm	624	34	66.7	11	9	ABR45194	ABR45194	Novel hum
552	35	68.6	125	6	ABR53900	Abt53900	Human mb	625	34	66.7	11	9	ABR45194	ABR45194	Novel hum
553	35	68.6	127	6	AEA16219	Aea16219	Anti-huma	626	34	66.7	11	9	ABR45194	ABR45194	Novel hum
554	35	68.6	127	6	AEA16219	Aea16219	Anti-huma	627	34	66.7	11	9	ABR45194	ABR45194	Novel hum
555	35	68.6	128	3	AAV56717	Aav56717	Amino aci	628	34	66.7	11	9	AAV02502	AAV02502	Novel hum
556	35	68.6	129	3	AAV56717	Aav56717	Amino aci	629	34	66.7	11	9	AAV02502	AAV02502	Novel hum
557	35	68.6	129	3	AAV56717	Aav56717	Amino aci	630	34	66.7	11	9	AAV02502	AAV02502	Novel hum
558	35	68.6	134	3	AAV93720	Aav93720	The kappa	631	34	66.7	11	9	AAV02511	AAV02511	Novel hum
559	35	68.6	134	6	ABR55901	Abt55901	Human mb	632	34	66.7	11	9	AAV02511	AAV02511	Novel hum
560	35	68.6	136	6	ABR55901	Abt55901	Human mb	633	34	66.7	11	9	AAV02511	AAV02511	Novel hum
561	35	68.6	214	8	ABM84937	Abm84937	Human dia	634	34	66.7	11	9	AAV02511	AAV02511	Novel hum
562	35	68.6	225	8	ABM84937	Abm84937	Human dia	635	34	66.7	11	9	AAV02511	AAV02511	Novel hum
563	35	68.6	234	2	AAAR20058	Aar20058	Light cha	636	34	66.7	11	9	AAV02511	AAV02511	Novel hum
564	35	68.6	234	2	AAAR20058	Aar20058	Light cha	637	34	66.7	11	9	AAV02511	AAV02511	Novel hum
565	35	68.6	235	3	AAAR20058	Aar20058	Light cha	638	34	66.7	11	9	AAV02511	AAV02511	Novel hum
566	35	68.6	235	3	AAAR20058	Aar20058	Light cha	639	34	66.7	11	9	AAV02511	AAV02511	Novel hum
567	35	68.6	235	3	AAAR20058	Aar20058	Light cha	640	34	66.7	11	9	AAV02511	AAV02511	Novel hum
568	35	68.6	236	6	ADA91403	Ada91403	Anti-Abet	641	34	66.7	11	9	AAV02511	AAV02511	Novel hum
569	35	68.6	236	6	ADA91403	Ada91403	Anti-Abet	642	34	66.7	11	9	AAV02511	AAV02511	Novel hum
570	35	68.6	239	5	AAU0905	Aau0905	Human mon	643	34	66.7	11	9	AAV02511	AAV02511	Novel hum
571	35	68.6	240	3	AAV15128	Aav15128	Anti-mutl	644	34	66.7	11	9	AAV02511	AAV02511	Novel hum
572	35	68.6	241	5	ABP45921	Abp45921	Human Bly	645	34	66.7	11	9	AAV02511	AAV02511	Novel hum
573	35	68.6	241	5	ABP45921	Abp45921	Human Bly	646	34	66.7	11	9	AAV02511	AAV02511	Novel hum
574	35	68.6	241	5	ABP45921	Abp45921	Human Bly	647	34	66.7	11	9	AAV02511	AAV02511	Novel hum
575	35	68.6	241	5	ABP45921	Abp45921	Human Bly	648	34	66.7	11	9	AAV02511	AAV02511	Novel hum
576	35	68.6	241	5	ABP45921	Abp45921	Human Bly	649	34	66.7	11	9	AAV02511	AAV02511	Novel hum
577	35	68.6	242	5	AAU09092	Aau09092	Insulin/1	650	34	66.7	11	9	AAV02511	AAV02511	Novel hum
578	35	68.6	242	5	AAU09092	Aau09092	Insulin/1	651	34	66.7	11	9	AAV02511	AAV02511	Novel hum
579	35	68.6	244	5	AAU09092	Aau09092	Insulin/1	652	34	66.7	11	9	AAV02511	AAV02511	Novel hum
580	35	68.6	245	5	AAU09092	Aau09092	Insulin/1	653	34	66.7	11	9	AAV02511	AAV02511	Novel hum
581	35	68.6	245	5	AAU09092	Aau09092	Insulin/1	654	34	66.7	11	9	AAV02511	AAV02511	Novel hum
582	35	68.6	245	5	AAU09092	Aau09092	Insulin/1	655	34	66.7	11	9	AAV02511	AAV02511	Novel hum
583	35	68.6	249	5	ABP45921	Abp45921	Human Bly	656	34	66.7	11	9	AAV02511	AAV02511	Novel hum
584	35	68.6	249	5	ABP45921	Abp45921	Human Bly	657	34	66.7	11	9	AAV02511	AAV02511	Novel hum
585	35	68.6	249	5	ABP45921	Abp45921	Human Bly	658	34	66.7	11	9	AAV02511	AAV02511	Novel hum
586	35	68.6	249	5	ABP45921	Abp45921	Human Bly	659	34	66.7	11	9	AAV02511	AAV02511	Novel hum
587	35	68.6	251	9	ADG96451	Adg96451	Single ch	660	34	66.7	11	9	AAV02511	AAV02511	Novel hum
588	35	68.6	251	9	ADG96451	Adg96451	Single ch	661	34	66.7	11	9	AAV02511	AAV02511	Novel hum
589	35	68.6	251	9	ADG96451	Adg96451	Single ch	662	34	66.7	11	9	AAV02511	AAV02511	Novel hum
590	35	68.6	251	9	ADG96451	Adg96451	Single ch	663	34	66.7	11	9	AAV02511	AAV02511	Novel hum
591	35	68.6	251	9	ADG96451	Adg96451	Single ch	664	34	66.7	11	9	AAV02511	AAV02511	Novel hum
592	35	68.6	251	9	ADG96451	Adg96451	Single ch	665	34	66.7	11	9	AAV02511	AAV02511	Novel hum
593	35	68.6	251	9	ADG96451	Adg96451	Single ch	666	34	66.7	11	9	AAV02511	AAV02511	Novel hum
594	35	68.6	251	9	ADG96451	Adg96451	Single ch	667	34	66.7	11	9	AAV02511	AAV02511	Novel hum
595	35	68.6	251	9	ADG96451	Adg96451	Single ch	668	34	66.7	11	9	AAV02511	AAV02511	Novel hum
596	35	68.6	251	9	ADG96451	Adg96451	Single ch	669	34	66.7	11	9	AAV02511	AAV02511	Novel hum
597	35	68.6	251	9	ADG96451	Adg96451	Single ch	670	34	66.7	11	9	AAV02511	AAV02511	Novel hum
598	35	68.6	251	9	ADG96451	Adg96451	Single ch	671	34	66.7	11	9	AAV02511	AAV02511	Novel hum
599	35	68.6	251	9	ADG96451	Adg96451	Single ch	672	34	66.7	11	9	AAV02511	AAV02511	Novel hum
600	35	68.6	251	9	ADG96451	Adg96451	Single ch	673	34	66.7	11	9	AAV02511	AAV02511	Novel hum
601	35	68.6	251	9	ADG96451	Adg96451	Single ch	674	34	66.7	11	9	AAV02511	AAV02511	Novel hum
602	35	68.6	251	9	ADG96451	Adg96451	Single ch	675	34	66.7	11	9	AAV02511	AAV02511	Novel hum
603	35	68.6	251	9	ADG96451	Adg96451	Single ch	676	34	66.7	11	9	AAV02511	AAV02511	Novel hum
604	35	68.6	251	9	ADG96451	Adg96451	Single ch	677	34	66.7	11	9	AAV02511	AAV02511	Novel hum
605	35	68.6	251	9	ADG96451	Adg96451	Single ch	678	34	66.7	11	9	AAV02511	AAV02511	Novel hum
606	35	68.6	251	9	ADG96451	Adg96451	Single ch	679	34	66.7	11	9	AAV02511	AAV02511	Novel hum
607	35	68.6	251	9	ADG96451	Adg96451	Single ch	680	34	66.7	11	9	AAV02511	AAV02511	Novel hum
608	35	68.6	251	9	ADG96451	Adg96451	Single ch	681	34	66.7	11	9	AAV02511	AAV02511	Novel hum

682	34	66.7	95	7	ADF09989	Adf09989	Antibody	755	34	66.7	107	6	ABO27451	AbO27451	Anti-Rh(D
683	34	66.7	95	7	ADP10180	Adf10180	Antibody	756	34	66.7	107	6	ABO27401	AbO27401	Anti-Rh(D
684	34	66.7	95	7	ADP10094	Adf10094	VEGF anti-	757	34	66.7	107	6	ABO27453	AbO27453	Anti-Rh(D
685	34	66.7	95	7	ADP09856	Adf09856	Anti-MUC1	758	34	66.7	107	6	ABO27471	AbO27471	Anti-Rh(D
686	34	66.7	95	7	ADJ80242	AdJ80242	Vkappa ge	759	34	66.7	107	6	ABO27403	AbO27403	Anti-Rh(D
687	34	66.7	95	7	ADJ80241	AdJ80241	Vkappa ge	760	34	66.7	107	6	ABO27463	AbO27463	Anti-Rh(D
688	34	66.7	95	7	ADJ80274	AdJ80274	Vkappa ge	761	34	66.7	107	6	ABO27402	AbO27402	Anti-Rh(D
689	34	66.7	95	7	ADP03925	Adp03925	Murine-ex	762	34	66.7	107	6	ABO27397	AbO27397	Anti-Rh(D
690	34	66.7	95	8	ADPO07343	Ado07343	Human ant	763	34	66.7	107	6	ABO27470	AbO27470	Anti-Rh(D
691	34	66.7	95	8	ADPO07310	Ado07310	Human ant	764	34	66.7	107	6	ABO27468	AbO27468	Anti-Rh(D
692	34	66.7	95	8	ADCO07311	Adco07311	Human ant	765	34	66.7	107	6	ABO27404	AbO27404	Anti-Rh(D
693	34	66.7	95	8	ADU86537	Adu86537	Immunoglo	766	34	66.7	107	7	ADCO51596	AdCO51596	Human TAG
694	34	66.7	95	8	ADY54709	Ady54709	Human V k	767	34	66.7	107	7	ADP03948	AdP03948	Murine-ex
695	34	66.7	95	9	ADY75448	Ady75448	Human ger	768	34	66.7	107	7	ADP03949	AdP03949	Murine-ex
696	34	66.7	95	9	ADY75416	Ady75416	Human ger	769	34	66.7	107	7	ADP03928	AdP03928	Murine-ex
697	34	66.7	95	9	ADY75415	Ady75415	Human ger	770	34	66.7	107	7	ADP03927	AdP03927	Murine-ex
698	34	66.7	95	9	AEA53913	Aea53913	Novel hum	771	34	66.7	107	8	ADG34381	AdG34381	Humanised
699	34	66.7	95	9	AEA53904	Aea53904	Novel hum	772	34	66.7	107	8	ADN49404	AdN49404	Human ant
700	34	66.7	95	9	AEA53979	Aea53979	Novel hum	773	34	66.7	107	8	ADO07301	AdO07301	Human pro
701	34	66.7	95	9	AEA53988	Aea53988	Novel hum	774	34	66.7	107	8	ADO06815	AdO06815	Virucidal
702	34	66.7	95	9	AEA53961	Aea53961	Novel hum	775	34	66.7	107	8	ADO06843	AdO06843	Virucidal
703	34	66.7	95	9	ABE13579	Aeb13579	Human var	776	34	66.7	107	8	ADP22402	AdP22402	Human ant
704	34	66.7	95	9	ABE13580	Aeb13580	Human var	777	34	66.7	107	8	ADQ09013	AdQ09013	Rat anti-
705	34	66.7	95	9	ABE13632	Aeb13632	Human var	778	34	66.7	107	8	ADT55242	AdT55242	Human ant
706	34	66.7	95	9	ABE13633	Aeb13633	Human var	779	34	66.7	107	8	ADV21397	AdV21397	Human ant
707	34	66.7	95	9	ABE13649	Aeb13649	Human var	780	34	66.7	107	9	ADV21365	AdV21365	Human ant
708	34	66.7	95	9	AEC20816	Aec20816	Human var	781	34	66.7	107	9	ADY26774	AdY26774	Anti-NGF
709	34	66.7	96	5	ABG27155	Abg27155	Germ-line	782	34	66.7	107	9	ADY74802	AdY74802	Human Ig
710	34	66.7	96	8	ADR28576	Adr28576	Human ant	783	34	66.7	107	9	AEA12440	Aea12440	Rat anti-
711	34	66.7	96	8	AEA53877	Aea53877	Novel hum	784	34	66.7	107	9	AEA12455	Aea12455	Rat anti-
712	34	66.7	96	9	AEA53985	Aea53985	Novel hum	785	34	66.7	107	9	AEA12433	Aea12433	Rat anti-
713	34	66.7	96	9	AEA53964	Aea53964	Novel hum	786	34	66.7	107	9	AEA12450	Aea12450	Rat anti-
714	34	66.7	96	9	AEA53996	Aea53996	Novel hum	787	34	66.7	107	9	AEA12435	Aea12435	Rat anti-
715	34	66.7	101	2	AAR22577	Aar22577	Light cha	788	34	66.7	107	9	AEA12460	Aea12460	Rat anti-
716	34	66.7	102	2	ADY33965	Ady33965	Anti-tile	789	34	66.7	107	9	AEA12445	Aea12445	Rat anti-
717	34	66.7	103	4	AAAG93599	Aag93599	Human ant	790	34	66.7	107	9	AEA12438	Aea12438	Rat anti-
718	34	66.7	103	6	ABO27406	AbO27406	Anti-Rh(D	791	34	66.7	107	9	AEA12448	Aea12448	Rat anti-
719	34	66.7	105	2	AAW52237	Aaw52237	Antibody	792	34	66.7	107	9	AEA12453	Aea12453	Rat anti-
720	34	66.7	105	7	ADPO3985	Adp03985	Murine-ex	793	34	66.7	107	9	AEA12400	Aea12400	Rat anti-
721	34	66.7	106	7	ABR61522	AbR61522	Human SA-	794	34	66.7	107	9	AEA12458	Aea12458	Rat anti-
722	34	66.7	106	8	ADJ22107	AdJ22107	Anti-plat	795	34	66.7	107	9	AEA12443	Aea12443	Rat anti-
723	34	66.7	106	8	ADR47411	Adr47411	Human ger	796	34	66.7	107	9	AEA12402	Aea12402	Rat anti-
724	34	66.7	106	8	ADY72816	Ady72816	Anti-hepa	797	34	66.7	107	9	AEA17749	Aea17749	Hybridoma
725	34	66.7	106	8	ADY72815	Ady72815	Anti-hepa	798	34	66.7	107	9	AEA41073	Aea41073	Germ-line
726	34	66.7	106	9	ADX01785	Adx01785	SARS coro	799	34	66.7	107	9	AEA40465	Aea40465	Anti-VEGF
727	34	66.7	106	9	ABE45972	Aeb45972	Human mon	800	34	66.7	107	9	ABE19291	Aeb19291	IgG kappa
728	34	66.7	107	2	AAR54261	Aar54261	Anti-HIV	801	34	66.7	107	9	ABE45968	Aeb45968	Human mon
729	34	66.7	107	2	AAR54260	Aar54260	Anti-HIV	802	34	66.7	108	2	AAR54258	Aar54258	Anti-HIV
730	34	66.7	107	2	AAW01283	Aaw01283	VL region	803	34	66.7	108	2	AAW01281	Aaw01281	VL region
731	34	66.7	107	2	AAW01284	Aaw01284	VL region	804	34	66.7	108	2	AAW13530	Aaw13530	Anti-mela
732	34	66.7	107	2	AAW80817	Aaw80817	Amino aci	805	34	66.7	108	2	AAW13521	Aaw13521	Anti-mela
733	34	66.7	107	2	AAW80972	Aaw80972	Kappa lig	806	34	66.7	108	3	AAW98242	Aaw98242	Anti-gp12
734	34	66.7	107	3	AAV98245	Aav98245	Anti-gp12	807	34	66.7	108	3	AAV95133	Aav95133	Anti-gp12
735	34	66.7	107	3	AAV98244	Aav98244	Anti-gp12	808	34	66.7	108	4	AAW62772	Aaw62772	Human HIV
736	34	66.7	107	3	AAV95136	Aav95136	Anti-gp12	809	34	66.7	108	4	AAAG93589	Aag93589	Human ant
737	34	66.7	107	3	AAV95135	Aav95135	Anti-gp12	810	34	66.7	108	4	AAAG93600	Aag93600	Human ant
738	34	66.7	107	4	AAAG65567	Aag65567	Amino aci	811	34	66.7	108	4	AAAG93655	Aag93655	Human ant
739	34	66.7	107	4	AAAG93566	Aag93566	Human ant	812	34	66.7	108	4	AAAG93651	Aag93651	Human ant
740	34	66.7	107	4	AAAG93596	Aag93596	Human ant	813	34	66.7	108	6	ABP96009	AbP96009	HSA antib
741	34	66.7	107	4	AAAG93597	Aag93597	Human ant	814	34	66.7	108	6	ABP96010	AbP96010	HSA antib
742	34	66.7	107	4	AAAG93566	Aag93566	Human ant	815	34	66.7	108	6	AAO16704	Aao16704	Human ant
743	34	66.7	107	4	AAAG93663	Aag93663	Human ant	816	34	66.7	108	6	AAO16706	Aao16706	Human ant
744	34	66.7	107	4	AAAG93644	Aag93644	Human ant	817	34	66.7	108	6	AAE35210	Aae35210	Human IGE
745	34	66.7	107	4	AAAG93664	Aag93664	Human ant	818	34	66.7	108	6	ABO27462	AbO27462	Anti-Rh(D
746	34	66.7	107	4	AAAG93661	Aag93661	Human ant	819	34	66.7	108	6	ABO27407	AbO27407	Anti-Rh(D
747	34	66.7	107	4	AAAG93594	Aag93594	Human ant	820	34	66.7	108	6	ABO27396	AbO27396	Anti-Rh(D
748	34	66.7	107	4	AAAG93595	Aag93595	Human ant	821	34	66.7	108	6	ABO27458	AbO27458	Anti-Rh(D
749	34	66.7	107	5	AAO17151	Aao17151	Human end	822	34	66.7	108	7	ADL91345	AdL91345	VL chain
750	34	66.7	107	5	ABP96012	Abp96012	HSA antib	823	34	66.7	108	7	ADL91337	AdL91337	VL chain
751	34	66.7	107	6	ABR54915	AbR54915	Light cha	824	34	66.7	108	8	ADL92461	AdL92461	Single do
752	34	66.7	107	6	ABO04835	AbO04835	Human epi	825	34	66.7	108	8	ADL92386	AdL92386	Anti-HSA
753	34	66.7	107	6	AAO23067	Aao23067	Murine K8	826	34	66.7	108	8	ADL92463	AdL92463	Single do
754	34	66.7	107	6				827	34	66.7	108	8			

828	34	66.7	108	8	AD036372	Ad036372	Intracell1	901	34	66.7	111	4	AA663655	AA663655	Amino aci
829	34	66.7	108	8	AD036364	Ad036364	Intracell1	902	34	66.7	111	6	ABJ38614	ABJ38614	Hepatitis
830	34	66.7	108	8	AD036397	Ad036397	Intracell1	903	34	66.7	111	8	ADG64755	ADG64755	Humanised
831	34	66.7	108	8	ADP66652	Adp66652	Anti-RAS	904	34	66.7	111	8	ADP47305	ADP47305	Human pho
832	34	66.7	108	8	ADP96654	Adp96654	Anti-RAS	905	34	66.7	111	8	ADP47306	ADP47306	Human pho
833	34	66.7	108	8	ADQ75245	Adq75245	Immunoglo	906	34	66.7	111	8	ADP47301	ADP47301	Human pho
834	34	66.7	108	8	ADQ75237	Adq75237	Immunoglo	907	34	66.7	113	2	AAW13924	AAW13924	Light cha
835	34	66.7	108	8	ADP47299	Adp47299	Human pho	908	34	66.7	113	2	ADD28277	ADD28277	Human het
836	34	66.7	108	8	ADP47294	Adp47294	Human pho	909	34	66.7	113	9	ADY50130	ADY50130	Endocell
837	34	66.7	108	8	ADP47107	Adp47107	Human pho	910	34	66.7	114	2	AAW13922	AAW13922	Light cha
838	34	66.7	108	8	ADP47113	Adp47113	Human pho	911	34	66.7	114	4	AA655563	AA655563	Amino aci
839	34	66.7	108	8	ADQ14601	Adq14601	Single-do	912	34	66.7	114	7	ADD28276	ADD28276	Human het
840	34	66.7	108	8	ADQ77184	Adq77184	VK C3 seq	913	34	66.7	115	2	AA62929	AA62929	Human V-k
841	34	66.7	108	8	ADQ77191	Adq77191	Dummy VK	914	34	66.7	115	2	AAW03947	AAW03947	Human V-k
842	34	66.7	108	8	ADQ77182	Adq77182	VK dummy	915	34	66.7	115	2	AAW03947	AAW03947	DNA fragm
843	34	66.7	108	8	ADQ77182	Adq77182	VK X8 seq	916	34	66.7	115	2	AAW62183	AAW62183	Human vka
844	34	66.7	108	8	ADQ90912	Adq90912	VK/CK pro	917	34	66.7	115	2	AAW62183	AAW62183	Human DNA
845	34	66.7	108	8	ADQ99346	Adq99346	Anti-RAS	918	34	66.7	115	2	AAV40430	AAV40430	Amino aci
846	34	66.7	108	8	ADQ78333	Adq78333	Vkappa du	919	34	66.7	116	9	ADW04873	ADW04873	PAP-A im
847	34	66.7	108	8	ADQ78331	Adq78331	DPkappa9-	920	34	66.7	116	9	ADY50090	ADY50090	PAP-A im
848	34	66.7	108	8	ADQ788240	Adq788240	Human ant	921	34	66.7	116	9	ADY50090	ADY50090	Endocell
849	34	66.7	108	8	ADQ788240	Adq788240	Human ant	922	34	66.7	120	9	AA653330	AA653330	Novel hum
850	34	66.7	108	8	ADQ788240	Adq788240	Human ant	923	34	66.7	120	9	AA653360	AA653360	Novel hum
851	34	66.7	108	8	ADQ788240	Adq788240	Human ant	924	34	66.7	121	9	AA653372	AA653372	Novel hum
852	34	66.7	108	9	ADQ788240	Adq788240	Human ant	925	34	66.7	121	9	AA653334	AA653334	Novel hum
853	34	66.7	108	9	ADQ788240	Adq788240	Human ant	926	34	66.7	121	9	AA653358	AA653358	Novel hum
854	34	66.7	108	9	ADQ788240	Adq788240	Human ant	927	34	66.7	121	9	AA653376	AA653376	Novel hum
855	34	66.7	108	9	ADQ788240	Adq788240	Human ant	928	34	66.7	122	2	AAW24538	AAW24538	Novel hum
856	34	66.7	108	9	ADQ788240	Adq788240	Human ant	929	34	66.7	122	2	AAW24538	AAW24538	Novel hum
857	34	66.7	108	9	ADQ788240	Adq788240	Human ant	930	34	66.7	124	8	ADQ84981	ADQ84981	H23 antiq
858	34	66.7	108	9	ADQ788240	Adq788240	Human ant	931	34	66.7	126	9	AA612635	AA612635	Modified
859	34	66.7	108	9	ADQ788240	Adq788240	Human ant	932	34	66.7	127	6	AA612639	AA612639	Modified
860	34	66.7	108	9	ADQ788240	Adq788240	Human ant	933	34	66.7	127	6	AA612639	AA612639	Modified
861	34	66.7	108	9	ADQ788240	Adq788240	Human ant	934	34	66.7	127	6	AA612639	AA612639	Modified
862	34	66.7	108	9	ADQ788240	Adq788240	Human ant	935	34	66.7	127	9	AA612639	AA612639	Modified
863	34	66.7	108	9	ADQ788240	Adq788240	Human ant	936	34	66.7	132	2	AA612639	AA612639	Modified
864	34	66.7	108	9	ADQ788240	Adq788240	Human ant	937	34	66.7	137	2	AA612639	AA612639	Modified
865	34	66.7	108	9	ADQ788240	Adq788240	Human ant	938	34	66.7	165	7	ADQ82845	ADQ82845	Human het
866	34	66.7	108	9	ADQ788240	Adq788240	Human ant	939	34	66.7	165	9	ADQ82845	ADQ82845	Human het
867	34	66.7	108	9	ADQ788240	Adq788240	Human ant	940	34	66.7	214	8	ADQ82845	ADQ82845	Human het
868	34	66.7	108	9	ADQ788240	Adq788240	Human ant	941	34	66.7	214	8	ADQ82845	ADQ82845	Human het
869	34	66.7	108	9	ADQ788240	Adq788240	Human ant	942	34	66.7	214	8	ADQ82845	ADQ82845	Human het
870	34	66.7	108	9	ADQ788240	Adq788240	Human ant	943	34	66.7	214	8	ADQ82845	ADQ82845	Human het
871	34	66.7	108	9	ADQ788240	Adq788240	Human ant	944	34	66.7	214	8	ADQ82845	ADQ82845	Human het
872	34	66.7	108	9	ADQ788240	Adq788240	Human ant	945	34	66.7	214	9	ADQ82845	ADQ82845	Human het
873	34	66.7	108	9	ADQ788240	Adq788240	Human ant	946	34	66.7	214	9	ADQ82845	ADQ82845	Human het
874	34	66.7	108	9	ADQ788240	Adq788240	Human ant	947	34	66.7	214	9	ADQ82845	ADQ82845	Human het
875	34	66.7	108	9	ADQ788240	Adq788240	Human ant	948	34	66.7	214	9	ADQ82845	ADQ82845	Human het
876	34	66.7	108	9	ADQ788240	Adq788240	Human ant	949	34	66.7	214	7	ADQ82845	ADQ82845	Human het
877	34	66.7	108	9	ADQ788240	Adq788240	Human ant	950	34	66.7	224	4	ADQ82845	ADQ82845	Human het
878	34	66.7	108	9	ADQ788240	Adq788240	Human ant	951	34	66.7	224	4	ADQ82845	ADQ82845	Human het
879	34	66.7	108	9	ADQ788240	Adq788240	Human ant	952	34	66.7	224	4	ADQ82845	ADQ82845	Human het
880	34	66.7	108	9	ADQ788240	Adq788240	Human ant	953	34	66.7	224	4	ADQ82845	ADQ82845	Human het
881	34	66.7	108	9	ADQ788240	Adq788240	Human ant	954	34	66.7	224	4	ADQ82845	ADQ82845	Human het
882	34	66.7	108	9	ADQ788240	Adq788240	Human ant	955	34	66.7	224	4	ADQ82845	ADQ82845	Human het
883	34	66.7	108	9	ADQ788240	Adq788240	Human ant	956	34	66.7	224	6	ADQ82845	ADQ82845	Human het
884	34	66.7	108	9	ADQ788240	Adq788240	Human ant	957	34	66.7	224	4	ADQ82845	ADQ82845	Human het
885	34	66.7	108	9	ADQ788240	Adq788240	Human ant	958	34	66.7	224	4	ADQ82845	ADQ82845	Human het
886	34	66.7	108	9	ADQ788240	Adq788240	Human ant	959	34	66.7	224	4	ADQ82845	ADQ82845	Human het
887	34	66.7	108	9	ADQ788240	Adq788240	Human ant	960	34	66.7	224	4	ADQ82845	ADQ82845	Human het
888	34	66.7	108	9	ADQ788240	Adq788240	Human ant	961	34	66.7	224	4	ADQ82845	ADQ82845	Human het
889	34	66.7	108	9	ADQ788240	Adq788240	Human ant	962	34	66.7	224	4	ADQ82845	ADQ82845	Human het
890	34	66.7	108	9	ADQ788240	Adq788240	Human ant	963	34	66.7	224	4	ADQ82845	ADQ82845	Human het
891	34	66.7	108	9	ADQ788240	Adq788240	Human ant	964	34	66.7	224	4	ADQ82845	ADQ82845	Human het
892	34	66.7	108	9	ADQ788240	Adq788240	Human ant	965	34	66.7	224	4	ADQ82845	ADQ82845	Human het
893	34	66.7	108	9	ADQ788240	Adq788240	Human ant	966	34	66.7	224	4	ADQ82845	ADQ82845	Human het
894	34	66.7	108	9	ADQ788240	Adq788240	Human ant	967	34	66.7	224	4	ADQ82845	ADQ82845	Human het
895	34	66.7	108	9	ADQ788240	Adq788240	Human ant	968	34	66.7	224	4	ADQ82845	ADQ82845	Human het
896	34	66.7	108	9	ADQ788240	Adq788240	Human ant	969	34	66.7	224	4	ADQ82845	ADQ82845	Human het
897	34	66.7	108	9	ADQ788240	Adq788240	Human ant	970	34	66.7	224	4	ADQ82845	ADQ82845	Human het
898	34	66.7	108	9	ADQ788240	Adq788240	Human ant	971	34	66.7	224	4	ADQ82845	ADQ82845	Human het
899	34	66.7	108	9	ADQ788240	Adq788240	Human ant	972	34	66.7	224	4	ADQ82845	ADQ82845	Human het
900	34	66.7	108	9	ADQ788240	Adq788240	Human ant	973	34	66.7	224	4	ADQ82845	ADQ82845	Human het

974	34	66.7	240	4	AAB46004	Aab46004 Human MUC
975	34	66.7	240	4	AAB46018	Aab46018 Human MUC
976	34	66.7	240	4	AAB46038	Aab46038 Human TP
977	34	66.7	240	4	AAB46042	Aab46042 Human TP
978	34	66.7	240	4	AAB46051	Aab46051 Human TP
979	34	66.7	240	4	AAB46008	Aab46008 Human MUC
980	34	66.7	240	4	AAB46017	Aab46017 Human MUC
981	34	66.7	240	4	AAB46021	Aab46021 Human MUC
982	34	66.7	240	4	AAB46041	Aab46041 Human TP
983	34	66.7	240	4	AAB46003	Aab46003 Human MUC
984	34	66.7	240	4	AAB46014	Aab46014 Human MUC
985	34	66.7	240	4	AAB46050	Aab46050 Human TP
986	34	66.7	240	4	AAB46006	Aab46006 Human MUC
987	34	66.7	240	4	AAB46020	Aab46020 Human MUC
988	34	66.7	240	4	AAB46039	Aab46039 Human TP
989	34	66.7	240	4	AAB46044	Aab46044 Human TP
990	34	66.7	240	4	AAB45999	Aab45999 Human MUC
991	34	66.7	240	4	AAB46047	Aab46047 Human TP
992	34	66.7	240	4	AAB46048	Aab46048 Human TP
993	34	66.7	240	4	AAB45996	Aab45996 Human MUC
994	34	66.7	240	4	AAB46019	Aab46019 Human MUC
995	34	66.7	240	4	AAB45995	Aab45995 Human MUC
996	34	66.7	240	4	AAB46005	Aab46005 Human MUC
997	34	66.7	240	4	AAB46046	Aab46046 Human TP
998	34	66.7	240	4	AAB46012	Aab46012 Human MUC
999	34	66.7	240	4	AAB46015	Aab46015 Human MUC
1000	34	66.7	240	4	AAB45991	Aab45991 Human MUC

ALIGNMENTS

RESULT 1

AAB62014

ID AAB62014 standard; peptide: 11 AA.

AC AAB62014;

DT 01-OCT-1998 (first entry)

DE Light chain variable region complementarily determining region 1.

XX Complementarily determining region; light chain variable region;

KW humanised antibody; MEM24F(ab)-8; anti-CD11a antibody;

KW human CD11a I domain; MEM24 epitope; alpha subunit;

KW lymphocyte function-associated antigen 1; LFA-1; immunosassay;

KW in vivo imaging; diagnosis; CD11a-associated disease.

XX Mus sp.

OS Homo sapiens.

XX WO9823761-A1.

PN 04-JUN-1998.

PD 20-OCT-1997; 97MO-US019041.

PE 27-NOV-1996; 96US-00757205.

PR (GETH) GENENTECH INC.

PA Jardiou PM, Presta LG;

PI WPI, 1998-322737/28.

XX New humanised anti-CD11a antibody - used in immunoassays for CD11a, and

XX also to treat conditions such as immunological or inflammatory disease.

XX Claim 8; Page 2; 66pp; English.

XX AAB62014-16 represent complementarily determining regions of the light

XX chain variable region of humanised antibody MEM24F(ab)-8. The fragments

CC were used to make a humanised anti-CD11a antibody that binds specifically

CC to the human CD11a I domain (MEM24 epitope). CD11a refers to the alpha
 CC subunit of lymphocyte function-associated antigen 1 (LFA-1) from any
 CC mammal. The humanised anti-CD11a antibodies are used to determine
 CC presence of CD11a in usual immunoassays or by in vivo imaging,
 CC particularly for diagnosis of CD11a-associated diseases (typically immune
 CC responses and inflammation such as psoriasis, Crohn's disease, rheumatoid
 CC arthritis, transplant rejection, leukaemia, etc

SQ Sequence 11 AA;

Query Match 100.0%; Score 51; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0026;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 RASKTSKYL A 11

Db 1 RASKTSKYL A 11

RESULT 2

AAB62340

ID AAB62340 standard; peptide: 11 AA.

AC AAB62340;

DT 22-JUN-2000 (first entry)

DE Humanised anti-CD11a antibody light chain CDRI SEQ ID NO:13.

XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;

XX antitumour; antiviral; inflammation; immunological response; LFA-1;

KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;

KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;

KW viral infection; transplant rejection; graft rejection.

XX Homo sapiens.

OS Mus sp.

XX US6037454-A.

PN 14-MAR-2000.

PD 20-NOV-1997; 97US-00974899.

PE 27-NOV-1996; 96US-0031971P.

PR (GETH) GENENTECH INC.

PA Jardiou PM, Presta LG;

PI WPI, 2000-282241/24.

XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.

XX inflammation and transplant rejection, contains human heavy variable

XX region complementarily determining regions.

XX Claim 4; Col 57-58; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that

XX binds specifically to the human CD11a I-domain. The Ab has anti-

XX inflammatory, immunosuppressant, antitumour and antiviral activities. The

XX Ab blocks lymphocyte function-associated antigen (LFA-1) which is

XX involved in leucocyte adhesion associated with inflammatory and

XX immunological responses. The Ab are used: (i) optionally when coupled to

XX a cytotoxin, to treat or prevent disorders mediated by lymphocyte

XX function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,

XX inflammatory bowel disease, eczema, systemic lupus erythematosus,

XX rhinitis, leukaemia, viral infections and many others, also for

XX inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for

XX tumor pretreatment; (iv) for delivery of enzymes that convert prodrugs

XX to active anticancer agent; and (v) for affinity chromatography. The Ab

XX retain about the same activity in adhesion and mixed lymphocyte response

XX assays as the murine antibodies from which they are derived. The murine

CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
 CC sequence represents the light chain variable region CDR1 of the humanised
 CC anti-CD11a Ab
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 51; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASKTISKYLA 11
 Db 1 RASKTISKYLA 11
 RESULT 3
 ADG39001
 ID ADG39001 standard; peptide; 11 AA.
 XX
 AC ADG39001;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Humanised Mouse anti-CD11a antibody light chain variable region CDR1.
 XX
 KM Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
 KM VL; cluster of differentiation 11a; mixed lymphocyte response assay;
 KM Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 KM ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 KM psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 KM rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KM diabetes mellitus; prodrug activating enzyme; humanised;
 KM complementarity determining region; CDR.
 XX
 OS Synthetic.
 OS Mus sp.
 PN US2003207336-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 28-FEB-2001; 2001US-00795798.
 XX
 PR 27-NOV-1996; 96US-0031971P.
 PR 20-NOV-1997; 97US-00974899.
 PR 20-OCT-1999; 99US-00420745.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-051511/05.
 XX
 PT Humanized anti-CD11a antibody useful for treating lymphocyte function-
 PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 XX
 PS Claim 8; SEQ ID NO 13; 43pp; English.
 XX
 CC The invention relates to a humanised anti-cluster of differentiation
 CC (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 CC a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the antibody by culturing the cell so that the
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The

CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is a CDR (complementarity determining region) of the
 CC light chain variable region (VL) of the humanised mouse anti-CD11a I
 CC domain monoclonal antibody MHM24.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 51; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASKTISKYLA 11
 Db 1 RASKTISKYLA 11
 RESULT 4
 ADR03416
 ID ADR03416 standard; peptide; 11 AA.
 XX
 AC ADR03416;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MHM24 CDR-11 peptide.
 XX
 KM CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KM rhinovirus infection; inflammatory skin disease; psoriasis;
 KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KM adult respiratory distress syndrome; allergic disease; eczema;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculosis; sarcoidosis; polyomyelitis;
 KM chronic obstructive pulmonary disease; poison ivy; poison oak;
 KM skin hypersensitivity disorder; lymphocytic leukaemia; hairy cell leukaemia;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD11a monoclonal antibody; MHM24; variable light chain;
 KM VL; murine; human; fusion protein; complementarity determining region;
 KM CDR.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 PN US2004146507-A1.
 XX
 PD 29-JUL-2004.
 XX
 PF 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 53; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful

for treating and preventing infectious diseases such as human immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin disease such as psoriasis, inflammatory bowel diseases such as Crohn's disease and ulcerative colitis, adult respiratory distress syndrome, allergic diseases such as eczema and asthma, autoimmune diseases such as rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes mellitus, Reynaud's syndrome, immunological diseases such as tuberculosis, sarcoidosis, polyomyelitis and chronic obstructive pulmonary disease (COPD), CNS inflammatory disorder, skin hypersensitivity disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is humanised murine anti-human CD11a monoclonal antibody (MHM24) CDR-L1 peptide. This sequence is used in the exemplification of the invention.

OY	1 RASKTISKYLÄ 11
D6	1 RASKTISKYLÄ 11

RESULT 5
AAW62017
ID AAW62017 standard; peptide; 108 AA

CC	Leukaemia, etc
XX	
SQ	Sequence 108 AA;

Qy	1	RASKTISKYLA	11
Db	24	RASKTISKYLA	34

RESULT 6
AAW63528
ID AAW63528 standard; protein; 108 AA

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 |||||
 DB 24 RASKTISKYLA 34

RESULT 7

AAW63529
 ID AAW63529 standard; protein; 108 AA.

XX AAW63529;
 AC AAW63529;
 XX
 XX
 DT 06-OCT-1998 (first entry)
 XX
 XX

DE Humanised MEM24 light chain.

XX Antibody mutant production; species-dependent antibody; malignancy;
 KW infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KW intercellular adhesion molecule-1; inflammatory diseases; CD11a; therapy;
 KW autoimmune disease; transplant rejection; tumour cell invasion;
 KW human immune deficiency virus infection; light chain.

XX Synthetic.
 OS
 XX
 XX

PN MO9823746-A1.
 XX
 XX

PD 04-JUN-1998.
 XX
 XX

PF 29-OCT-1997; 97WO-US020169.
 XX
 XX

PR 27-NOV-1996; 96US-00756150.
 XX
 XX

PA (GETH) GENENTECH INC.
 XX
 XX

PI Jardieu PM, Presta LG;
 XX
 XX

DR WPI; 1998-322726/28.
 XX
 XX

PT Mutants of species-dependent antibodies with affinity for non-human
 mammalian antigen - greater than for parent antibody, particularly used
 for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 directed against CD11a.
 PT
 XX
 XX

PS Disclosure; Page 53; 71pp; English.

XX This sequence represents the light chain of the humanised antibody MEM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 CC
 XX

SQ Sequence 108 AA;

Query Match 100.0%; Score 51; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 |||||
 DB 24 RASKTISKYLA 34

RESULT 8

AAW82344
 ID AAW82344 standard; protein; 108 AA.

XX AAW82344;
 AC AAW82344;
 XX
 XX

DT 22-JUN-2000 (first entry)
 XX
 XX

DE Murine MEM24 light chain amino acid sequence SEQ ID NO:1.

XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 KW antitumour; antiviral; inflammation; immunological response; LFA-1;
 KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
 KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KW viral infection; transplant rejection; graft rejection.

XX Mus sp.
 OS
 XX

PN US6037454-A.
 XX
 XX

PD 14-MAR-2000.
 XX
 XX

PF 20-NOV-1997; 97US-00974899.
 XX
 XX

PR 27-NOV-1996; 96US-0031971P.
 XX
 XX

PA (GETH) GENENTECH INC.
 XX
 XX

PI Jardieu PM, Presta LG;
 XX
 XX

DR WPI; 2000-282241/24.
 XX
 XX

PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 inflammation and transplant rejection, contains human heavy variable
 region complementarily determining regions.
 PT
 XX
 XX

PS Example; Fig 1; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that
 CC binds specifically to the human CD11a I-domain. The Ab has anti-
 CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
 CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 CC involved in leucocyte adhesion associated with inflammatory and
 CC immunological responses. The Ab are used: (i) optionally when coupled to
 CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
 CC rhinitis, leukaemia, viral infections and many others, also for
 CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine
 CC anti-CD11a antibody MEM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MEM24 had IC50 0.13 nM. The present
 CC sequence represents the amino acid sequence of murine MEM24 light chain,
 CC which is used in the exemplification of the present invention
 CC
 XX

SQ Sequence 108 AA;

Query Match 100.0%; Score 51; DB 3; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 |||||
 DB 24 RASKTISKYLA 34

RESULT 9

ID	AA82343
ID	AA82343 standard; protein; 108 AA.
XX	
AC	AA82343;
XX	
DT	22-JUN-2000 (first entry)
XX	
DE	Humanised anti-CD11a antibody light chain variable region SEQ ID NO:2.
XX	
KW	Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant; antitumour; antiviral; inflammation; immunological response; LFA-1; lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema; inflammatory bowel disease; systemic lupus erythematosus; leukaemia; viral infection; transplant rejection; graft rejection.
KM	
XX	
OS	Homo sapiens.
OS	Mus sp.
XX	
PN	US6037454-A.
XX	
PD	14-MAR-2000.
XX	
PF	20-NOV-1997; 97US-00974839.
XX	
PR	27-NOV-1996; 96US-0031971P.
XX	
PA	(GETH) GENENTECH INC.
PI	Jardieu PM, Presta LG;
DR	WPI, 2000-282241/24.
XX	
PT	New humanized anti-CD11a antibody, useful for treating or preventing e.g. inflammation and transplant rejection, contains human heavy variable region complementarily determining regions.
PS	Claim 5; Fig 1; 38pp; English.
XX	
CC	The present invention describes a humanised anti-CD11a antibody (Ab) that binds specifically to the human CD11a I-domain. The Ab has anti- inflammatory, immunosuppressant, antitumor and antiviral activities. The Ab blocks lymphocyte function-associated antigen (LFA-1) which is involved in leucocyte adhesion associated with inflammatory and immunological responses. The Ab are used: (i) optionally when coupled to a cytotoxin, to treat or prevent disorders mediated by lymphocyte function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis, inflammatory bowel disease, eczema, systemic lupus erythematosus, rhinitis, leukaemia, viral infections and many others, also for inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs to active anticancer agent; and (v) for affinity chromatography. The Ab retain about the same activity in adhesion and mixed lymphocyte response assays as the murine antibodies from which they are derived. The murine anti-CD11a antibody MRM24 has IC50 0.09 nM for preventing adhesion between Jurkat cells (expressing LFA-1) and normal epidermal keratinocytes that express ICAM-1 (intracellular adhesion molecule-1). The fully humanized version of MRM24 had IC50 0.13 nM. The present sequence represents the light chain variable region of the humanised anti- CD11a Ab
XX	
SQ	Sequence 108 AA;

Query Match Similarity	100.0%	Score 51;	DB 3;	Length 108;
Best Local Similarity	100.0%	Pred. NO. 0.033;		
Matches 11; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0
OY	1 RASKTISKYLA	11		
Db	24 RASKTISKYLA	34		

RESULT 1
ADG38989

ID	ADG38989 standard; protein; 108 AA.
XX	
AC	ADG38989;
DT	
XX	
DE	26-FEB-2004 (first entry)
XX	
XX	Mouse anti-CD11a antibody light chain variable region.
KM	Mouse; CD11a, I-domain; monoclonal antibody; light chain variable region;
KM	VL; cluster of differentiation 11a; mixed lymphocyte response assay;
KM	Jurkat cell; epidermal keratinocytes; intercellular adhesion molecule;
KM	ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
KM	psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
KM	rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KM	diabetes mellitus; prodrug activating enzyme.
XX	
OS	Mus sp.
XX	
PN	US200307336-A1.
XX	
PD	06-NOV-2003.
XX	
PF	28-FEB-2001; 2001US-00795798.
XX	
PR	27-NOV-1996; 96US-0031971P.
PR	20-NOV-1997; 97US-00974899.
PR	20-OCT-1999; 99US-00420745.
XX	
PA	(GETH) GENENTECH INC.
PI	Jardieu PM, Presta LG;
DR	WPI; 2004-051511/05.
XX	
PT	Humanised anti-CD11a antibody useful for treating lymphocyte function-
PT	associated antigen mediated disorder e.g. psoriasis, Crohns disease,
PT	ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
PS	
XX	Example; SEQ ID NO 1; 43bp; English.
XX	
CC	The invention relates to a Humanised anti-cluster of differentiation
CC	(CD11a) antibody having specificity to human CD11a I-domain or CD11a with
CC	a kd value of not more than 1x10 ⁻⁸ M, or concentration for 50 %
CC	inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
CC	response assay or for preventing adhesion of Jurkat cells to normal human
CC	epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
CC	-1. Also included are a kit comprising the antibody and instructions for
CC	use to detect the CD11a protein, an isolated nucleic acid encoding the
CC	antibody, a vector comprising the nucleic acid, a host cell comprising
CC	the vector and producing the antibody by culturing the cell so that the
CC	antibody is expressed. The antibody binds to epitope M24 on CD11a. The
CC	antibody is useful for determining the presence of CD11a protein and for
CC	treating lymphocyte function-associated antigen 1 mediated disorder such
CC	as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
CC	rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
CC	and diabetes mellitus. The antibody is useful when conjugated to a
CC	prodrug activating enzyme, or as an affinity purification agent. The
CC	present sequence is the light chain variable region (VL) of the wild-type
CC	mouse anti-CD11a I domain monoclonal antibody M2M24.
XX	
5Q	Sequence 108 AA;

Query Match	100.0%	Score 51	DB 8	Length 106
Best Local Similarity	100.0%	Pred. No. 0.033		
Matches 11; Conservative	0	Mismatches	0	Gaps 0
QY	1 RAKTISKYLA	11		
DB	24 RAKTISKYLA	34		

RESULT 11
ADG38990

ID ADG38990 standard; protein; 108 AA.

XX ADG38990;

DT 26-FEB-2004 (first entry)

DE Humanised Mouse anti-CD11a antibody light chain variable region.

XX Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
XX VL; cluster of differentiation 11a; mixed lymphocyte response assay;
XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; produg activating enzyme; humanised.

OS Synthetic.
OS Mus sp.

XX US2003207336-A1.

XX 06-NOV-2003.

XX 28-FEB-2001; 2001US-00795798.

XX 27-NOV-1996; 96US-0031971P.

XX 20-NOV-1997; 97US-00974899.

XX 20-OCT-1999; 99US-00420745.

XX (GETH) GENENTECH INC.

XX Jarden PM, Presta LG;

XX WPI; 2004-051511/05.

XX Humanized anti-CD11a antibody useful for treating lymphocyte function-
XX associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
XX ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

XX Claim 9; SEQ ID NO 2; 43pp; English.

XX The invention relates to a Humanised anti-cluster of differentiation
XX (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
XX a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
XX inhibition (IC50) (nm) value of not more than 1 nm in mixed lymphocyte
XX response assay or for preventing adhesion of Jurkat cells to normal human
XX epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
XX -1. Also included are a kit comprising the antibody and instructions for
XX use to detect the CD11a protein, an isolated nucleic acid encoding the
XX antibody, a vector comprising the nucleic acid, a host cell comprising
XX the vector and producing the antibody by culturing the cell so that the
XX antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The
XX antibody is useful for determining the presence of CD11a protein and for
XX treating lymphocyte function-associated antigen 1 mediated disorder such
XX as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
XX rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
XX and diabetes mellitus. The antibody is useful when conjugated to a
XX produg activating enzyme, or as an affinity purification agent. The
XX present sequence is the light chain variable region (VL) of the humanised
XX mouse anti-CD11a I domain monoclonal antibody MHM24.

XX Sequence 108 AA;

XX Query Match 100.0%; Score 51; DB 8; Length 108;

XX Best Local Similarity 100.0%; Pred. No. 0.033;

XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 RASKITSKYA 11

XX 24 RASKITSKYA 34

XX RESULT 12

ID ADR03365 standard; protein; 108 AA.

XX ADR03365;

DT 21-OCT-2004 (first entry)

DE Humanised MHM24 F(ab)-8 antibody variable light chain protein.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
XX rhinovirus infection; inflammatory skin disease; psoriasis;
XX inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX adult respiratory distress syndrome; allergic disease; eczema; asthma;
XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
XX SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
XX tuberculosis; sarcoidosis; polymyositis;
XX chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
XX skin hypersensitivity disorder; poison ivy; poison oak;
XX B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
XX graft versus host disease; cancer; gene therapy;
XX murine anti-human CD11a monoclonal antibody; MHM24; variable light chain;
XX VL; murine; human; fusion protein.

OS Mus sp.

OS Homo sapiens.

XX US2004146507-A1.

XX 29-JUL-2004.

XX 03-DEC-2003; 2003US-00727737.

XX 27-NOV-1996; 96US-0031945P.

XX 20-NOV-1997; 97US-00975329.

XX (GETH) GENENTECH INC.

XX Jarden PM, Presta LG;

XX WPI; 2004-552640/53.

XX New antibody mutant of a species-dependent antibody, useful for treating
XX PT and preventing infectious diseases, psoriasis, inflammatory bowel
XX disease, allergic conditions, autoimmune diseases, or cancer.

XX Example; SEQ ID NO 2; 54pp; English.

XX The present invention relates to an antibody mutant of a species-
XX dependent antibody with beneficial properties. The invention is useful
XX for treating and preventing infectious diseases such as human
XX immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
XX disease such as psoriasis, inflammatory bowel diseases such as Crohn's
XX disease and ulcerative colitis, adult respiratory distress syndrome,
XX allergic diseases such as eczema and asthma, autoimmune diseases such as
XX rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
XX mellitus, Reynaud's syndrome, immunological diseases such as
XX tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
XX disease (COPD), CNS inflammatory disorder, skin hypersensitivity
XX disorders such as poison ivy and poison oak, B-cell malignancies such as
XX chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
XX disease and cancer. The invention is also useful in gene therapy. The
XX present sequence is humanised murine anti-human CD11a monoclonal antibody
XX (MHM24) F(ab)-8 variable light chain protein. This sequence is used in
XX the exemplification of the invention.

XX Sequence 108 AA;

XX Query Match 100.0%; Score 51; DB 8; Length 108;

XX Best Local Similarity 100.0%; Pred. No. 0.033;

XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 RASKITSKYA 11

Db 24 RASKTISKYLA 34

RESULT 13

ADRO3364 ID ADR03364 standard; protein; 108 AA.

AC ADR03364;

DT 21-OCT-2004 (first entry)

DE Murine MEM24 antibody variable light chain protein.

CD11a antibody; human immunodeficiency virus infection; HIV infection;
rhinovirus infection; inflammatory skin disease; psoriasis;
inflammatory bowel disease; Crohn's disease; ulcerative colitis;
adult respiratory distress syndrome; allergic disease; eczema; asthma;
autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
tuberculosis; sarcoidosis; polymyositis;
chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
skin hypersensitivity disorder; poison ivy; poison oak; hairy cell leukaemia;
B-cell malignancy; chronic lymphocytic leukaemia; cancer; gene therapy;
graft versus host disease; cancer; murine anti-human CD11a monoclonal antibody; MEM24; variable light chain;
VL; murine.

OS Mus sp.

PN US2004146507-A1.

PD 29-JUL-2004.

PF 03-DEC-2003; 2003US-00727737.

PR 27-NOV-1996; 96US-0031945P.

PR 20-NOV-1997; 97US-00975329.

PA (GETH) GENENTECH INC.

PI Jardieu PM, Presta LG;

DR WPI; 2004-552640/53.

PT New antibody mutant of a species-dependent antibody, useful for treating
PT and preventing infectious diseases, psoriasis, inflammatory bowel
PT disease, allergic conditions, autoimmune diseases, or cancer.
XX Example; SEQ ID NO 1; 54pp; English.

CC The present invention relates to an antibody mutant of a species-
CC dependent antibody with beneficial properties. The invention is useful
CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such as
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as
CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC disorders such as poison ivy and poison oak, B-cell malignancies such as
CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is murine anti-human CD11a monoclonal antibody (MEM24)
CC variable light chain protein. This sequence is used in the
CC exemplification of the invention.

XX Sequence 108 AA;

Query Match 100.0%; Score 51; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RASKTISKYLA 11
Db 24 RASKTISKYLA 34

RESULT 14

ADM38457 ID ADM38457 standard; protein; 108 AA.

AC ADM38457;

DT 24-MAR-2005 (first entry)

DE CD11a light chain variable region #2.

monoclonal antibody; CD11a; light-chain variable region;
heavy-chain variable region.

OS Homo sapiens.

PN CN1439651-A.

PD 03-SEP-2003.

PF 20-FEB-2002; 2002CN-00110866.

PR 20-FEB-2002; 2002CN-00110866.

PA (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.

PI Wang H, Wang J;

DR WPI; 2004-169719/17.

PT Recombinant human CD11a monoclonal antibody and its preparation and
PT medicinal composition.
XX Claim 1; Page 14; 16pp; Chinese.

CC The present invention relates to a recombinant monoclonal antibody for
CC human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
CC No.5 in light-chain variable region and the amino acid sequence shown by
CC SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
CC bioactivity and the expression in host cell are greatly increased. The
CC DNA molecule for coding the antibody, its preparation process and the
CC medicinal composition containing it are also disclosed. The present
CC sequence represents a light chain variable region of human CD11a.

XX Sequence 108 AA;

Query Match 100.0%; Score 51; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
Db 24 RASKTISKYLA 34

RESULT 15
ADX80645 ID ADX80645 standard; protein; 108 AA.

AC ADX80645;

DT 05-MAY-2005 (first entry)

DE Humanized CD11a variable light chain amino acid sequence, seq id 5.

XX Protein purification; leaching; protein A affinity chromatography; CD11a;
KW antibody.

XX OS Synthetic.
XX PN US2005038231-A1.
XX PD 17-FEB-2005.
XX PF 24-JUN-2004; 2004US-00877532.
XX PR 28-JUL-2003; 2003US-0490500P.
XX PA (GETH) GENENTECH INC.
XX PI Fahrner RL, Laverdiere A, McDonald PJ, Oleary RM;
XX DR WPI; 2005-172327/18.
XX PT Purifying a protein, e.g. antibody or immunoadhesin, comprises reducing
XX PT the temperature of a composition subjected to protein A affinity
XX PT chromatography to 3-20 degrees C, where protein A leaching is reduced.
XX PS Disclosure; SEQ ID NO 5; 27pp; English.
XX XX
XX CC The invention relates to a method of purifying a protein which comprises
XX CC a CH2/CH3 region by protein A affinity chromatography. The method
XX CC involves reducing the temperature of a composition comprising the protein
XX CC and one or more impurities subjected to protein A affinity chromatography
XX CC to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably
XX CC the protein is antibody. The antibody is selected from Trautzumab,
XX CC humanized 2C4, humanized CD1a antibody, and humanized VEGF antibody.
XX CC Preferably, the antibody binds HER2 antigen, where the antibody is
XX CC Trautzumab or humanized 2C4. The protein is an immunoadhesin.
XX CC Specifically, a TNP receptor immunoadhesin. The methods are useful for
XX CC purifying a protein, which comprises a CH2/CH3 region by protein A
XX CC affinity chromatography and for reducing leaching of protein A during
XX CC protein A affinity chromatography. The current sequence represents the
XX CC variable light chain amino acid sequence of CD1a.
XX SQ Sequence 108 AA;
XX
XX Query Match 100.0%; Score 51; DB 9; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 0.033;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RASKTISKYLA 11
XX |||||
XX 24 RASKTISKYLA 34
XX DB
XX
XX RESULT 16
XX AAY29449
XX ID AAY29449 standard; protein; 109 AA.
XX XX
XX AC AAY29449;
XX XX
XX DT 05-OCT-1999 (first entry)
XX XX
XX DE Human light chain kappa-I consensus framework.
XX XX
XX KM Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
XX KM diagnosis; inflammatory disorder; conjugate; immunoglobulin;
XX KM fusion protein.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO93779-A1.
XX XX
XX PD 29-JUL-1999.
XX XX
XX PF 19-JAN-1999; 99WO-US001081.
XX XX
XX PT 22-JAN-1998; 98US-00012116.
XX PR 20-FEB-1998; 98WO-US003337.

PR 24-JUL-1998; 98US-00121952.
PR 24-JUL-1998; 98US-00122513.
XX XX
XX PA (GETH) GENENTECH INC.
XX XX
XX PI Hseil V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z, Zapata GA;
XX DR WPI; 1999-469134/39.
XX XX
XX PT New conjugates of nonproteaceous polymers with antibody fragments, used
XX PT for treating inflammatory disorders.
XX PS Disclosure; Fig 29; 36pp; English.
XX XX
XX CC The present invention describes a novel conjugate having one or more
XX CC antibody fragments covalently attached to one or more nonproteaceous
XX CC polymer molecules, where the apparent size of the conjugate is at least
XX CC about 500 kDa. Conjugates of antibody fragments which bind the human
XX CC interleukin (IL) 8 with a nonproteaceous polymer can be used for
XX CC treating inflammatory disorders e.g. acute lung injury, ischaemic
XX CC reperfusion disorder, and autoimmune diseases. They can also be used for
XX CC treating e.g. inflammatory skin diseases including psoriasis and atopic
XX CC dermatitis, systemic scleroderma and sclerosis, and asthmatic diseases.
XX CC The conjugates can also be used as reagents in an animal model system for
XX CC in vivo study of the biological functions of the antigen recognised by
XX CC the conjugate. The present sequence represents the human light chain
XX CC kappa-I consensus framework from the present invention
XX SQ Sequence 109 AA;
XX
XX Query Match 100.0%; Score 51; DB 2; Length 109;
XX Best Local Similarity 100.0%; Pred. No. 0.034;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RASKTISKYLA 11
XX |||||
XX 24 RASKTISKYLA 34
XX DB
XX
XX RESULT 17
XX AAY77752
XX ID AAY77752 standard; protein; 109 AA.
XX XX
XX AC AAY77752;
XX XX
XX DT 06-JUN-2000 (first entry)
XX XX
XX DE Human light chain kl consensus framework.
XX XX
XX KM Interleukin-8; IL-8; monoclonal antibody; Mb; anti-IL-8; 6G4.2.5V11N35A;
XX KM inflammatory disorder; adult respiratory distress syndrome; chimeric;
XX KM affinity purification; 6G4.2.5.
XX XX
XX OS Homo sapiens.
XX XX
XX PN US6025158-A.
XX XX
XX PD 15-FEB-2000.
XX XX
XX PF 20-FEB-1998; 98US-00027449.
XX XX
XX PR 21-FEB-1997; 97US-0038664P.
XX PR 22-JAN-1998; 98US-0074330P.
XX XX
XX PA (GETH) GENENTECH INC.
XX XX
XX PI Presta LG, Leong SR, Gonzalez TN;
XX XX
XX DR WPI; 2000-181809/16.
XX XX
XX PT New nucleic acid molecule encodes a polypeptide which is an anti-
XX PT interleukin-8 monoclonal antibody or antibody fragment useful for the
XX PT production of anti-interleukin-8 monoclonal antibodies or fragments.

XX Example; Fig 29; 188bp; English.
PS
XX The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
CC (Mab). The anti-IL-8 Mab comprises a sequence containing the CDRs
CC (complementarily determining regions) of the humanized anti-IL-8
CC 6G4.2.5V11N35A light chain; and amino acids 24-253 of the humanized anti-
CC IL-8 6G4.2.5V11N35A heavy chain. The anti-IL-8 Mabs and fragments can be
CC used in diagnosis, for affinity purification of IL-8 from recombinant
CC cell culture or natural sources and for the treatment of inflammatory
CC disorders e.g. adult respiratory distress syndrome. Nucleic acids
CC encoding the anti-IL-8 Mab can be associated in a vector with another
CC gene encoding another protein or protein fragment to produce a fusion
CC protein which can make isolation and/or purification of the protein an
CC easier process
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 51; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||
|||
Db 24 RASKTISKYLA 34

RESULT 18
AAB30309
ID AAB30309 standard; protein; 109 AA.
XX
AC AAB30309;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human light chain kappa consensus framework SEQ ID NO: 47.
XX
KW Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
KW adult respiratory distress syndrome; multiple organ failure;
KW bacterial pneumonia; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
PN US6133426-A.
XX
PD 17-OCT-2000.
XX
PF 20-FEB-1998; 98US-00026985.
XX
PT 21-FEB-1997; 97US-0038664P.
XX
PR 22-JAN-1998; 98US-0074330P.
XX
PA (GETH) GENENTECH INC.
XX
PI Presta LG, Leong SR, Gonzalez TN;
XX
DR WPI; 2000-686027/67.
XX
PT Humanized anti-interleukin 8 monoclonal antibody variant useful for
PT treating inflammatory disorders, such as adult respiratory distress
PT syndrome, hypovolemic shock and ulcerative colitis.
XX
PS Disclosure; Col 161-162; 240pp; English.
XX
CC The present invention provides a number of humanised monoclonal anti-IL-8
CC antibodies which can be used in the diagnosis and treatment of
CC inflammatory disorders, including adult respiratory distress syndrome,
CC septic shock, multiple organ failure, bacterial pneumonia and
CC inflammatory bowel disease. The present sequence comprises one of the
CC antibodies of the invention
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 51; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||
|||
Db 24 RASKTISKYLA 34

RESULT 19
ABU13786
ID ABU13786 standard; protein; 109 AA.
XX
AC ABU13786;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human light chain kappa consensus framework sequence.
XX
DE Antibody; monoclonal antibody; 5.12.14; 6G4.2.5; interleukin-8; mab;
KW antiinflammatory; respiratory; acute lung injury; polyethylene glycol;
KW PEG; lung injury; adult respiratory distress syndrome; ARDS; asthma;
KW inflammatory disease; inflammatory bowel disease; psoriasis; sclerosis;
KW ischaemic reperfusion disorder; stroke; multiple sclerosis; meningitis;
KW osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis;
KW alcoholic hepatitis; cystic fibrosis; human.
XX
OS Homo sapiens.
XX
PN US6468532-B1.
XX
PD 22-OCT-2002.
XX
PF 20-JAN-1999; 99US-00234340.
XX
PT 22-JAN-1998; 98US-0074330P.
XX
PR 20-FEB-1998; 98US-0075467P.
XX
PR 24-JUL-1998; 98US-0094003P.
XX
PR 24-JUL-1998; 98US-0094013P.
XX
PA (GETH) GENENTECH INC.
XX
PI Hseil V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
XX
DR WPI; 2003-138230/13.
XX
PT Treating acute lung injury in mammal by administering to mammal a 500 kD
PT conjugate comprising F(ab')₂ antibody fragment that binds to human
PT interleukin-8, covalently attached to one or two polyethylene glycol
PT molecules.
XX
PS Example G; Fig 29; 259pp; English.
XX
CC The invention relates to treating acute lung injury in a mammal,
CC comprising administering to the mammal an effective amount of a conjugate
CC of a single antibody fragment covalently attached to 1 or 2 polyethylene
CC glycol (PEG) molecules, where the antibody fragment is a F(ab')₂
CC comprising: (a) first chain that is either a light chain or a heavy chain
CC ; (b) a first opposite chain that is either a heavy chain opposite the
CC first light chain or a light chain opposite the first heavy chain; (c) a
CC second chain that is either a light chain or a heavy chain; and (d) a
CC second opposite chain that is either a heavy chain opposite the second
CC light chain or a light chain opposite the second heavy chain; where every
CC PEG molecule is covalently attached to a first cysteine residue in the
CC first or second chain that would ordinarily form a disulphide bridge with
CC a second cysteine residue in the first or second opposite chain, where
CC the disulphide bridge is avoided by substitution of another amino acid
CC residue for the second cysteine residue in the first or second opposite
CC chain, where the F(ab')₂ comprises an antigen binding site that binds to
CC human interleukin-8 (IL-8), and where the apparent site of the conjugate
CC is at least about 500 kD. The antigen binding sites may be derived from
CC murine monoclonal antibodies 5.12.14 or 6G4.2.5. The method is useful for
CC treating lung injury, including adult respiratory distress syndrome

CC (ARDS) in a mammal and inflammatory diseases (such as asthma,
 CC inflammatory bowel disease, psoriasis and sclerosis), ischemic
 CC reperfusion disorders, stroke, multiple sclerosis, meningitis,
 CC osteoarthritis, septic shock, autoimmune disease (e.g. rheumatoid
 CC arthritis), alcoholic hepatitis, cystic fibrosis and many other diseases
 CC and disorders listed in the specification. The present sequence
 CC represents a human antibody sequence included for comparison with the
 CC mouse humanised monoclonal antibody sequences

XX Sequence 109 AA;

XX
 XX Query Match 100.0%; Score 51; DB 6; Length 109;
 XX Best Local Similarity 100.0%; Pred. No. 0.034;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
 |||||
 |||||
 Db 24 RASKTISKYLA 34

RESULT 20
 ABUS9499 standard; protein; 109 AA.

XX
 XX AC ABUS9499;
 XX
 XX DT 22-APR-2003 (first entry)
 XX
 XX DE Human light chain kappa consensus framework.

XX
 XX Interleukin-8; IL-8; humanised antibody; antibody; 5.12.14; 6G4.2.5;
 KW inflammatory disorder; psoriasis; atopic dermatitis; sclerosis;
 KW systemic scleroderma; inflammatory bowel disease; Crohn's disease;
 KW ulcerative colitis; ischaemia; reperfusion; myocardial infarction;
 KW stroke; adult respiratory distress syndrome; rheumatoid arthritis;
 KW alcoholic hepatitis; acute lung injury; asthma; cerebral oedema;
 KW myocardial ischaemia; cranial trauma; asphyxia; Behcet's disease;
 KW dermatomyositis; polymyositis; multiple sclerosis; meningitis;
 KW encephalitis; uveitis; osteoarthritis; lupus nephritis; trauma;
 KW autoimmune disease; Sjogren's syndrome; vasculitis; septicemia;
 KW central nervous system inflammatory disorder; sepsis; sarcoidosis;
 KW multiple organ injury syndrome; bacterial pneumonia; glomerulonephritis;
 KW inflammation of the lung; human.

XX
 XX OS Homo sapiens.
 XX
 XX PN US6458355-B1.
 XX
 XX PD 01-OCT-2002.
 XX
 XX PF 24-JUL-1998; 98US-00121952.
 XX
 XX PR 22-JAN-1998; 98US-0074330P.
 XX
 XX PR 20-FEB-1998; 98US-0075467P.
 XX
 XX PA (GETH) GENENTECH INC.
 XX
 XX PI Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 XX
 XX DR WPI; 2003-208759/20.
 XX
 XX PT Treating inflammatory disorder in a mammal, involves administering a
 PT conjugate of polyethylene glycol and a single antibody fragment
 PT comprising antigen binding site that binds to human interleukin-8, to
 PT mammal.
 XX
 XX PS Example 3G; Fig 29; 259pp; English.
 XX
 XX CC The invention relates to treating an inflammatory disorder in a mammal,
 CC comprising administering to the mammal, an effective amount of a
 CC conjugate of a single antibody fragment (e.g. the heavy or light chains
 CC of the humanised mouse monoclonal antibodies 5.12.14 and 6G4.2.5, which
 CC also have their intramolecular disulphide bridges ablated by substitution

CC mutations) covalently attached to one or two polyethylene glycol (PEG)
 CC molecules. The antibodies comprise an antigen binding site that binds to
 CC human interleukin-8 (IL-8), and the apparent size of the conjugate is at
 CC least 500 kDa. The method is useful for treating an inflammatory disorder
 CC e.g. ischemic reperfusion disorder such as surgical tissue reperfusion
 CC injury, myocardial ischaemia or myocardial infarction, or hypovolemic
 CC shock, in a mammal e.g. human. The method is useful for treating
 CC inflammatory disorders including psoriasis, atopic dermatitis, systemic
 CC scleroderma and sclerosis, responses associated with inflammatory bowel
 CC disease, ischemic reperfusion disorders, myocardial ischemic
 CC conditions, cerebral oedema secondary to stroke, cranial trauma,
 CC asphyxia, adult respiratory distress syndrome, acute-lung injury,
 CC Behcet's disease, dermatomyositis, polymyositis, multiple sclerosis,
 CC dermatitis, meningitis, encephalitis, uveitis, osteoarthritis, lupus
 CC nephritis, autoimmune diseases such as rheumatoid arthritis, Sjogren's
 CC syndrome, vasculitis, central nervous system inflammatory disorder,
 CC multiple organ injury syndrome secondary to septicemia or trauma,
 CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
 CC mediated diseases including glomerulonephritis, sepsis, sarcoidosis,
 CC immunopathologic responses to tissue/organ transplantation, inflammations
 CC of the lung, inflammatory bowel disease such as ulcerative colitis and
 CC asthma. The present sequence represents the light or heavy chain of human
 CC IgG, used to design the humanising mutations in the two mouse antibodies

XX
 XX Sequence 109 AA;

XX
 XX Query Match 100.0%; Score 51; DB 6; Length 109;
 XX Best Local Similarity 100.0%; Pred. No. 0.034;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
 |||||
 |||||
 Db 24 RASKTISKYLA 34

RESULT 21
 AAE39082 standard; protein; 109 AA.

XX
 XX AC AAE39082;
 XX
 XX DT 18-DEC-2003 (first entry)
 XX
 XX DE Human light chain kappa consensus framework protein.

XX
 XX Interleukin-8 mediated disease; adult respiratory distress syndrome; IL;
 KW bacterial pneumonia; inflammatory bowel disease; hypovolemic shock; ARDS;
 KW ulcerative colitis; ischemic reperfusion injury; myocardial infarction;
 KW acute lung injury; inflammatory disease; asthma; antibody; human.

XX
 XX OS Homo sapiens.
 XX
 XX PN US2003021790-A1.
 XX
 XX PD 30-JAN-2003.
 XX
 XX PF 29-NOV-2000; 2000US-00726258.
 XX
 XX PR 22-JAN-1998; 98US-0074330P.
 XX
 XX PR 20-FEB-1998; 98US-0075467P.
 XX
 XX PR 24-JUL-1998; 98US-0094003P.
 XX
 XX PR 20-JAN-1999; 99US-00234182.
 XX
 XX PA (GETH) GENENTECH INC.
 XX
 XX PI Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
 XX
 XX DR WPI; 2003-605694/57.
 XX
 XX PT Novel conjugates comprising antibody fragments covalently attached to
 PT nonproteinaceous polymer molecules, useful for treating inflammatory
 PT diseases, acute lung injury, ischemic reperfusion injury, pneumonia and

PT asthma.
XX
XX Example; Fig 29; 266pp; English.
XX
CC The invention relates to novel conjugates comprising antibody fragments
CC covalently attached to nonproteinaceous polymer molecules. The invention
CC is useful for treating interleukin (IL)-8 mediated diseases or disorders
CC such as inflammatory diseases, acute lung injury e.g. adult respiratory
CC distress syndrome (ARDS), ischemic reperfusion injury e.g. myocardial
CC infarction, hypovolemic shock, inflammatory bowel disease e.g. ulcerative
CC colitis, bacterial pneumonia and asthma. The invention is also useful as
CC a reagent in an animal model system for in vivo study of the biological
CC functions of the antigen recognised by the conjugate. The present
CC sequence is human light chain kappa consensus framework protein. This
CC sequence is used in the exemplification of the invention
SQ Sequence 109 AA;
Query Match 100.0%; Score 51; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKTISKYLA 11
DB 24 RASKTISKYLA 34
RESULT 22
ADFI1669
ID ADFI1669 standard; protein; 214 AA.
XX
XX ADFI1669;
XX
XX 26-FEB-2004 (first entry)
XX
XX anti-CD11a rhumAb light chain amino acid sequence #SEQ ID 3.
XX
XX Purifying; target protein; non-affinity purification;
XX high-performance tangential flow filtration; HPRFF; pharmaceutical;
XX diagnostic; therapeutic; antibody.
XX
XX Synthetic.
XX
XX WO2003102132-A2.
XX
XX 11-DEC-2003.
XX
XX 25-APR-2003; 2003WO-US013054.
XX
XX 26-APR-2002; 2002US-0375953P.
XX
XX (GETH) GENENTECH INC.
XX
XX Fahner RL, Folman D, Lebretton B, Van Reis R;
XX
XX WPI; 2004-043096/04.
XX
XX Purifying target protein from mixture containing host cell protein
XX involves subjecting mixture to non-affinity purification, high-
XX performance tangential flow filtration and isolating purified protein.
XX
XX Disclosure; SEQ ID NO 3; 77pp; English.
XX
XX The invention relates to a method for purifying a target protein from a
XX mixture containing a host cell protein. This method comprises subjecting
XX the mixture to a non-affinity purification followed by high-performance
XX tangential flow filtration (HPRFF) and isolating the protein in a purity
XX containing less than 100 parts/million (ppm) of the host cell protein,
XX where the method of the invention includes no affinity purification
XX process. The method of the invention is useful for purifying a target
XX protein from a mixture containing a host cell protein, and is useful for
XX incorporating the isolated protein into a pharmaceutical formulation.
XX Proteins purified using the method of the invention are useful in a

CC pharmaceutical respect, and are also useful in various diagnostic and
CC therapeutic purposes. The method of the invention is efficient in
CC purifying a target protein from a mixture containing a host cell protein,
CC and may also be effectively performed at low cost. The current sequence
CC represents the anti-CD11a rhumAb light chain amino acid sequence. This
CC particular protein was used to demonstrate the method of the invention.
SQ Sequence 214 AA;
Query Match 100.0%; Score 51; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKTISKYLA 11
DB 24 RASKTISKYLA 34
RESULT 23
ABB07177
ID ABB07177 standard; protein; 101 AA.
XX
XX ABB07177;
XX
XX 13-MAR-2002 (first entry)
XX
XX Mouse 09 antibody kappa light chain 2 variable region.
XX
XX Neuromodulatory; central nervous system; CNS; SHIGM22; LYM 22; AKR4;
XX ebvHlgM M6119D10; ebv HlgM CB2B68; CB21E12; CB21E7; MS119E5; virucide;
XX antiparkinsonian; neuroprotective; nootropic; vulnerary; mouse.
XX
XX Mus sp.
XX
XX WO200185797-A1.
XX
XX 15-NOV-2001.
XX
XX 30-MAY-2000; 2000WO-US014902.
XX
XX 10-MAY-2000; 2000US-00568351.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
XX Rodriguez M, Miller DJ, Pease LR;
XX
XX WPI; 2002-066596/09.
XX
XX N-PSDB; ABA94224.
XX
XX Novel neuromodulatory agent (a human Igm monoclonal antibody), promoting
XX neurite outgrowth, regeneration, remyelination and neuroprotection in
XX central nervous system, useful to treat post-infectious
XX encephalomyelitis.
XX
XX Disclosure; Fig 36A-B; 219pp; English.
XX
XX The invention provides a neuromodulatory agent (I) capable of promoting
XX neurite outgrowth, regeneration, remyelination and neuroprotection in
XX central nervous system (CNS). (I) is capable of inducing remyelination,
XX promoting cellular proliferation of glial cells, and promoting Ca2+
XX signalling with oligodendrocytes. An humanised antibody to (I) can be
XX selected from antibody SHIGM22 (LYM 22), ebvHlgM M6119D10, ebv HlgM
XX CB2B68, AKR4, CB21E12, CB21E7 or MS119E5. (I) is useful for stimulating
XX remyelination of CNS axons, stimulating proliferation of glial cells in
XX CNS axons, or treating demyelinating disease of CNS in a mammal in need
XX of such therapy. (I) is capable of binding to structures and cells within
XX CNS. (I) is preferably useful for treating a demyelinating disease of CNS
XX of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
XX (TMEV) or for treating a human being having multiple sclerosis, or a
XX human or domestic animal with a viral demyelinating disease, or a post-
XX neural disease of CNS. (I) is also useful for an in vitro method of
XX stimulating the proliferation of glial cells from mixed cell culture. (I)
XX is also useful for stimulating remyelination of CNS axons. The antibodies

CC are useful for preventing infection by a bacterium, virus or like
 CC pathogen that causes demyelination or other neurodegenerative condition
 CC in a subject. Methods where (I) is administered to a patient are useful
 CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
 CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
 CC disease, CNS diseases, and other conditions in the CNS where nerves are
 CC damaged as by trauma. The present sequence represents the mouse 09
 CC antibody kappa light chain 2 variable region

SO Sequence 101 AA;

Query Match 92.2%; Score 47; DB 5; Length 101;
 Best Local Similarity 90.9%; Pred. No. 0.2;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 ||||:|||||
 DB 24 RASKTISKYLA 34

RESULT 24
 AD126670
 ID AD126670 standard; protein; 101 AA.
 AC AD126670;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE Mouse anti oligodendrocyte antibody O9 V kappa 2 protein.
 XX
 KW Mouse; antibody; IGM; remyelination; neuronal growth; autoantibody;
 KW demyelination disease; multiple sclerosis; central nervous system; CNS;
 KW axon; glial cell proliferation;
 KW Theiler's murine encephalomyelitis virus infection; CNS injury;
 KW spinal cord injury.
 XX
 OS Mus sp.
 XX
 PN US2003185827-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 13-NOV-2001; 2001US-00010729.
 XX
 PR 29-APR-1994; 94US-00236520.
 PR 08-AUG-1996; 96US-00692084.
 PR 07-JAN-1997; 97US-00779784.
 PR 28-MAY-1999; 99US-00322862.
 PR 30-MAY-2000; 2000US-00580787.
 PR 05-DEC-2000; 2000US-00730473.
 XX
 PA (MAYO-) MAYO FOUND.
 XX
 PI Rodriguez M, Miller DJ, Pease LR;
 XX
 DR WPI: 2004-119219/12.
 DR N-PSDB; AD126671.
 XX
 XX New human immunoglobulin M antibody for treating or preventing a
 PT demyelinating disease of the central nervous system in a human or
 PT domestic animal, such as multiple sclerosis.
 XX
 XX Example 11; Fig 54; 159pp; English.
 XX
 CC The invention relates to an antibody (I) produced by injecting an
 CC immunocompetent host with an antibody peptide, and harvesting the
 CC antibody, where the peptide comprises a human anti-IGM antibody fragment
 CC given in the specification, or active fragments. Also included are
 CC stimulating remyelination of central nervous system (CNS) axons in a
 CC mammal (comprising administering a monoclonal antibody, or mixtures,
 CC monomers, active fragments, or recombinant antibodies derived from it,
 CC characterised by their ability to bind structures and cells within the
 CC CNS, including oligodendrocytes), stimulating the proliferation of glial

CC cells in CNS axons in a mammal (comprising administering a monoclonal
 CC antibody, or mixtures, monomers, active fragments, or recombinant
 CC antibodies derived from it, characterised by their ability to bind
 CC structures and cells within the CNS), treating or preventing a
 CC demyelinating disease of the CNS in a mammal (comprising administering a
 CC monoclonal antibody, or mixtures, monomers, active fragments, or
 CC recombinant antibodies derived from it, characterised by their ability to
 CC bind structures and cells within the CNS, and to stimulate remyelination
 CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
 CC cells from mixed cell culture, stimulating remyelination of CNS axons in
 CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 CC antibody (or a peptide analogue, hapten, or active fragment of it, where
 CC the DNA sequence consists of a sequence encoding an anti IGM antibody), a
 CC probe capable of screening for the antibody, an assay for screening drugs
 CC and other agents for the ability to modulate the production or mimic the
 CC activities of mAb SHIGM22, SHIGM46, or combinations of them, a
 CC recombinant virus transformed with recombinant antibody nucleic acids or
 CC vector, imaging a portion of the CNS using the antibody and diagnosing or
 CC monitoring demyelination and/or remyelination of the CNS comprising using
 CC CNS image. The antibody is used to stimulate remyelination of CNS axons,
 CC and to stimulate the proliferation of glial cells in CNS axons,
 CC optionally in vitro. The antibody is used to treat or prevent a
 CC demyelinating disease of the CNS in a human or domestic animal, such as
 CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 CC preferably the mammal is a mouse infected with Strain DA of Theiler's
 CC murine encephalomyelitis virus. The antibody is used to treat a spinal
 CC cord injury and used to screen drugs and other agents for the ability to
 CC modulate the production or mimic the activities of the antibody. The
 CC antibody can be used to image a portion of the CNS which can be used to
 CC diagnose or monitor demyelination and/or remyelination of the CNS. The
 CC present sequence is a variable region of a mouse anti-IGM antibody (or
 CC fragment).

SO Sequence 101 AA;

Query Match 92.2%; Score 47; DB 8; Length 101;
 Best Local Similarity 90.9%; Pred. No. 0.2;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 ||||:|||||
 DB 24 RASKTISKYLA 34

RESULT 25
 ADV66159
 ID ADV66159 standard; protein; 107 AA.
 AC ADV66159;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE Human EPCAM-specific antibody light chain variable domain - SEQ ID 82.
 XX
 KW bispecific single chain antibody; epithelial cell adhesion molecule;
 KW EPCAM; tumor; cancer; cytostatic; light chain variable region.
 XX
 OS Unidentified.
 XX
 PN WO2004106383-A1.
 XX
 PD 09-DEC-2004.
 XX
 PF 26-MAY-2004; 2004WO-EP005687.
 XX
 PR 31-MAY-2003; 2003EP-00012133.
 PR 31-MAY-2003; 2003EP-00012134.
 XX
 PA (MICR-) MICROMET AG.
 XX
 PI Kufner P, Berry M, Offner S, Brischwein K, Wolf A, Raum T,
 PI Kohleisen B, Lenkner-Schuetz U, Baerentele P;
 XX

DR WPI; 2005-021271/02.
DR N-PSDB; ADV66158.
XX
PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
XX disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 10; SEQ ID NO 82; 227pp; English.
XX
CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents an antibody
CC light chain variable domain that is specific for human EPCAM.
XX
SQ Sequence 107 AA;
Query Match 92.2%; Score 47; DB 9; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.21; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 0;
QY 1 RASKTISKYLA 11
DB 24 RASKSISKYLA 34
RESULT 26
AD283517
ID AD283517 standard; protein; 107 AA.
XX
AC AD283517;
XX
DT 14-JUL-2005 (first entry)
XX
DE AntiEPCam single chain antibody SEQ ID NO 139.
XX
KM neoplasia; inflammation; immune disorder; infection; allergy;
KM graft versus host disease; Cytostatic; Antiinflammatory;
KM immunosuppressive; Virocide; Antibacterial; Antiallergic; Antiparasitic;
KM EPCam; antibody.
XX
OS Synthetic.
XX
FN WO2005040220-A1.
XX
PD 06-MAY-2005.
XX
PP 15-OCT-2004; 2004WO-EP011646.
XX
PR 16-OCT-2003; 2003EP-00023581.
XX
PA (MICR-) MICROMET AG.
XX
PI Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baeuerle P;
PI Carr FJ, Hamilton AA, Williams S;
XX
DR WPI; 2005-333494/34.
DR N-PSDB; AD283516.
XX
PT New cytotoxically active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.
XX
PS Example 8; SEQ ID NO 139; 639pp; English.
XX
CC The invention relates to a cytotoxically active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,

CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of an anti-EPCam single chain antibody.
XX
SQ Sequence 107 AA;
Query Match 92.2%; Score 47; DB 9; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.21; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 0;
QY 1 RASKTISKYLA 11
DB 24 RASKSISKYLA 34
RESULT 27
AD126700
ID AD126700 standard; protein; 108 AA.
XX
AC AD126700;
XX
DT 15-APR-2004 (first entry)
XX
DE Mouse anti Igm antibody OI kappa light chain protein.
XX
KM Mouse; antibody; Igm; remyelination; neuronal growth; autoantibody;
KM demyelination disease; multiple sclerosis; central nervous system; CNS;
KM axon; glial cell proliferation;
KM Theiler's murine encephalomyelitis virus infection; CNS injury;
KM spinal cord injury.
XX
OS Mus sp.
XX
FN US2003185827-A1.
XX
PD 02-OCT-2003.
XX
PP 13-NOV-2001; 2001US-00010729.
XX
PR 29-APR-1994; 94US-00236520.
PR 08-AUG-1996; 96US-00692084.
PR 07-JAN-1997; 97US-0079784.
PR 28-MAY-1999; 99US-00322862.
PR 30-MAY-2000; 2000US-00580787.
PR 05-DEC-2000; 2000US-00730473.
XX
PA (MAYO-) MAYO FOUND.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2004-119219/12.
DR N-PSDB; AD126701.
XX
PT New human immunoglobulin M antibody for treating or preventing a
PT demyelinating disease of the central nervous system in a human or
PT domestic animal, such as multiple sclerosis.
XX
PS Example 19; Fig 68; 159pp; English.
XX
CC The invention relates to an antibody (I) produced by injecting an
CC immunocompetent host with an antibody peptide, and harvesting the
CC antibody, where the peptide comprises a human anti-Igm antibody fragment
CC given in the specification, or active fragments. Also included are
CC stimulating remyelination of central nervous system (CNS) axons in a

CC mammal (comprising administering a monoclonal antibody, or mixtures,
 CC monomers, active fragments, or recombinant antibodies derived from it,
 CC characterised by their ability to bind structures and cells within the
 CC CNS, including oligodendrocytes), stimulating the proliferation of glial
 CC cells in CNS axons in a mammal (comprising administering a monoclonal
 CC antibody, or mixtures, monomers, active fragments, or recombinant
 CC antibodies derived from it, characterised by their ability to bind
 CC structures and cells within the CNS), treating or preventing a
 CC demyelinating disease of the CNS in a mammal (comprising administering a
 CC monoclonal antibody, or mixtures, monomers, active fragments, or
 CC recombinant antibodies derived from it, characterised by their ability to
 CC bind structures and cells within the CNS, and to stimulate remyelination
 CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
 CC cells from mixed cell culture, stimulating remyelination of CNS axons in
 CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 CC antibody (or a peptide analogue, hapten, or active fragment of it, where
 CC the DNA sequence consists of a sequence encoding an anti Igm antibody), a
 CC probe capable of screening for the antibody, an assay for screening drugs
 CC and other agents for the ability to modulate the production or mimic the
 CC activities of MAb 8H1GM2, 8H1GM46, or combinations of them, a
 CC recombinant virus transformed with recombinant antibody nucleic acids or
 CC vector, imaging a portion of the CNS using the antibody and diagnosing or
 CC monitoring demyelination and/or remyelination of the CNS comprising using
 CC CNS image. The antibody is used to stimulate remyelination of CNS axons,
 CC and to stimulate the proliferation of glial cells in CNS axons,
 CC optionally in vitro. The antibody is used to treat or prevent a
 CC demyelinating disease of the CNS in a human or domestic animal, such as
 CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 CC preferably the mammal is a mouse infected with Strain DA of Theiler's
 CC murine encephalomyelitis virus. The antibody is used to treat a spinal
 CC cord injury and used to screen drugs and other agents for the ability to
 CC modulate the production or mimic the activities of the antibody. The
 CC antibody can be used to image a portion of the CNS which can be used to
 CC diagnose or monitor demyelination and/or remyelination of the CNS. The
 CC present sequence is a variable region of a mouse anti-Igm antibody (or
 CC fragment).

SO Sequence 108 AA;

Query Match 92.2%; Score 47; DB 8; Length 108;

Best Local Similarity 90.9%; Pred. No. 0.21;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTSKYIA 11
 ||||:|||||
 Db 24 RASKTSKYIA 34

RESULT 28

AA64819 ID AAR64819 standard; protein; 234 AA.

XX AAR64819;

DT 25-MAR-2003 (revised)

DT 15-JUL-1995 (first entry)

XX OMVU10 ScFv fragment.

KM ScFv; single chain Fv; expression cassette; Aspergillus; Mucor;
 KM Neurospora; Penicillium; OMVU10; monoclonal antibody; OMVU10;
 KM Streptococcus; antibody engineering.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 28..32

FT Region /label= CDR1

FT Region /note= "complementarity determining region 1"

FT Region /label= CDR11

FT Region /note= "complementarity determining region 2"

FT /label= CDR111
 FT /note= "complementarity determining region 3"
 FT Peptide 115..129
 FT /label= Linker
 FT Region 130..234
 FT /label= VL
 FT /note= "MAb OMVU10 VL"
 FT Region 154..163
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 179..185
 FT /label= CDR11
 FT /note= "complementarity determining region 2"
 FT Region 218..225
 FT /label= CDR111
 FT /note= "complementarity determining region 3"

PN WO9429457-A2.

PD 22-DEC-1994.

PF 09-JUN-1994; 94WO-BP001906.

PR 09-JUN-1993; 93EP-00201660.

PR 09-JUN-1993; 93EP-00201661.

PR 14-JUN-1993; 93EP-00201706.

XX (UNITL) UNILEVER NV.

PA (UNITL) UNILEVER PLC.

PA (NEDE) NEDERLAND ORG TMO.

PI Franken LGJ, Van Gorpcom RFM, Heessing JGM, Van Den Hondel CAMUJ;

PI Musters W, Verbakel JMA, Verrips CT;

DR WPI; 1995-036484/05.

DR N-PSDB; AAQ76287.

XX Prodn. of single chain Fv antibody fragments - as fusion proteins using a

PT transformed mould of the genus Aspergillus, Mucor, Neurospora or

PT Penicillium.

XX Example 4; Page 30-31; 70pp; English.

XX An ScFv fragment of OMVU10, a MAb raised against oral streptococci, was

CC constructed by PCR amplification of OMVU10 heavy and light chain

CC sequences, and expressed from pUR4457. The ScFv-encoding Peti-XhoI

CC fragment of pUR4457 is given in AAQ76287, and the encoded protein in

CC AAR64819. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-

CC MAR-2003 to correct PI field.)

XX Sequence 234 AA;

Query Match 92.2%; Score 47; DB 2; Length 234;

Best Local Similarity 90.9%; Pred. No. 0.51;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTSKYIA 11
 ||||:|||||
 Db 153 RASKTSKYIA 163

RESULT 29

AA17957 ID AAY17957 standard; protein; 242 AA.

XX AAY17957;

DT 04-AUG-1999 (first entry)

XX Mouse scFv fragment 3-1.

XX Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;

KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.

```

XX OS Mus sp.
XX XX WO9925818-A1.
XX PD 27-MAY-1999.
XX XX 16-NOV-1998; 98WO-EP007313.
XX PF 17-NOV-1997; 97EP-00120096.
XX PR (KUFE/) KUFER P.
XX PA Kufer P, Raum T, Borschert K, Zetcl F, Luterduese R;
XX PI WPI: 1999-338004/28.
XX DR N-PSDB; AAX77240.
XX PT Phage display system for identification of binding site domains retaining
XX PT capacity to bind an epitope.
XX PS Claim 27; Fig 6.3; 152pp; English.
XX CC The invention relates to a method of identifying binding site domains
XX CC (BSD) that retain the capacity of binding to a predetermined epitope when
XX CC positioned C-terminal of at least one further domain in a recombinant bi-
XX CC or multivalent polypeptide. The method comprises (a) testing a panel of
XX CC BSD displayed on the surface of a biological display system as part of a
XX CC fusion protein for binding to a predetermined epitope, where the fusion
XX CC protein comprises an additional domain positioned N-terminal of the BSD
XX CC and an amino acid sequence that mediates anchoring of the fusion protein
XX CC to the surface of the display system; and (b) identifying a BSD that
XX CC binds to the predetermined epitope. The method is useful to identify bi-
XX CC or multivalent polypeptides that comprise antibody binding sites capable
XX CC of efficiently binding to the corresponding antigen. The polypeptides or
XX CC antibodies identified by the method are useful therapeutically and
XX CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
XX CC fragments that bind independently of their position within bifunctional
XX CC single-chain fusion proteins can be isolated from combinatorial antibody
XX CC libraries using the new in vitro method. Sequences AAY17957-965 represent
XX CC mouse scFv fragments
XX CC
XX SQ Sequence 242 AA;
XX
XX Query Match 92.2%; Score 47; DB 2; Length 242;
XX Best Local Similarity 90.9%; Pred. No. 0.53;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKTISKYLA 11
Db 159 RASKSISKYLA 169

```

```

XX PR 17-NOV-1997; 97EP-00120096.
XX XX (KUFE/) KUFER P.
XX PA Kufer P, Raum T, Borschert K, Zetcl F, Luterduese R;
XX PI WPI: 1999-338004/28.
XX DR N-PSDB; AAX77244.
XX PT Phage display system for identification of binding site domains retaining
XX PT capacity to bind an epitope.
XX PS Claim 27; Fig 6.7; 152pp; English.
XX CC The invention relates to a method of identifying binding site domains
XX CC (BSD) that retain the capacity of binding to a predetermined epitope when
XX CC positioned C-terminal of at least one further domain in a recombinant bi-
XX CC or multivalent polypeptide. The method comprises (a) testing a panel of
XX CC BSD displayed on the surface of a biological display system as part of a
XX CC fusion protein for binding to a predetermined epitope, where the fusion
XX CC protein comprises an additional domain positioned N-terminal of the BSD
XX CC and an amino acid sequence that mediates anchoring of the fusion protein
XX CC to the surface of the display system; and (b) identifying a BSD that
XX CC binds to the predetermined epitope. The method is useful to identify bi-
XX CC or multivalent polypeptides that comprise antibody binding sites capable
XX CC of efficiently binding to the corresponding antigen. The polypeptides or
XX CC antibodies identified by the method are useful therapeutically and
XX CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
XX CC fragments that bind independently of their position within bifunctional
XX CC single-chain fusion proteins can be isolated from combinatorial antibody
XX CC libraries using the new in vitro method. Sequences AAY17957-965 represent
XX CC mouse scFv fragments
XX CC
XX SQ Sequence 242 AA;
XX
XX Query Match 92.2%; Score 47; DB 2; Length 242;
XX Best Local Similarity 90.9%; Pred. No. 0.53;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKTISKYLA 11
Db 159 RASKSISKYLA 169

```

DR N-PSDB; AAX77242.
XX
XX Phase display system for identification of binding site domains retaining
PT capacity to bind an epitope.
XX
XX Claim 27; Fig 6.5; 152pp; English.
XX
XX The invention relates to a method of identifying binding site domains
CC (BSD) that retain the capacity of binding to a predetermined epitope when
CC positioned C-terminal of at least one further domain in a recombinant bi-
CC or multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and
CC diagnostically, for e.g. cancer and autoimmune diseases. scFv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method. Sequences AAY17957-965 represent
CC mouse scFV fragments
XX
SQ Sequence 242 AA;
Query Match 92.2%; Score 47; DB 2; Length 242;
Best Local Similarity 90.9%; Pred. No. 0.53;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKTISKYLA 11
|||:|||||
Db 159 RASKSISKYLA 169
RESULT 32
AAB10863
ID AAB10863 standard; protein; 392 AA.
XX
XX AAB10863;
AC
XX
XX 02-FEB-2001 (first entry)
DT
XX
XX S11-VEGF2 construct protein in pSectagA SEQ ID NO: 38.
DE
XX
XX MVP; multivalent protein; treatment; dressing; skin; muscle; musculature;
KW nervous system; inner organ; hematopoietic system; immune system; joint;
KW support tissue; immunization.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX WO200053790-A1.
XX
XX 14-SEP-2000.
PD
XX
XX 26-FEB-2000; 2000WO-EP001612.
PF
XX
XX 10-MAR-1999; 99DE-0101419.
PR
XX
XX (AVET) AVENTIS PHARMA DEUT GMBH.
PA
XX
XX Kontermann R, Nettelbeck D, Sedlacek H, Mueller R;
PI
XX
XX WPI: 2000-572272/53.
DR
XX
XX N-PSDB; AAA98173.
DR
XX
XX Cell specific multivalent proteins useful for targeting specific cells
PT for the treatment of disease.
PT
XX
XX Example 2; Page 66-67; 81pp; German.

XX
XX This invention describes a method for the production of a novel cell
CC specific multivalent protein (MVP). The invention also describes (1) a
CC nucleic acid construct, which encodes an MVP; (2) a bacterium, yeast or
CC mammalian cell, in which the nucleic acid construct of (1) is introduced;
CC (3) the MVP bound to a vector; (4) production of an MVP; (5) an MVP
CC comprising a scFv with a binding site for the adenoviral fibre protein or
CC CD3 molecule and two VSBF units, bound by a peptide linker; and (6) a
CC complex comprising at least two MVPs as above (in which each single
CC ligand can be 0-1). The MVP, optionally bound to a vector, is useful for
CC production of a remedy to treat cells outside tissue by dressings for
CC skin, muscle, nervous systems, inner organs, hematopoietic systems, immune
CC systems, musculature, support tissues or joints and to immunize to
CC prevent or treat diseases
XX
SQ Sequence 392 AA;
Query Match 92.2%; Score 47; DB 3; Length 392;
Best Local Similarity 90.9%; Pred. No. 0.9;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKTISKYLA 11
|||:|||||
Db 186 RASKSISKYLA 196
RESULT 33
AD283409
ID AD283409 standard; protein; 491 AA.
XX
XX AD283409;
AC
XX
XX 14-JUL-2005 (first entry)
DT
XX
XX C-terminal BpCam binder SEQ ID NO 31.
DE
XX
XX neoplasm; inflammation; immune disorder; infection; allergy;
KW graft versus host disease; Cytostatic; Antiinflammatory;
KW Immunosuppressive; Virocide; Antibacterial; Antiallergic; Antiparasitic;
KW BpCam.
XX
XX Synthetic.
OS
XX WO2005040220-A1.
XX
XX 06-MAY-2005.
PD
XX
XX 15-OCT-2004; 2004WO-EP011646.
PF
XX
XX 16-OCT-2003; 2003EP-00023581.
PR
XX
XX (MIGR-) MICROMET AG.
PA
XX
XX Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
PI Carr FJ, Hamilton AA, Williams S;
PI
XX
XX WPI: 2005-333494/34.
DR
XX
XX N-PSDB; AD283408.
DR
XX
XX New cytotoxically active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.
PT
XX
XX Claim 20; SEQ ID NO 31; 639pp; English.
PS
XX
XX The invention relates to a cytotoxically active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,
CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological

CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxicity active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of an anti-EpCam binder.

XX
 SQ Sequence 491 AA;

Query Match 92.2%; Score 47; DB 9; Length 491;
 Best Local Similarity 90.9%; Pred. No. 1.2;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 ||||:|||||
 Db 408 RASKSISKYLA 418

RESULT 34

ADV66089 ID ADV66089 standard; protein; 494 AA.

XX AC ADV66089;

XX DT 24-FEB-2005 (first entry)

XX DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 12.

XX bispecific single chain antibody; epithelial cell adhesion molecule;
 XX EpCAM; CD3; tumor; cancer; cytostatic.

XX OS Unidentified.

XX PN WO2004106383-A1.

XX PD 09-DEC-2004.

XX PF 26-MAY-2004; 2004WO-EP005687.

XX PR 31-MAY-2003; 2003EP-00012133.

XX PR 31-MAY-2003; 2003EP-00012134.

XX PA (MICR-) MICROMET AG.

PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkeri-Schuetz U, Baeruerle P;

DR WPI; 2005-021271/02.

DR N-PSDB; ADV66088.

XX New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.

XX PS Claim 12; SEQ ID NO 12; 227pp; English.

XX The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.

XX SQ Sequence 494 AA;

Query Match 92.2%; Score 47; DB 9; Length 494;
 Best Local Similarity 90.9%; Pred. No. 1.2;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 ||||:|||||
 Db 405 RASKSISKYLA 415

RESULT 35

ADV66123 ID ADV66123 standard; protein; 497 AA.

XX AC ADV66123;

XX DT 24-FEB-2005 (first entry)

XX DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 46.

XX bispecific single chain antibody; epithelial cell adhesion molecule;
 XX EpCAM; CD3; tumor; cancer; cytostatic.

XX OS Unidentified.

XX PN WO2004106383-A1.

XX PD 09-DEC-2004.

XX PF 26-MAY-2004; 2004WO-EP005687.

XX PR 31-MAY-2003; 2003EP-00012133.

XX PR 31-MAY-2003; 2003EP-00012134.

XX PA (MICR-) MICROMET AG.

PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkeri-Schuetz U, Baeruerle P;

XX WPI; 2005-021271/02.

XX DR N-PSDB; ADV66122.

XX New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.

XX PS Claim 12; SEQ ID NO 46; 227pp; English.

XX The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.

XX SQ Sequence 497 AA;

Query Match 92.2%; Score 47; DB 9; Length 497;
 Best Local Similarity 90.9%; Pred. No. 1.2;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 ||||:|||||
 Db 408 RASKSISKYLA 418

RESULT 36

ADV66125 ID ADV66125 standard; protein; 497 AA.

XX AC ADV66125;

XX DT 24-FEB-2005 (first entry)

XX DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 48.

XX bispecific single chain antibody; epithelial cell adhesion molecule;
 KW EpCAM; CD3; tumor; cancer; cytostatic.
 XX Unidentified.
 OS WO2004106383-A1.
 XX
 XX 09-DEC-2004.
 PD
 XX 26-MAY-2004; 2004WO-EP005687.
 XX
 XX 31-MAY-2003; 2003EP-00012133.
 PR 31-MAY-2003; 2003EP-00012134.
 XX
 XX (MICR-) MICROMET AG.
 PA
 XX Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkeri-Schuetz U, Baenerle P;
 XX
 XX WPI; 2005-021271/02.
 DR N-PSDB; ADV66124.
 DR
 XX New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.
 XX
 XX Claim 12; SEQ ID NO 48; 227pp; English.
 XX
 XX The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.
 XX
 SQ Sequence 497 AA;
 Query Match 92.2%; Score 47; DB 9; Length 497;
 Best Local Similarity 90.9%; Pred. No. 1.2;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 ||||:||||
 Db 408 RASKSISKYLA 418

RESULT 37
 AD283427
 ID AD283427 standard; protein; 506 AA.
 XX
 AC AD283427;
 XX
 DT 14-JUL-2005 (first entry)
 XX
 DE Deimmunized construct 3-ixanti-CD3.
 XX
 OS neoplasm; inflammation; immune disorder; infection; allergy;
 KW graft versus host disease; Cytostatic; Antiinflammatory;
 KW immunosuppressive; Vitruide; Antibacterial; Antiallergic; Antiparasitic.
 XX
 OS Synthetic.
 XX
 XX WO2005040220-A1.
 PN
 XX 06-MAY-2005.
 PD
 XX 15-OCT-2004; 2004WO-EP011646.
 PF
 PR 16-OCT-2003; 2003EP-00023581.
 XX

PA (MICR-) MICROMET AG.
 XX
 XX Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baenerle P;
 PI Carr FU, Hamilton AA, Williams S;
 XX
 XX WPI; 2005-333494/34.
 DR N-PSDB; AD283426.
 DR
 XX New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.
 PT proliferative disease.
 XX
 XX Claim 20; SEQ ID NO 49; 639pp; English.
 PS
 XX The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of deimmunized construct 3-ixanti-CD3.
 XX
 SQ Sequence 506 AA;
 Query Match 92.2%; Score 47; DB 9; Length 506;
 Best Local Similarity 90.9%; Pred. No. 1.2;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 ||||:||||
 Db 43 RASKSISKYLA 53

RESULT 38
 AAB10864
 ID AAB10864 standard; protein; 510 AA.
 XX
 AC AAB10864;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE S11-scVEGF2 construct DNA in pSectra9 SEQ ID NO: 40.
 XX
 XX MVP; multivalent protein; treatment; dressing; skin; mucus; musculature;
 KW nervous system; inner organ; hematopoietic system; immune system; joint;
 KW support tissue; immunization.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS
 XX WO2000053790-A1.
 PN
 XX 14-SEP-2000.
 PD
 XX 26-FEB-2000; 2000WO-EP001612.
 PF
 XX 10-MAR-1999; 99DE-01010419.
 PR
 XX (AVET) AVENTIS PHARMA DEUT GMBH.
 PA
 XX Kontermann R, Nettelbeck D, Sedlaczek H, Mueller R;
 PI WPI; 2000-572272/53.
 DR

CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
CC polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
CC detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a DITHP protein which has antigen
CC recognition activity. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
XX
SQ Sequence 238 AA;

Query Match 80.4%; Score 41; DB 6; Length 238;
Best Local Similarity 81.8%; Pred. No. 8.5;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
|||:|||||
DB 49 RASRTSTYLA 59

RESULT 41
ADC64782
ID ADC64782 standard; protein; 238 AA.
XX
AC ADC64782;
XX
DT 18-DEC-2003 (first entry)
XX
DE Hu-C12-3 clone amino acid sequence SEQ ID NO:3.
XX
KW humanised; polypeptide antigen; protein antigen; decreased antigenicity;
KW CD8; T lymphoblast; CD8 T cell; cancer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN KR2002066383-A.
XX
PD 16-AUG-2002.
XX
PF 07-FEB-2002; 2002KR-00006974.
XX
PR 08-FEB-2001; 2001KR-00006212.
XX
PA (IMMUNO-) IMMUNOMICS CO LTD.
XX
PI Kwon BS;
XX
DR WPI; 2003-145050/14.
XX
PT New humanized polypeptide antigen with decreased antigenicity and it's
XX encoding gene, for the treatment of tumors and AIDS.
XX
PS Disclosure; Page 12; 18pp; Korean.

XX
CC The present invention describes a humanised polypeptide antigen with
CC decreased antigenicity, which binds to 4-1BB of CD8 T lymphoblasts to
CC activate CD8 T cells, and it's encoding gene. The humanised polypeptide
CC antigen can be used in the treatment of cancer. The present sequence
CC represents a humanised polypeptide antigen clone amino acid sequence from
CC the present invention.
XX
SQ Sequence 238 AA;

Query Match 80.4%; Score 41; DB 7; Length 238;
Best Local Similarity 90.0%; Pred. No. 8.5;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYL 10
|||||||
DB 155 RASKTISDYL 164

RESULT 42
AEA45016
ID AEA45016 standard; peptide; 11 AA.

XX
AC AEA45016;
XX
DT 11-AUG-2005 (first entry)
XX
DE Apolipoprotein E C-terminal domain related sequence, SEQ ID 214.

XX
KW Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
KW Alzheimer's disease; Amyloidosis; Parkinson's disease; Huntingtons chorea;
KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
KW motor neurone disease; chronic obstructive pulmonary disease.
XX

OS Homo sapiens.
XX
PN GB2408508-A.
XX
PD 01-JUN-2005.

XX
PF 26-NOV-2004; 2004GB-00026043.
XX
PR 28-NOV-2003; 2003US-0525174P.
XX
PA (ASTR) ASTRAZENCA AB.
XX
PA (DVAX-) DVAX CORP.

XX
PI Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
PI Hufon S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;
XX
DR WPI; 2005-408785/42.

XX
PT New human antibody or antibody fragment which binds to a sequence of the
PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
PT manufacturing a medicament for treating or preventing an amyloid disorder
PT e.g. Alzheimers disease.
XX
PT

XX
Example 8; SEQ ID NO 214; 392pp; English.

XX
CC The present invention relates to a human antibody or antibody fragment,
CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD);
CC AEA44803) and also to human plaques. The antibody or its fragment is
CC useful for manufacturing a medicament for treating or preventing an
CC amyloid disorder such as Alzheimers disease, primary systemic
CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
CC familial amyloid polynuropathy I, familial amyloid polynuropathy III,
CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
CC amyloid, type II diabetes, hereditary renal amyloidosis, Pituitary-gland
CC amyloidosis, infection localized amyloidosis, Medullary carcinoma of the

CC chryzoid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
 CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
 CC disease, Gerstmann-Strausner-Scheinker Disease (GSS), Kuru, Parkinsons
 CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
 CC chronic obstructive pulmonary disease. The present sequence was used to
 CC illustrate the invention.

XX Sequence 11 AA;

Query Match 78.4%; Score 40; DB 9; Length 11;
 Best Local Similarity 80.0%; Pred. No. 0.44;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
 |||::|||
 Db 1 RASQTSRYL 10

RESULT 43

AEA45037
 ID AEA45037 standard; peptide; 11 AA.

AC AEA45037;

DT 11-AUG-2005 (first entry)

DE Apolipoprotein B C-terminal domain related sequence, SEQ ID 235.

KM Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotoxic;
 KM Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein B;
 KM Alzheimer's disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
 KM Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
 KM Spongiform encephalopathy; Creutzfeldt Jakob disease;
 KM motor neurone disease; chronic obstructive pulmonary disease.

OS Homo sapiens.

PN GB2408508-A.

PD 01-JUN-2005.

PF 26-NOV-2004; 2004GB-00026043.

PR 28-NOV-2003; 2003US-0525174P.

PA (ASTR) ASTRAZENCA AB.

PI (DYNX-) DYNX CORP.

PI Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
 PI Hufton S, Andersson CV, Lindquist J, Sunemark D, Leonov S;

DR WPI; 2005-408785/42.

XX New human antibody or antibody fragment which binds to a sequence of the
 PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
 PT manufacturing a medicament for treating or preventing an amyloid disorder
 PT e.g. Alzheimers disease.

PS Disclosure; SEQ ID NO 235; 392pp; English.

XX The present invention relates to a human antibody or antibody fragment,
 CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD);
 CC AEA44803) and also to human plaques. The antibody or its fragment is
 CC useful for manufacturing a medicament for treating or preventing an
 CC amyloid disorder such as Alzheimers disease, primary systemic
 CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
 CC familial non-neuropathic amyloidosis, familial amyloid polynuropathy III,
 CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
 CC angioptosis, Familial British Dementia, Hemodialysis-related amyloidosis,
 CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
 CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
 CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
 CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs

CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
 CC disease, Gerstmann-Strausner-Scheinker Disease (GSS), Kuru, Parkinsons
 CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
 CC chronic obstructive pulmonary disease. The present sequence was used to
 CC illustrate the invention.

XX Sequence 11 AA;

Query Match 78.4%; Score 40; DB 9; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.44;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKRYLA 11
 |||::|||
 Db 1 RASQTSRYLA 11

RESULT 44

ADL91341
 ID ADL91341 standard; protein; 108 AA.

AC ADL91341;

DT 20-MAY-2004 (first entry)

DE VL chain clone A12 of an intracellularly binding immunoglobulin SegID 32.

KM antibody; variable chain; cytosolic; cytoplasmic degradation;
 KM intracellular relocation; specific antigen positive cancer; leukaemia;
 KM lymphoma; intracellularly binding immunoglobulin; BCR-ABL.

OS Unidentified.

PN WO200307945-A1.

PD 25-SEP-2003.

PF 14-MAR-2003; 2003WO-GB001077.

PR 14-MAR-2002; 2002GB-00006043.

PR 15-NOV-2002; 2002GB-00026723.

PR 15-NOV-2002; 2002GB-00026727.

PA (MEDI-) MEDICAL RES COUNCIL.

PI Lobato-Caballero MN, Rabbits TH;

PI WPI; 2003-779088/73.

XX Use of an intracellularly binding immunoglobulin comprising at least one
 PT antibody variable chain, in preparing a medicament for degrading one or
 PT more specific antigens, or for treating specific antigen positive cancer,
 PT e.g. leukemia.

PS Example 1; SEQ ID NO 32; 86pp; English.

XX This invention relates to novel immunoglobulin molecules that comprise at
 CC least one antibody variable chain VH or VL framework region and are
 CC capable of binding to a specific antigens within an intracellular
 CC environment. Specifically, it refers to antibodies that can form an
 CC insoluble complex with a cognate antigen, such that it can then be target
 CC for degradation via the lysosome or proteosome systems. The present
 CC invention describes the specific target antigen as the oncogenic fusion
 CC protein BCR-ABL or the RAS antigen, such that this method can be used to
 CC prepare a cytostatic medicament for the cytoplasmic degradation or
 CC intracellular relocation of such an antigen or for the treatment of the
 CC specific antigen positive cancer i.e. leukaemia or lymphoma. Furthermore,
 CC the immunoglobulins may also be used for therapeutic, prophylactic or
 CC diagnostic applications both in vitro and in vivo, as well as for assay
 CC and reagent applications or in functional genomics. This polypeptide
 CC sequence is a variable light chain (VL) framework region of an
 CC intracellularly binding anti-ABL antibody of the invention.

SQ Sequence 108 AA;

Query Match 78.4%; Score 40; DB 7; Length 108;
 Best Local Similarity 72.7%; Pred. No. 5.6;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
 |||: |||||
 DB 24 RASRAIAKYLA 34

RESULT 45

ADO36368
 ID ADO36368 standard; protein; 108 AA.

AC ADO36368;

DT 26-AUG-2004 (first entry)

DE Intracellular interaction-related scfv protein SeqID32.

XX immunoglobulin single domain; intracellular environment;

KW intracellular interaction; immunoglobulin domain; scfv;

XX single chain variable fragment.

OS Unidentified.

PN WO2004046185-A2.

PD 03-JUN-2004.

PF 14-NOV-2003; 2003WO-GB004942.

PR 15-NOV-2002; 2002GB-00026729.

PA (MEDI-) MEDICAL RES COUNCIL.

PI Rabbits TH, Tanaka T;

XX WPI; 2004-431946/40.

PT Determining the ability of an immunoglobulin single domain to bind to a
 target in an intracellular environment by assessing the intracellular
 interaction between the immunoglobulin domain and the target by
 monitoring the signal.

PS Disclosure; SEQ ID NO 32; 66pp; English.

XX This invention relates to a novel method of determining the ability of an
 CC immunoglobulin single domain to bind to a target in an intracellular
 CC environment comprising assessing the intracellular interaction between
 CC the immunoglobulin domain and the target by monitoring the signal. The
 CC method comprises providing a first molecule and a second molecule, where
 CC stable interaction of the first and second molecules leads to the
 CC generation of a signal; providing a single intracellular immunoglobulin
 CC domain which is associated with the first molecule, where the single
 CC immunoglobulin domain is free of complementary immunoglobulin domains;
 CC providing an intracellular target which is associated with the second
 CC molecule, such that association of the immunoglobulin domain and the
 CC target leads to stable interaction of the first and second molecules and
 CC generation of the signal; and assessing the intracellular interaction
 CC between the immunoglobulin domain and the target by monitoring the
 CC signal. The methods are useful for determining the ability of an
 CC immunoglobulin single domain to bind to a target in an intracellular
 CC environment. The present sequence is that of a single chain variable
 CC fragment (scfv) protein which was used to illustrate the method of the
 CC invention.

SQ Sequence 108 AA;

Query Match 78.4%; Score 40; DB 8; Length 108;
 Best Local Similarity 72.7%; Pred. No. 5.6;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
 |||: |||||
 DB 24 RASRAIAKYLA 34

RESULT 46

ADO75241
 ID ADO75241 standard; protein; 108 AA.

AC ADO75241;

DT 09-SEP-2004 (first entry)

DE Immunoglobulin light chain variable domain A12 sequence.

XX immunoglobulin; variable domain.

OS Unidentified.

PN WO2004046189-A2.

PD 03-JUN-2004.

PF 14-NOV-2003; 2003WO-GB004964.

PR 15-NOV-2002; 2002GB-00026731.

PA (MEDI-) MEDICAL RES COUNCIL.

PI Rabbits TH, Chung G, Tanaka T, Lobato-Caballero MN, Forster A;

XX WPI; 2004-431950/40.

PT Preparing a double stranded nucleic acid comprises providing a set of
 PT three or more overlapping oligonucleotides which anneal to form the + and
 PT - strands of a nucleic acid that encodes at least part of an
 PT immunoglobulin variable domain.

PS Disclosure; SEQ ID NO 32; 53pp; English.

XX The invention relates to a method of preparing a double stranded nucleic
 CC acid, which encodes an immunoglobulin comprising providing a set of three
 CC or more overlapping oligonucleotides which anneal to form the + and -
 CC strands of a nucleic acid that encodes at least part of an immunoglobulin
 CC variable domain. The methods are useful for preparing nucleic acids,
 CC preferably immunoglobulin genes. This sequence represents one of the
 CC immunoglobulin variable light chain produced by the method of the
 CC invention.

SQ Sequence 108 AA;

Query Match 78.4%; Score 40; DB 8; Length 108;
 Best Local Similarity 72.7%; Pred. No. 5.6;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
 |||: |||||
 DB 24 RASRAIAKYLA 34

RESULT 47

AEA45113
 ID AEA45113 standard; protein; 108 AA.

AC AEA45113;

DT 11-AUG-2005 (first entry)

DE Apolipoprotein E C-terminal domain related sequence, SEQ ID 311.

XX Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephroretropic;
 KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;

KW Alzheimer's disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
 KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
 KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
 KW motor neurone disease; chronic obstructive pulmonary disease.
 XX
 OS Homo sapiens.
 XX
 PN GB2408508-A.
 XX
 XX 01-JUN-2005.
 PD
 XX 26-NOV-2004; 2004GB-00026043.
 XX
 XX 28-NOV-2003; 2003US-0525174P.
 PR
 XX (ASTR) ASTRAZENECA AB.
 XX (DVAX-) DVAX CORP.
 PA
 PI Nordstedt C, Goldschmidt T, Henderlix M, Hoet R, Hoogenboom H;
 PI Hufon S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;
 DR WPI; 2005-408785/42.
 XX
 XX New human antibody or antibody fragment which binds to a sequence of the
 PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
 PT manufacturing a medicament for treating or preventing an amyloid disorder
 PT e.g. Alzheimers disease.
 XX
 PS Disclosure; SEQ ID NO 311; 392pp; English.
 XX
 CC The present invention relates to a human antibody or antibody fragment,
 CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD);
 CC AEA44803) and also to human plaques. The antibody or its fragment is
 CC useful for manufacturing a medicament for treating or preventing an
 CC amyloid disorder such as Alzheimers disease, primary systemic
 CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
 CC familial amyloid polynuropathy I, familial amyloid polynuropathy III,
 CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
 CC angioathy, Familial British Dementia, Hemodialysis-related amyloidosis,
 CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
 CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
 CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
 CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
 CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
 CC disease, Gerstmann-Strausler-Scheinker Disease (GSS), Kuru, Parkinsons
 CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
 CC chronic obstructive pulmonary disease. The present sequence was used to
 CC illustrate the invention.
 CC
 SQ Sequence 108 AA;
 XX
 XX
 Query Match 78.4%; Score 40; DB 9; Length 108;
 Best Local Similarity 72.7%; Pred. No. 5.6;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RASKTISKYLA 11
 |||::|||:
 Db 25 RASQTSRYLA 35

RESULT 48
 AEA45092
 ID AEA45092 standard; protein; 108 AA.
 XX
 AC AEA45092;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Apolipoprotein E C-terminal domain related sequence, SEQ ID 290.
 XX
 KW Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
 KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
 KW Alzheimers disease; amyloidosis; Parkinsons disease; Huntingtons chorea;

KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
 KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
 KW motor neurone disease; chronic obstructive pulmonary disease.
 XX
 OS Homo sapiens.
 XX
 PN GB2408508-A.
 XX
 XX 01-JUN-2005.
 PD
 XX 26-NOV-2004; 2004GB-00026043.
 XX
 XX 28-NOV-2003; 2003US-0525174P.
 PR
 XX (ASTR) ASTRAZENECA AB.
 XX (DVAX-) DVAX CORP.
 PA
 PI Nordstedt C, Goldschmidt T, Henderlix M, Hoet R, Hoogenboom H;
 PI Hufon S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;
 DR WPI; 2005-408785/42.
 XX
 XX New human antibody or antibody fragment which binds to a sequence of the
 PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
 PT manufacturing a medicament for treating or preventing an amyloid disorder
 PT e.g. Alzheimers disease.
 XX
 PS Disclosure; SEQ ID NO 290; 392pp; English.
 XX
 CC The present invention relates to a human antibody or antibody fragment,
 CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD);
 CC AEA44803) and also to human plaques. The antibody or its fragment is
 CC useful for manufacturing a medicament for treating or preventing an
 CC amyloid disorder such as Alzheimers disease, primary systemic
 CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
 CC familial amyloid polynuropathy I, familial amyloid polynuropathy III,
 CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
 CC angioathy, Familial British Dementia, Hemodialysis-related amyloidosis,
 CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
 CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
 CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
 CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
 CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
 CC disease, Gerstmann-Strausler-Scheinker Disease (GSS), Kuru, Parkinsons
 CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
 CC chronic obstructive pulmonary disease. The present sequence was used to
 CC illustrate the invention.
 CC
 SQ Sequence 108 AA;
 XX
 XX
 Query Match 78.4%; Score 40; DB 9; Length 108;
 Best Local Similarity 80.0%; Pred. No. 5.6;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 1 RASKTISKYL 10
 |||::|||:
 Db 25 RASQTSRYL 34

RESULT 49
 AAR30814
 ID AAR30814 standard; protein; 11 AA.
 XX
 AC AAR30814;
 XX
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1993 (first entry)
 XX
 DE Humanised antibody light chain CDR 1.
 XX
 KW Complementarity determining region; CDR; rat; monoclonal; antibody;
 KW YFC51.1; CD18; humanised; antigen; leukocyte; lung; sepsis; asthma;
 KW endotoxic shock; adult respiratory distress syndrome; inflammation;

KW immunotoxin.
 XX
 OS Rattus rattus.
 XX
 PN WO9302191-A1.
 XX
 PD 04-FEB-1993.
 XX
 PF 15-JUL-1992; 92WO-GB001289.
 XX
 PR 16-JUL-1991; 91GB-00015364.
 XX
 PA (WELL) WELLCOME FOUND LTD.
 XX
 PI Waldmann H, Sims M, Crowe S;
 XX
 DR WPI; 1993-058788/07.
 DR N-PSDB; AAQ35171.
 XX
 PT New humanised antibody specific for human CD-18 antigen - inhibits influx
 PT of leukocytes into the lungs, useful for treating endotoxic shock, adult
 PT respiratory distress syndrome, asthma, etc.
 XX
 PS Claim 1; Page 33; 59pp; English.
 XX
 CC The sequences given in AAR30814-16 represent the light chain complement-
 CC arily determining regions (CDRs) of the rat monoclonal antibody YFC51.1.1
 CC (see also AAR30820-21). YFC51.1.1 is a CD18 antibody. These CDRs can be
 CC used in a humanised antibody with specificity for CD18 antigen. The
 CC antibody may be useful in treating leukocyte-mediated conditions, such as
 CC inhibiting influx of leukocytes into the lung and other organs during
 CC sepsis, endotoxic shock or adult respiratory distress syndrome. The
 CC antibodies may also be used to treat asthma and inflammation and may form
 CC part of an immunotoxin. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 11 AA;
 SQ
 Query Match 76.5%; Score 39; DB 2; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.7;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASKTISKYLA 11
 :|||:||||
 Db 1 KASKSISNYLA 11
 RESULT 50
 AAU09909
 ID AAU09909 standard; peptide; 11 AA.
 XX
 AC AAU09909;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Rat mAb YFC51-1 light chain variable region CDR1 peptide sequence.
 XX
 KW Rat; mAb YFC1-1 light chain variable region; vasotropic;
 KW antiinflammatory; collagen disease; immunosuppressive; antiasthmatic;
 KW insulin-dependent diabetes mellitus; inflammatory bowel disease;
 KW ulcerative colitis; graft rejection; allergic disease; antipsoriatic;
 KW antiarthritic; nephrotropic; antithyroid; restenosis; dermatological;
 KW anaphylaxis; cell adhesion inhibitor; vascular injury;
 KW autoimmune disease; immunoglobulin; complementarity determining region;
 KW CDR; CD18; CCR2; atherosclerosis.
 XX
 OS Rattus sp.
 XX
 PN WO200170266-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US008266.
 XX

PR 17-MAR-2000; 2000US-00528267.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Horvath CJ, Rao PE;
 XX
 DR WPI; 2001-607511/69.
 XX
 PT Inhibiting stenosis or restenosis of a blood vessel following vascular
 PT injury or angioplasty in a subject by administering agent which inhibits
 PT recruitment or adhesion of neutrophils, mononuclear cells to injury site.
 XX
 PS Claim 30; Fig 10; 108pp; English.
 XX
 CC The present invention relates to a new method of inhibiting stenosis or
 CC restenosis of a blood vessel following vascular injury in a subject. The
 CC new method comprises administering to the subject agents which inhibit
 CC the adhesion and/or recruitment of neutrophils and mononuclear cells to a
 CC site of vascular injury by binding CD18 or CCR2. The method of the
 CC invention inhibits stenosis or restenosis of a blood vessel following
 CC vascular injury arising from a vascular intervention procedure such as
 CC vascular by-pass or transplantation surgery. The method is also useful
 CC for treating a subject having an inflammatory disease or condition
 CC mediated by neutrophil and mononuclear cell activity e.g. asthma and
 CC graft versus host disease. Chronic inflammatory diseases of the lung,
 CC collagen diseases, and insulin-dependent diabetes mellitus can also be
 CC treated. The method is further useful for treating inflammatory bowel
 CC diseases, such as ulcerative colitis. Additional diseases or conditions
 CC include inflammatory or allergic diseases and conditions, including
 CC systemic anaphylaxis of hypersensitivity responses, drug allergies,
 CC psoriasis and inflammatory dermatoses, autoimmune diseases such as
 CC arthritis, graft rejection and other diseases including atherosclerosis.
 CC The present sequence represents complementarity determining region 1 (CDR
 CC 1) of the rat mAb YFC51.1 light chain variable region. This sequence is
 CC one of three CDRs (AAU09909-AAU09911) that can be used to inhibit
 CC stenosis or restenosis
 CC
 SQ Sequence 11 AA;
 SQ
 Query Match 76.5%; Score 39; DB 4; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.7;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASKTISKYLA 11
 :|||:||||
 Db 1 KASKSISNYLA 11

Search completed: January 17, 2006, 11:58:49
 Job time : 81.8333 secs

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:48:18 ; Search time 10.3333 Seconds
(without alignments)
102.424 Million cell updates/sec

Title: US-10-665-658-13
Perfect score: 51
Sequence: 1 RASKTISKXYLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	92.2	98	2 PH1083	Ig light chain V r
2	47	92.2	106	2 S26345	Ig light chain V r
3	47	92.2	127	2 S04574	Ig kappa chain pre
4	43	84.3	103	2 H30502	Ig kappa chain V r
5	38	74.5	108	1 K1HVOU	Ig kappa chain V-I
6	37	72.5	78	2 S34102	Ig kappa chain V r
7	37	72.5	86	2 S16837	Ig kappa chain V r
8	37	72.5	86	2 S16830	Ig kappa chain V r
9	37	72.5	86	2 S16826	Ig kappa chain V-I
10	37	72.5	86	2 S16826	Ig kappa chain V r
11	37	72.5	92	2 S37506	Ig kappa chain V r
12	37	72.5	92	2 S37512	Ig kappa chain V r
13	37	72.5	92	2 S37522	Ig kappa chain V r
14	37	72.5	92	2 S37516	Ig kappa chain V r
15	37	72.5	106	2 PC4282	Ig kappa chain (an
16	37	72.5	108	2 G44151	Ig kappa chain V r
17	37	72.5	111	2 S23628	Ig kappa chain V r
18	37	72.5	114	2 S54905	Ig kappa chain V r
19	37	72.5	115	1 K3HVG	Ig kappa chain pre
20	37	72.5	128	2 AS6701	Ig kappa chain V r
21	37	72.5	128	2 S40379	Ig kappa chain V-J
22	37	72.5	129	2 S40363	Ig kappa chain - h
23	37	72.5	144	2 PL0106	Ig kappa chain pre
24	36	70.6	107	2 S57444	Ig kappa chain V-J
25	36	70.6	107	2 S47183	Ig kappa chain - h
26	36	70.6	109	2 S31578	Ig kappa chain - h
27	36	70.6	125	2 S40344	Ig kappa chain V-J
28	36	70.6	510	2 T38076	conserved hypotet
29	35	68.6	71	2 S21526	Ig kappa chain V r

30	35	68.6	82	2 S34090	Ig kappa chain V r
31	35	68.6	86	2 S16832	Ig kappa chain V r
32	35	68.6	87	2 S21523	Ig kappa chain V r
33	35	68.6	88	2 S21525	Ig kappa chain V r
34	35	68.6	88	2 S21520	Ig kappa chain V r
35	35	68.6	88	2 S34104	Ig kappa chain V r
36	35	68.6	88	2 S21524	Ig kappa chain V r
37	35	68.6	95	2 S21524	Ig kappa chain V r
38	35	68.6	95	2 PH0866	Ig kappa chain V r
39	35	68.6	95	2 PH0863	Ig kappa chain V-J
40	35	68.6	101	2 S44117	Ig kappa chain V r
41	35	68.6	106	2 C33936	Ig kappa chain V r
42	35	68.6	107	2 S36268	Ig kappa chain V r
43	35	68.6	107	2 S36275	Ig kappa chain V r
44	35	68.6	107	2 S40366	Ig kappa chain V-I
45	35	68.6	108	1 K1HVOU	Ig kappa chain V r
46	35	68.6	108	2 S34007	Ig kappa chain V r
47	35	68.6	108	2 S30521	Ig kappa chain pre
48	35	68.6	117	2 C21056	Ig kappa chain V r
49	35	68.6	124	2 S40318	Ig kappa chain V r
50	35	68.6	124	2 S40336	Ig kappa chain V r
51	35	68.6	127	2 S11240	Ig kappa chain V r
52	35	68.6	128	2 S46372	Ig kappa chain var
53	35	68.6	131	2 S40352	Ig kappa chain V r
54	35	68.6	132	2 S38646	Ig kappa chain V r
55	34	66.7	43	2 S21065	Ig kappa chain V r
56	34	66.7	86	2 S34086	Ig kappa chain V r
57	34	66.7	87	2 S34084	Ig kappa chain V r
58	34	66.7	87	2 S34083	Ig kappa chain V r
59	34	66.7	88	2 S21522	Ig kappa chain V r
60	34	66.7	88	2 S21528	Ig kappa chain V r
61	34	66.7	92	2 S37504	Ig kappa chain V r
62	34	66.7	106	2 PL0267	Ig kappa chain V r
63	34	66.7	107	2 S36264	Ig kappa chain V r
64	34	66.7	108	2 S19674	Ig kappa chain V r
65	34	66.7	108	2 S44122	Ig kappa chain V r
66	34	66.7	108	2 S47182	Ig kappa chain - h
67	34	66.7	108	2 B49047	Ig kappa chain V r
68	34	66.7	109	2 S31981	Ig kappa chain - h
69	34	66.7	109	2 S32001	Ig kappa chain - h
70	34	66.7	109	2 S31980	Ig kappa chain - h
71	34	66.7	109	2 S31979	Ig kappa chain - h
72	34	66.7	115	2 S11697	Ig kappa chain pre
73	34	66.7	116	2 A27594	Ig kappa chain pre
74	34	66.7	117	2 S24206	Ig kappa chain V r
75	34	66.7	123	2 S40331	Ig kappa chain - h
76	34	66.7	123	2 S35479	Ig kappa chain pre
77	34	66.7	127	2 S40367	Ig kappa chain V r
78	34	66.7	129	1 K1HVMK	Ig kappa chain pre
79	34	66.7	205	2 S28998	Ig kappa chain regu
80	34	66.7	234	2 S28998	G protein-coupled
81	34	66.7	253	2 AH3390	secretion activato
82	34	66.7	295	2 C84709	cytidine deaminase
83	34	66.7	415	2 C84709	hypothetical prote
84	34	66.7	467	2 B72331	hypothetical prote
85	34	66.7	482	2 D89828	Ig heavy chain V r
86	33	64.7	72	2 H36025	Ig light chain V r
87	33	64.7	81	2 P36025	Ig light chain V r
88	33	64.7	85	2 P36025	Ig light chain V r
89	33	64.7	86	2 S16825	Ig kappa chain V r
90	33	64.7	86	2 S16840	Ig kappa chain V r
91	33	64.7	94	2 E33730	Ig kappa chain V r
92	33	64.7	96	2 G33730	Ig kappa chain V r
93	33	64.7	97	2 PH1064	Ig light chain V r
94	33	64.7	98	2 S41813	Ig kappa chain V r
95	33	64.7	101	2 B37262	Ig kappa chain V r
96	33	64.7	103	2 S44121	Ig kappa chain V-J
97	33	64.7	103	2 S19975	Ig kappa chain V r
98	33	64.7	104	2 S26330	Ig kappa chain V r
99	33	64.7	104	2 S26329	Ig kappa chain V r
100	33	64.7	106	2 PC2397	anti-tetanus toxin
101	33	64.7	108	2 S31977	Ig kappa chain - h
102	33	64.7	109	2 S31998	Ig kappa chain - h
103	33	64.7	109	2 S31983	Ig kappa chain - h

103	33	64.7	110	2	PN0535	Ig kappa chain V r
104	33	64.7	117	1	K1H12	Ig kappa chain pre
105	33	64.7	117	2	S46371	Ig kappa chain V-J
106	33	64.7	125	2	S40333	Ig kappa chain V-J
107	33	64.7	125	2	S09365	Ig kappa chain - m
108	33	64.7	129	2	S29627	Ig kappa chain V r
109	33	64.7	359	2	S55653	hypothetical prote
110	33	64.7	393	1	IBBYFC	ferrochelatase (BC
111	33	64.7	434	2	G64444	amidase - Methanoc
112	33	64.7	556	2	S49754	probable membrane
113	33	64.7	656	1	G64596	DNA ligase (NAD) (
114	33	64.7	656	2	A71916	DNA ligase - Helic
115	33	64.7	957	2	T15976	hypothetical prote
116	33	64.7	1011	2	S45573	myosin IA - fruit
117	33	64.7	1616	2	T17884	S-layer protein -
118	33	64.7	39	2	PH0878	Ig kappa chain V r
119	33	64.7	91	2	S37521	Ig kappa chain V r
120	33	64.7	93	2	S38564	Ig kappa chain V r
121	33	64.7	107	1	K1H10R	Ig kappa chain V-I
122	33	64.7	107	2	S69901	Ig kappa chain (c1
123	33	64.7	107	2	S31186	Ig kappa chain V r
124	33	64.7	107	2	A28044	Ig kappa chain V r
125	33	64.7	107	2	D48677	Ig kappa chain V-J
126	33	64.7	107	2	B28044	Ig kappa chain V r
127	33	64.7	107	2	B49026	Ig kappa chain V r
128	33	64.7	107	2	S69906	Ig kappa chain (c1
129	33	64.7	108	1	KWMSAR	Ig kappa chain V r
130	33	64.7	108	2	PL0282	Ig kappa chain V r
131	33	64.7	108	2	C26405	Ig kappa chain V r
132	33	64.7	108	2	S38862	Ig kappa chain V r
133	33	64.7	108	2	S69902	Ig kappa chain (c1
134	33	64.7	108	2	S69900	Ig kappa chain (c1
135	33	64.7	108	2	S69903	Ig kappa chain (c1
136	33	64.7	115	2	A53276	Ig kappa chain V r
137	33	64.7	115	2	UL0080	Ig kappa chain pre
138	33	64.7	128	2	A26406	Ig kappa chain V r
139	33	64.7	132	2	S40334	Ig kappa chain - h
140	33	64.7	261	1	A69615	2,3-dihydro-2,3-di
141	33	64.7	286	1	A82159	hypothetical prote
142	33	64.7	354	2	T43507	DNA repair protein
143	33	64.7	397	2	S38283	urea transport pro
144	33	64.7	432	2	S60440	probable membrane
145	33	64.7	466	2	D72733	glutamate synthase
146	33	64.7	474	2	E75069	glutamate synthase
147	33	64.7	475	2	G59105	hypothetical prote
148	33	64.7	476	2	A48664	toxin synthesis tr
149	33	64.7	495	2	I57680	potassium channel
150	33	64.7	558	2	T21468	hypothetical prote
151	33	64.7	566	2	T42227	methylenetetrahydr
152	33	64.7	598	2	H69011	hypothetical prote
153	33	64.7	641	2	T38659	methylenetetrahydr
154	33	64.7	661	2	S19646	DNA repair protein
155	33	64.7	776	2	A97756	DNA topoisomerase
156	33	64.7	776	2	H71688	DNA topoisomerase
157	33	64.7	815	2	T00456	protein kinase hom
158	33	64.7	821	2	B82746	DNA topoisomerase
159	33	64.7	865	1	ISRCTP	DNA topoisomerase
160	33	64.7	865	2	AP0654	DNA topoisomerase
161	33	64.7	865	2	F90859	DNA topoisomerase
162	33	64.7	868	2	A85760	DNA topoisomerase
163	33	64.7	868	2	D83269	DNA topoisomerase
164	33	64.7	868	2	G64119	DNA topoisomerase
165	33	64.7	871	2	AB0270	DNA topoisomerase
166	33	64.7	876	2	B82163	DNA topoisomerase
167	33	64.7	885	2	S61189	probable membrane
168	33	64.7	892	2	AH2736	DNA topoisomerase
169	33	64.7	892	2	F97517	DNA topoisomerase
170	33	64.7	899	2	B87553	DNA topoisomerase
171	33	64.7	901	2	A13592	DNA topoisomerase
172	33	64.7	919	1	OYFKG	phosphoenolpyruvat
173	33	64.7	1495	2	S61023	hypothetical prote
174	33	64.7	1737	2	A59235	unconventional myo
175	33	64.7	1992	1	S02771	myosin heavy chain
176	32	62.7	2262	2	S16664	large protein L -
177	31	60.8	91	2	S17622	Ig kappa chain V r
178	31	60.8	97	2	PH1068	Ig light chain V r
179	31	60.8	98	2	PH1069	Ig light chain V r
180	31	60.8	98	2	PH1062	Ig light chain V r
181	31	60.8	101	2	S20810	Ig kappa chain V r
182	31	60.8	105	2	PH0087	Ig kappa chain V r
183	31	60.8	106	2	B47329	Ig kappa chain V r
184	31	60.8	108	1	K1HUDE	Ig kappa chain V-I
185	31	60.8	108	1	KWMS49	Ig kappa chain V r
186	31	60.8	108	1	KWMSA4	Ig kappa chain V r
187	31	60.8	109	2	UN0296	Ig kappa chain V-J
188	31	60.8	117	2	S46376	Ig kappa chain V-J
189	31	60.8	120	2	S46370	Ig kappa chain V-J
190	31	60.8	122	2	S40314	Ig kappa chain - h
191	31	60.8	125	2	S40350	Ig kappa chain - h
192	31	60.8	128	2	S31488	Ig kappa chain pre
193	31	60.8	129	2	S32806	Ig kappa chain pre
194	31	60.8	200	2	H86556	riboflavin synthas
195	31	60.8	200	2	E72066	riboflavin synthas
196	31	60.8	216	2	S40720	hypothetical prote
197	31	60.8	217	2	P82612	hypothetical prote
198	31	60.8	230	1	Q0SAC2	hypothetical prote
199	31	60.8	230	2	A87730	protein 123H5A.1 (
200	31	60.8	249	2	T41110	hypothetical prote
201	31	60.8	251	2	D86822	hypothetical prote
202	31	60.8	263	2	T38635	hypothetical prote
203	31	60.8	276	2	H81707	inclusion membrane
204	31	60.8	349	2	AD0990	probable membrane
205	31	60.8	353	2	F64175	hypothetical prote
206	31	60.8	359	2	T31821	hypothetical prote
207	31	60.8	364	2	C86015	hypothetical prote
208	31	60.8	369	2	AB2733	NADH ubiquinone ox
209	31	60.8	369	2	D97514	complex I 24k chai
210	31	60.8	376	2	C91169	hypothetical prote
211	31	60.8	376	2	S47693	hypothetical 38.5k
212	31	60.8	389	2	D87460	ribonuclease D (lm
213	31	60.8	416	2	H69252	alcohol dehydrogen
214	31	60.8	441	2	H82617	follypolyglutamate
215	31	60.8	468	1	NM1VNA	exo-alpha-stalidas
216	31	60.8	507	2	T00871	probable cytochrom
217	31	60.8	548	2	F96663	hypothetical prote
218	31	60.8	627	2	H86254	hypothetical prote
219	31	60.8	689	2	E89898	hypothetical prote
220	31	60.8	690	2	C83958	DNA topoisomerase
221	31	60.8	692	2	AC1234	DNA topoisomerase
222	31	60.8	692	2	A11596	DNA topoisomerase
223	31	60.8	697	2	C97120	topoisomerase I (l
224	31	60.8	699	2	F95146	DNA topoisomerase
225	31	60.8	701	2	D98014	DNA topoisomerase
226	31	60.8	710	2	P86778	DNA topoisomerase
227	31	60.8	780	2	T03156	ribonucleoside-dip
228	31	60.8	806	2	T25614	hypothetical prote
229	31	60.8	1017	2	T24349	myosin IA - Caenor
230	31	60.8	1021	2	G75403	DNA topoisomerase
231	31	60.8	1123	2	T47687	adaptor protein/a
232	31	60.8	1643	2	T07961	myosin heavy chain
233	31	60.8	62	2	I30601	Ig kappa chain V-I
234	30.5	59.8	109	2	S47181	Ig kappa chain - h
235	30.5	59.8	270	2	G69953	conserved hypotet
236	30.5	59.8	270	2	E83821	conserved hypotet
237	30.5	59.8	272	2	B89937	hypothetical prote
238	30.5	59.8	274	2	A11256	hypothetical prote
239	30.5	59.8	274	2	A81619	hypothetical prote
240	30	58.8	67	2	AC1954	hypothetical prote
241	30	58.8	92	2	D28840	Ig kappa chain V r
242	30	58.8	95	2	S45324	Ig kappa chain V r
243	30	58.8	96	2	B82321	conserved hypotet
244	30	58.8	101	2	C28840	Ig kappa chain V r
245	30	58.8	101	2	B28840	Ig kappa chain V r
246	30	58.8	107	2	T69017	anti-HIV envelope
247	30	58.8	107	2	S12954	Ig kappa chain V r
248	30	58.8	108	1	K1H1WS	Ig kappa chain V-I

249	30	58.8	108	2	S19970	Ig kappa chain V r	322	30	58.8	891	2	G64875	aconitate hydratase
250	30	58.8	109	2	S38494	Ig lambda chain -	323	30	58.8	925	2	D59105	hypothetical prote
251	30	58.8	111	2	E90111	hypothetical prote	324	30	58.8	932	2	T40216	probable histone t
252	30	58.8	112	2	E70433	flagellar switch p	325	30	58.8	941	2	B96553	hypothetical prote
253	30	58.8	117	1	K4RNP2	Ig kappa chain pre	326	30	58.8	942	2	C96589	hypothetical prote
254	30	58.8	117	2	S41812	Ig kappa chain V r	327	30	58.8	986	2	UC4825	glucan 1,4-beta-gl
255	30	58.8	117	2	S41814	Ig kappa chain V r	328	30	58.8	1121	2	S54504	hypothetical prote
256	30	58.8	117	2	B21056	Ig kappa chain pre	329	30	58.8	1133	1	S41478	DNA repair protein
257	30	58.8	117	2	S21527	Ig kappa chain pre	330	30	58.8	1164	2	AC2136	multifunctional pe
258	30	58.8	117	2	S41810	Ig kappa chain V r	331	30	58.8	1408	2	S16148	gene serate prote
259	30	58.8	123	2	AG0283	probable exported	332	30	58.8	1437	2	F69680	DNA-directed DNA p
260	30	58.8	125	2	S40316	Ig kappa chain - h	333	30	58.8	1474	2	F69009	probable membrane
261	30	58.8	125	2	S40315	Ig kappa chain - h	334	30	58.8	1957	2	S68453	sodium channel pro
262	30	58.8	127	2	PH1224	Ig kappa chain pre	335	30	58.8	2662	2	T19756	hypocutellin synth
263	30	58.8	129	2	S48641	lysosyme (EC 3.2.1	336	30	58.8	5369	2	T44807	mycosubtilin synth
264	30	58.8	214	2	H75552	riboflavin synthase	337	29	57.8	270	2	AB1680	conserved hypochet
265	30	58.8	227	2	F97276	CPSD/CAPA conserve	338	29	56.9	56	2	B72804	gp36 protein - Myc
266	30	58.8	230	2	B36908	aspartate racemase	339	29	56.9	86	2	S16827	Ig kappa chain V r
267	30	58.8	233	2	F81195	conserved hypochet	340	29	56.9	86	2	S78488	Ig kappa chain V r
268	30	58.8	236	2	F69128	hypothetical prote	341	29	56.9	92	1	KVRB38	Ig kappa chain V-I
269	30	58.8	237	2	AD3396	NADH2 dehydrogenas	342	29	56.9	95	2	PH0864	Ig kappa chain V-I
270	30	58.8	245	2	G81831	probable integral	343	29	56.9	108	1	K1HUEU	Ig kappa chain V r
271	30	58.8	246	2	B95911	hypothetical prote	344	29	56.9	108	2	B26405	Ig kappa chain V r
272	30	58.8	262	2	A84240	molybdopterin oxid	345	29	56.9	108	2	S18112	conserved hypochet
273	30	58.8	263	2	A90120	hypothetical prote	346	29	56.9	112	2	E98025	Ig kappa chain pre
274	30	58.8	271	2	S76802	hypothetical prote	347	29	56.9	114	2	E71034	Ig kappa chain V-I
275	30	58.8	272	2	A13628	peptidylprolyl iso	348	29	56.9	115	1	KWMSK2	pilin (pilS5 locus
276	30	58.8	272	2	S28013	outc. protein - Erv	349	29	56.9	116	2	B26555	Ig kappa chain - h
277	30	58.8	272	2	A47021	pectic enzyme secr	350	29	56.9	116	2	S19120	Ig kappa chain pre
278	30	58.8	289	2	S66773	hypothetical prote	351	29	56.9	122	2	S40370	Ig kappa chain V-U
279	30	58.8	294	2	B72605	probable high-affi	352	29	56.9	123	2	A29380	Ig kappa chain V r
280	30	58.8	311	2	A42982	rfas protein - Esc	353	29	56.9	123	2	G89162	Ig kappa chain - h
281	30	58.8	320	2	AF0378	ferrochelatase (EC	354	29	56.9	125	2	S04936	Ig kappa chain pre
282	30	58.8	320	2	AC2432	hypothetical prote	355	29	56.9	125	2	A39396	histone H1-like pr
283	30	58.8	324	2	E91186	probable transcrip	356	29	56.9	125	2	A71477	probable histone-1
284	30	58.8	324	2	D86033	probable transcrip	357	29	56.9	126	2	A34904	Ig kappa chain pre
285	30	58.8	330	2	S74456	regulatory protein	358	29	56.9	128	2	S40345	Ig kappa chain V-U
286	30	58.8	334	2	A72109	hypothetical prote	359	29	56.9	129	2	S52792	Ig kappa chain - h
287	30	58.8	334	2	B86512	hypothetical prote	360	29	56.9	129	2	S40317	Ig kappa chain - h
288	30	58.8	346	2	C88961	ABC transporter, p	361	29	56.9	129	2	S40332	Ig kappa chain - h
289	30	58.8	356	2	D97057	stage II sporulati	362	29	56.9	129	2	A99399	hypothetical prote
290	30	58.8	400	2	T64018	hypothetical prote	363	29	56.9	129	2	H97938	hypothetical prote
291	30	58.8	403	2	B88470	protein C28H8.11 l	364	29	56.9	130	2	KL0113	Ig kappa chain pre
292	30	58.8	417	2	AG0864	N-acetylmuramoyl-L	365	29	56.9	130	2	KWMS32	Ig kappa chain pre
293	30	58.8	433	2	AD3570	galactarate dehydr	366	29	56.9	135	2	H70543	hypothetical prote
294	30	58.8	447	2	B65064	probable amidase l	367	29	56.9	136	2	F64033	hypothetical prote
295	30	58.8	447	2	B91088	probable amidase l	368	29	56.9	141	2	H64340	hypothetical prote
296	30	58.8	447	2	D85933	probable amidase 2	369	29	56.9	146	2	A59492	protamine P1 - Sty
297	30	58.8	447	2	T34887	probable transposa	370	29	56.9	155	2	T42929	hypothetical prote
298	30	58.8	457	2	E85215	hypothetical prote	371	29	56.9	174	2	A10457	protoporphyrinogen
299	30	58.8	514	2	T04429	probable D-galacta	372	29	56.9	177	2	G85973	hypothetical 20.6k
300	30	58.8	524	2	E97697	D-galactarate dehy	373	29	56.9	186	2	H91128	hypothetical prote
301	30	58.8	533	2	AF0180	hypothetical prote	374	29	56.9	186	2	G85973	hypothetical prote
302	30	58.8	533	2	AE2923	proline-rich prote	375	29	56.9	206	2	A72579	MADS box protein a
303	30	58.8	534	2	S21961	hypothetical prote	376	29	56.9	224	2	T14474	conserved hypochet
304	30	58.8	552	2	T15396	methy1-accepting c	377	29	56.9	224	2	B89811	Ig kappa chain - s
305	30	58.8	566	2	A72254	hypothetical prote	378	29	56.9	230	2	S33161	streptococcal pyro
306	30	58.8	614	2	T42649	hypothetical prote	379	29	56.9	246	2	T00628	stereococcal pyro
307	30	58.8	644	2	G81961	ATP-dependent DNA	380	29	56.9	250	1	A26152	amino acid ABC tra
308	30	58.8	698	2	A57644	carntitine O-palmit	381	29	56.9	260	2	B82927	integrase-recombin
309	30	58.8	772	2	G02860	ATP-dependent ion	382	29	56.9	266	1	A42468	7alpha-hydroxyster
310	30	58.8	806	2	E97224	hypothetical prote	383	29	56.9	267	2	S21399	hypothetical prote
311	30	58.8	806	2	T15468	Na+/H+-exchanging	384	29	56.9	269	2	AC0497	probable haloacid
312	30	58.8	813	2	A46747	Na+/H+-exchanging	385	29	56.9	270	2	T06984	hypothetical prote
313	30	58.8	813	2	A46748	serine/chreonine-s	386	29	56.9	283	2	E98065	conserved hypochet
314	30	58.8	830	1	A57060	probable fibritial	387	29	56.9	284	2	B97075	pyruvate-formate 1
315	30	58.8	844	2	B83136	aconitate hydratase	388	29	56.9	290	2	D64355	hypothetical prote
316	30	58.8	891	2	A90860	aconitate hydratase	389	29	56.9				
317	30	58.8	891	2	E85759	aconitate hydratase	390	29	56.9				
318	30	58.8	891	2	E85759	aconitate hydratase	391	29	56.9				
319	30	58.8	891	2	E85759	aconitate hydratase	392	29	56.9				
320	30	58.8	891	2	E85759	aconitate hydratase	393	29	56.9				
321	30	58.8	891	2	E85759	aconitate hydratase	394	29	56.9				

395	29	56.9	312	2	F69842	3-oxoacyl- acyl-ca
396	29	56.9	313	2	T15855	hypothetical prote
397	29	56.9	314	2	C71824	hypothetical prote
398	29	56.9	316	2	G70110	L-lactate dehydrog
399	29	56.9	321	2	T31589	hypothetical prote
400	29	56.9	325	2	T36851	probable transcrip
401	29	56.9	326	2	G83881	transcription regu
402	29	56.9	335	2	A34290	membrane protein C
403	29	56.9	347	2	T24921	hypothetical prote
404	29	56.9	347	2	G72684	hypothetical prote
405	29	56.9	348	2	C96530	hypothetical prote
406	29	56.9	354	2	C83253	probable UDP-N-ace
407	29	56.9	357	2	S04990	integrase - phage
408	29	56.9	360	2	T23063	hypothetical prote
409	29	56.9	363	1	C72590	probable hexoxyltr
410	29	56.9	370	2	E70390	iron-sulfur cofact
411	29	56.9	371	2	C70337	carbamoyl phosphat
412	29	56.9	379	2	B64300	formate dehydrogen
413	29	56.9	386	2	B83536	probable acyl-CoA
414	29	56.9	387	2	G64489	hypothetical prote
415	29	56.9	389	2	T46722	conserved hypoteth
416	29	56.9	395	1	J00396	nodulation protein
417	29	56.9	398	2	F83099	nicotinate phospho
418	29	56.9	398	2	B86655	phosphoglycerate k
419	29	56.9	406	2	C84940	3-oxoacyl- lacyl-ca
420	29	56.9	408	2	S63528	phosphoglycerate k
421	29	56.9	409	2	G71935	type I restriction
422	29	56.9	410	2	C44490	retrovirus-related
423	29	56.9	415	2	H90198	phosphoglycerate k
424	29	56.9	417	2	C90273	exopolyphosphatase
425	29	56.9	447	2	E72320	hypothetical prote
426	29	56.9	448	2	H84680	hypothetical prote
427	29	56.9	449	2	S16748	proline-rich prote
428	29	56.9	453	2	G66695	hypothetical prote
429	29	56.9	458	2	T25557	hypothetical prote
430	29	56.9	463	2	B81141	xanthine/uracil pe
431	29	56.9	463	2	T48116	hypothetical prote
432	29	56.9	467	2	D95253	L-fucose kinase
433	29	56.9	469	2	B84496	probable retroelem
434	29	56.9	472	2	D71076	probable glutamate
435	29	56.9	482	2	B98118	thiaminokinase (BC
436	29	56.9	492	2	UC4828	cyclin B - yeast (
437	29	56.9	507	2	A81413	probable DNA repai
438	29	56.9	508	2	E72299	glutamate synthase
439	29	56.9	508	2	T23836	hypothetical prote
440	29	56.9	518	2	D71288	probable glutamate
441	29	56.9	542	2	T11925	hypothetical prote
442	29	56.9	550	2	T26343	hypothetical prote
443	29	56.9	551	2	S38086	hypothetical prote
444	29	56.9	554	2	T01240	laccase (BC 1.10.3
445	29	56.9	574	2	C82301	endoglucanase-rela
446	29	56.9	610	2	H71503	probable fad-depen
447	29	56.9	611	2	T28171	hypothetical prote
448	29	56.9	617	2	S10511	thrombin (BC 3.4.2
449	29	56.9	618	2	A35827	thrombin (BC 3.4.2
450	29	56.9	625	2	G90570	hypothetical prote
451	29	56.9	625	2	E90236	arganyl-tRNA synth
452	29	56.9	670	2	D90738	hypothetical prote
453	29	56.9	670	2	F85588	hypothetical prote
454	29	56.9	671	2	A40692	signal recognition
455	29	56.9	678	2	B70913	probable penicillin
456	29	56.9	679	2	A24788	pilin protein - Ne
457	29	56.9	681	2	S37809	transketolase (EC
458	29	56.9	683	2	E86358	PI2K8.13 protein -
459	29	56.9	702	2	T16533	hypothetical prote
460	29	56.9	741	2	G69514	hypothetical prote
461	29	56.9	747	1	A27366	AMP deaminase (EC
462	29	56.9	747	1	I39444	AMP deaminase (EC
463	29	56.9	754	2	S61113	YTA6 protein - Yea
464	29	56.9	768	2	A82009	DNA topoisomerase
465	29	56.9	768	2	H81236	transducer protein
466	29	56.9	773	1	T44989	kinesin-related pr
467	29	56.9	784	1	A55236	
468	29	56.9	797	2	D71621	hypothetical prote
469	29	56.9	820	2	H82302	ATP-dependent heil
470	29	56.9	871	2	A53429	acetylglutamate ki
471	29	56.9	970	2	A13605	potassium efflux s
472	29	56.9	1006	2	AD2195	hypothetical prote
473	29	56.9	1070	2	G84982	exodeoxyribonuclea
474	29	56.9	1099	2	AS9311	myosin VIII, ZMM3
475	29	56.9	1132	1	QSBPL	host specificity p
476	29	56.9	1132	2	H90834	host specificity p
477	29	56.9	1137	2	B90734	probable host spec
478	29	56.9	1138	2	D85584	probable tail comp
479	29	56.9	1168	1	MPAXIC	myosin heavy chain
480	29	56.9	1169	2	T18423	hypothetical prote
481	29	56.9	1175	2	F64489	hypothetical prote
482	29	56.9	1186	2	T51793	hypothetical prote
483	29	56.9	1206	2	T30555	nitric-oxide synth
484	29	56.9	1228	2	I40468	surface layer prot
485	29	56.9	1281	2	G83405	hypothetical prote
486	29	56.9	1390	2	T13153	polyprotein - Arab
487	29	56.9	1428	2	T08852	lutein A - Gallo
488	29	56.9	1764	2	S37827	hypothetical prote
489	29	56.9	2014	2	S46622	probable membrane
490	29	56.9	2155	2	T30197	alpha tectorin - m
491	29	56.9	7825	2	T15789	hypothetical prote
492	29	56.9	92	2	S37503	Ig kappa chain V r
493	29	56.9	99	2	JH0429	Ig kappa chain V-I
494	29	55.9	109	2	F30601	Ig kappa chain V-I
495	28.5	55.9	118	2	T03036	Ig light chain - h
496	28.5	55.9	517	2	T11665	probable cell divi
497	28	54.9	32	2	S38528	rRNA N-glycosidase
498	28	54.9	36	2	I46593	myosin - pig (frag
499	28	54.9	56	2	T07842	probable histone H
500	28	54.9	56	2	AG0629	conserved hypoteth
501	28	54.9	62	2	S42265	Ig kappa chain V r
502	28	54.9	76	2	T17960	hypothetical prote
503	28	54.9	80	2	E72267	hypothetical prote
504	28	54.9	82	2	AG0946	probable CopG-fam1
505	28	54.9	83	2	S78489	Ig kappa chain V r
506	28	54.9	84	2	S34099	Ig kappa chain V r
507	28	54.9	86	2	S16834	Ig kappa chain V r
508	28	54.9	86	2	S16824	Ig kappa chain V r
509	28	54.9	86	2	S16836	Ig kappa chain V r
510	28	54.9	86	2	S16838	Ig kappa chain V r
511	28	54.9	86	2	S16829	Ig kappa chain V r
512	28	54.9	86	2	S16835	Ig kappa chain V r
513	28	54.9	86	2	S16835	Ig kappa chain V r
514	28	54.9	87	2	T52592	Ig kappa chain V r
515	28	54.9	87	2	S34098	Ig kappa chain V r
516	28	54.9	88	2	S34087	Ig kappa chain V r
517	28	54.9	88	2	S34088	Ig kappa chain V r
518	28	54.9	91	2	S37525	Ig kappa chain V r
519	28	54.9	91	2	S37525	Ig kappa chain V r
520	28	54.9	92	2	S37523	Ig kappa chain V r
521	28	54.9	95	2	PH0862	Ig kappa chain V r
522	28	54.9	96	1	CCQFM2	cytochrome c2, iso
523	28	54.9	97	1	CCQFM2	cytochrome c2, iso
524	28	54.9	100	2	S76498	ribosomal protein
525	28	54.9	104	2	F86867	probable ps3 prote
526	28	54.9	107	2	S34005	Ig kappa chain V r
527	28	54.9	107	2	B48677	Ig kappa chain V-J
528	28	54.9	107	2	C48677	Ig light chain V-J
529	28	54.9	107	2	A48677	Ig kappa chain V-J
530	28	54.9	107	2	H75313	ribosomal protein
531	28	54.9	108	1	K1JHUN	Ig kappa chain V-I
532	28	54.9	108	2	S40377	Ig kappa chain - h
533	28	54.9	108	2	S36283	Ig lambda chain V
534	28	54.9	108	2	S11124	Ig kappa chain V r
535	28	54.9	110	2	S40326	Ig kappa chain V-J
536	28	54.9	110	2	S44118	Ig kappa chain V-J
537	28	54.9	111	1	KVMS40	Ig kappa chain V r
538	28	54.9	111	2	B37266	Ig kappa chain V r
539	28	54.9	113	2	S53482	hypothetical prote
540	28	54.9	115	1	K3HUCI	Ig kappa chain pr

541	28	54.9	115	2	A30553	Ig kappa chain pre	614	28	54.9	332	2	T00847	probable membrane
542	28	54.9	115	2	F30338	DNA transport mach	615	28	54.9	333	2	B97257	spore coat protein
543	28	54.9	115	2	C64160	hypothetical prote	616	28	54.9	335	2	A46678	endoglycosidase F2
544	28	54.9	117	1	Q3ECX1	hypothetical prote	617	28	54.9	337	2	S66515	protein kinase (EC
545	28	54.9	117	2	S40362	Ig kappa chain - h	618	28	54.9	340	2	C83827	molybdopterin bios
546	28	54.9	117	2	S42263	Ig kappa chain V r	619	28	54.9	343	2	H96976	tryptophan-tRNA sy
547	28	54.9	117	2	S43528	Ig kappa chain V r	620	28	54.9	345	2	T32416	hypothetical prote
548	28	54.9	117	2	D86031	hypothetical prote	621	28	54.9	348	2	B84448	hypothetical prote
549	28	54.9	117	2	P91184	hypothetical prote	622	28	54.9	350	2	T19609	nitrogenase cofact
550	28	54.9	120	2	S46374	Ig kappa chain V-J	623	28	54.9	352	2	S16047	probable nucleic-a
551	28	54.9	122	2	C90502	conserved hypotet	624	28	54.9	357	2	A97292	hypothetical prote
552	28	54.9	124	2	B96960	holo-acyl-carrier	625	28	54.9	357	2	B81292	hypothetical prote
553	28	54.9	125	2	AG1134	probable secreted	626	28	54.9	361	2	D59107	hypothetical prote
554	28	54.9	125	2	AF1134	Ig kappa chain pre	627	28	54.9	362	2	T42689	hypothetical prote
555	28	54.9	128	1	K3HU41	Ig kappa chain V-J	628	28	54.9	364	2	H87212	probable glucose e
556	28	54.9	128	2	S40343	Ig kappa chain V r	629	28	54.9	369	2	T24620	hypothetical prote
557	28	54.9	129	2	S52789	Ig kappa chain V r	630	28	54.9	371	2	G82369	emf protein VC0048
558	28	54.9	134	2	S11245	hypothetical prote	631	28	54.9	371	2	T08759	conserved hypotet
559	28	54.9	153	2	F81429	hypothetical prote	632	28	54.9	371	2	B88925	probable drug resl
560	28	54.9	153	2	AC2653	hypothetical prote	633	28	54.9	372	2	B72579	probable udp-gluc
561	28	54.9	163	2	E90522	hypothetical prote	634	28	54.9	376	2	H70745	membrane proteins
562	28	54.9	168	2	S72898	hypothetical prote	635	28	54.9	378	2	AD1188	membrane protein h
563	28	54.9	169	2	JN0514	filu protein - Sal	636	28	54.9	378	2	AD1546	bacteriochlorophyl
564	28	54.9	185	2	A75420	hypothetical prote	637	28	54.9	381	2	H65096	hypothetical prote
565	28	54.9	196	2	D87198	probable membrane	638	28	54.9	387	2	T24558	hypothetical prote
566	28	54.9	201	2	G86736	hypothetical prote	639	28	54.9	387	2	F82817	probable retroelem
567	28	54.9	205	2	S06867	crystalin (clone	640	28	54.9	387	2	H84461	hypothetical prote
568	28	54.9	206	2	AE0160	probable glutathio	641	28	54.9	388	2	T45896	acyl-CoA dehydrog
569	28	54.9	209	2	P90261	conserved hypotet	642	28	54.9	389	2	D90498	hypothetical prote
570	28	54.9	211	2	PS0045	nitrogenase (BC 1.	643	28	54.9	396	2	C75209	hypothetical prote
571	28	54.9	212	2	B89891	phosphate transp	644	28	54.9	397	2	E82860	lyttophan synthas
572	28	54.9	217	1	P69098	phosphate transp	645	28	54.9	397	2	E82860	hypothetical prote
573	28	54.9	219	2	S56899	probable membrane	646	28	54.9	400	2	A87700	threonine dehydrat
574	28	54.9	223	2	C41305	retrovirus-related	647	28	54.9	400	2	F81432	probable transamin
575	28	54.9	225	2	AG1350	hypothetical prote	648	28	54.9	407	2	T51543	TOM (target of myp
576	28	54.9	225	2	AB1721	hypothetical prote	649	28	54.9	408	2	F83379	conserved hypotet
577	28	54.9	235	2	G82381	conserved hypotet	650	28	54.9	412	2	T40899	probable proteinas
578	28	54.9	237	2	G75562	RNA polymerase ECF	651	28	54.9	412	2	T33638	hypothetical prote
579	28	54.9	242	2	G84052	probable NMD(P)H o	652	28	54.9	414	1	A38331	LEP100 protein pre
580	28	54.9	246	2	T35934	protein T01B10.5 l	653	28	54.9	415	2	D96524	protein T1N15.3 [l
581	28	54.9	249	2	A89592	proteasome compone	654	28	54.9	421	2	I56251	GTP binding protei
582	28	54.9	259	2	T37985	hypothetical prote	655	28	54.9	421	2	T43406	cullin-3 - fission
583	28	54.9	260	2	T33405	mannosyl-glycoprot	656	28	54.9	422	2	D86659	phosphoglutamate s
584	28	54.9	267	2	S19538	integrinase-recombin	657	28	54.9	424	2	F82503	hypothetical prote
585	28	54.9	268	2	H82893	38k ribosome-associ	658	28	54.9	430	2	E84212	hypothetical prote
586	28	54.9	269	2	JC7700	hypothetical prote	659	28	54.9	432	2	H64514	hypothetical prote
587	28	54.9	270	2	C86670	hypothetical prote	660	28	54.9	434	2	C96963	CBS domain; simila
588	28	54.9	274	2	G84353	hypothetical prote	661	28	54.9	440	1	TWBYM1	transcription fact
589	28	54.9	280	2	F97785	invasion protein h	662	28	54.9	440	2	F72038	RNA polymerase sig
590	28	54.9	281	2	H86159	hypothetical prote	663	28	54.9	440	2	A86587	RNA polymerase sig
591	28	54.9	284	2	F69759	atomatic hydrocarb	664	28	54.9	440	2	S74969	hypothetical prote
592	28	54.9	285	2	B86687	conserved hypotet	665	28	54.9	442	2	T28232	ORF MSV071 hypote
593	28	54.9	288	2	S34414	site-specific DNA-	666	28	54.9	444	2	T42537	probable transket
594	28	54.9	290	2	C70182	GTP-binding protei	667	28	54.9	444	2	F64420	hypothetical prote
595	28	54.9	292	2	AI1937	probable transcrip	668	28	54.9	450	2	AC2656	conserved hypotet
596	28	54.9	293	2	AH0633	hypothetical prote	669	28	54.9	453	2	T44310	H+-transporting tw
597	28	54.9	293	2	D95919	hypothetical prote	670	28	54.9	464	2	C84782	probable pyruvate
598	28	54.9	294	2	B97713	hypothetical prote	671	28	54.9	465	2	A64327	H+-transporting tw
599	28	54.9	298	2	S46996	B-cell receptor-as	672	28	54.9	465	2	C75028	probable H(+)-tran
600	28	54.9	300	2	F84594	hypothetical prote	673	28	54.9	465	2	F71213	H+-transporting AT
601	28	54.9	301	2	D70471	GTP-binding protei	674	28	54.9	465	2	T44675	conserved hypotet
602	28	54.9	305	2	G84256	hypothetical prote	675	28	54.9	472	2	AB3239	conserved hypotet
603	28	54.9	307	2	T39783	hypothetical prote	676	28	54.9	472	2	AG3171	glutamate synthase
604	28	54.9	309	2	S78291	probable transcrip	677	28	54.9	475	2	B75024	probable Zn-depend
605	28	54.9	309	2	AF3565	transporter BMEI10	678	28	54.9	475	2	G96927	probable glutamate
606	28	54.9	313	2	S17757	rRNA N-glycosidase	679	28	54.9	476	2	D71200	H+-transporting tw
607	28	54.9	320	2	C82476	site-specific reco	680	28	54.9	478	2	B56812	hypothetical prote
608	28	54.9	324	2	AB1269	delta-aminolevulin	681	28	54.9	478	2	T10030	hypothetical prote
609	28	54.9	325	2	T32282	hypothetical prote	682	28	54.9	482	2	A34948	cyclin-related cel
610	28	54.9	327	2	G81695	3-oxoacyl-(acyl-c	683	28	54.9	482	2	S01153	cell division cont
611	28	54.9	327	2	H71538	probable oxoacyl-c	684	28	54.9	484	2	T33504	hypothetical prote
612	28	54.9	331	2	A86713	cytochrome D ubiq	685	28	54.9	486	2	S57786	phosphogluconate d
613	28	54.9	331	2	A86278	hypothetical prote	686	28	54.9	486	2	C75154	hypothetical prote

687	28	54.9	489	1	NIBCAT	nitrogenase (EC 1.7.1.1)
688	28	54.9	490	2	A96745	probable cytosolic potassium channel
689	28	54.9	495	2	A40090	potassium channel
690	28	54.9	495	2	B39113	potassium channel
691	28	54.9	499	1	S17648	pyruvate kinase (E. coli)
692	28	54.9	499	2	S17649	pyruvate kinase (E. coli)
693	28	54.9	500	2	B95318	nitrogenase (EC 1.7.1.1)
694	28	54.9	500	2	B96739	nitrogenase (EC 1.7.1.1)
695	28	54.9	504	2	T10829	nitrogenase (EC 1.7.1.1)
696	28	54.9	513	2	T34546	nitrogenase (EC 1.7.1.1)
697	28	54.9	514	2	T47556	pyruvate kinase-i
698	28	54.9	517	2	T47134	hypothetical prote
699	28	54.9	550	2	T06379	SAR DNA-binding pr
700	28	54.9	552	1	B60000	nonstructural prot
701	28	54.9	553	2	F89960	hypothetical prote
702	28	54.9	564	2	E75179	DNA topoisomerase
703	28	54.9	564	2	D71034	probable type II D
704	28	54.9	565	2	B72660	probable type II D
705	28	54.9	568	2	T25162	frizzled-1 protein
706	28	54.9	573	2	H96744	probable cytosolic
707	28	54.9	582	2	H97306	TPR-repeat domain
708	28	54.9	585	2	F89953	pyruvate kinase (i
709	28	54.9	586	2	H86914	conserved hypothet
710	28	54.9	591	2	T03602	probable asparagin
711	28	54.9	599	2	H70143	hypothetical prote
712	28	54.9	602	2	A89868	hypothetical prote
713	28	54.9	616	2	S50998	transporter protei
714	28	54.9	621	2	T47843	dynammin-like prote
715	28	54.9	627	2	A97729	dnak protein limpo
716	28	54.9	632	2	T38126	probable electron
717	28	54.9	655	2	A57681	hypothetical prote
718	28	54.9	672	2	F71424	hypothetical prote
719	28	54.9	677	2	T18231	transketolase I -
720	28	54.9	680	1	XJBYTK	transketolase (EC
721	28	54.9	685	2	T40162	transketolase - fi
722	28	54.9	691	2	G69724	DNA topoisomerase
723	28	54.9	705	2	G86348	hypothetical prote
724	28	54.9	708	2	F87245	penicillin-bonding
725	28	54.9	711	2	S73898	DNA topoisomerase
726	28	54.9	723	2	H85092	hypothetical prote
727	28	54.9	726	2	T44187	infected cell prot
728	28	54.9	726	2	T44000	transport protein
729	28	54.9	745	2	T10924	3C3.15c protein -
730	28	54.9	767	2	T42974	ribonucleoside-dip
731	28	54.9	767	2	S64130	PRP22 protein homo
732	28	54.9	785	2	T38359	culin 3 homolog -
733	28	54.9	798	2	S62405	hypothetical prote
734	28	54.9	807	2	S25242	sucrose synthase (
735	28	54.9	812	2	D97438	hypothetical prote
736	28	54.9	816	2	T00919	hypothetical prote
737	28	54.9	817	2	T22442	hypothetical prote
738	28	54.9	819	2	G81698	leucyl-tRNA synthet
739	28	54.9	821	2	C64461	hypothetical prote
740	28	54.9	822	2	S66210	chloride channel p
741	28	54.9	830	1	B48723	replicational licens
742	28	54.9	852	2	T33824	hypothetical prote
743	28	54.9	860	2	JC4566	chitinase (EC 3.2.1
744	28	54.9	861	2	B84963	DNA topoisomerase
745	28	54.9	863	1	GNIYIH	retrovirus-related
746	28	54.9	886	1	JC5085	replicational licens
747	28	54.9	899	2	G36812	hypothetical prote
748	28	54.9	907	2	S23399	chloride channel p
749	28	54.9	952	1	OYMG	phosphoenolpyruvat
750	28	54.9	960	2	S22507	phosphoenolpyruvat
751	28	54.9	961	1	TSHUP4	thrombospondin 4 p
752	28	54.9	961	2	S67568	probable membrane
753	28	54.9	962	2	JC5808	G protein-coupled
754	28	54.9	968	2	T46568	ATP-dependent RNA
755	28	54.9	994	1	J00151	myosin heavy chain
756	28	54.9	1001	2	AG1979	hypothetical prote
757	28	54.9	1002	2	T30546	major surface glyc
758	28	54.9	1006	2	A53933	myosin I myr 4 - r
759	28	54.9	1021	2	T05901	hypothetical prote
760	28	54.9	1042	2	G64514	type I restriction
761	28	54.9	1042	2	T16169	hypothetical prote
762	28	54.9	1088	1	PIXPR	inner layer protei
763	28	54.9	1088	2	S39261	VPI protein - porc
764	28	54.9	1119	2	AC0045	probable membrane
765	28	54.9	1201	2	H69898	hypothetical prote
766	28	54.9	1251	2	S49645	probable membrane
767	28	54.9	1277	2	B84517	hypothetical prote
768	28	54.9	1281	2	T47214	nif-1 protein (lmp
769	28	54.9	1283	2	T29109	histidine kinase F
770	28	54.9	1286	1	S38058	hypothetical prote
771	28	54.9	1293	2	T27886	hypothetical prote
772	28	54.9	1298	2	T18359	nif-1 protein - Ne
773	28	54.9	1298	2	T18360	Os-1p - Neurospora
774	28	54.9	1314	2	A85176	hypothetical prote
775	28	54.9	1317	2	A54831	nuclear pore compl
776	28	54.9	1329	2	A84525	probable reticulum
777	28	54.9	1392	2	T01908	hypothetical prote
778	28	54.9	1423	1	S27941	serum albumin - se
779	28	54.9	1444	2	AH1239	DNA polymerase III
780	28	54.9	1444	2	AD1602	DNA polymerase III
781	28	54.9	1474	2	B85188	retrotransposon 1i
782	28	54.9	1478	2	T38712	ABC transporter SP
783	28	54.9	1515	2	T04204	hypothetical prote
784	28	54.9	1538	2	E70874	probable gp8b prot
785	28	54.9	1642	2	E15018	cobra venom factor
786	28	54.9	1714	2	E71609	Ser/Thr protein ki
787	28	54.9	1734	2	A41101	phorbol ester-bind
788	28	54.9	1758	2	T34393	hypothetical prote
789	28	54.9	1783	2	T42386	unconventional myo
790	28	54.9	1813	2	T19285	hypothetical prote
791	28	54.9	1860	2	T17485	peptide synthetase
792	28	54.9	1861	2	T13845	microtubule-associ
793	28	54.9	2088	2	E71436	hypothetical prote
794	28	54.9	2095	2	S29529	genome polyprotein
795	28	54.9	2329	2	S44625	C50C3.6 protein -
796	28	54.9	3061	1	JN0545	genome polyprotein
797	28	54.9	3216	2	C90538	hypothetical prote
798	28	54.9	3511	2	A59295	unconventional myo
799	28	54.9	3530	2	A59266	unconventional myo
800	28	54.9	92	2	S37502	Ig kappa chain V r
801	28	54.9	109	1	K3HUPM	Ig kappa chain V-I
802	28	54.9	114	2	S46375	Ig kappa chain V-J
803	28	54.9	392	2	B32370	cyclin B2 - Africa
804	28	54.9	398	2	S21529	cyclin B2 - mouse
805	28	54.9	398	2	T12530	hypothetical prote
806	28	54.9	399	2	S23596	cyclin B2 - chicke
807	28	54.9	423	2	S34226	cyclin B - rat
808	28	54.9	429	2	S34224	cyclin B - long-ta
809	28	54.9	430	2	A43285	cyclin B1 - mouse
810	28	54.9	430	2	I48316	cyclin B1 - mouse
811	28	54.9	430	2	JH0509	cyclin B - mouse
812	28	54.9	433	2	A32992	cyclin B1 - human
813	28	54.9	34	2	B26021	trialy protein - Bsc
814	28	54.9	36	2	S30981	gene 36 protein -
815	28	54.9	63	2	G95373	probable Nrea prot
816	28	54.9	67	2	A64321	archaeal histone -
817	28	54.9	67	2	D64416	archaeal histone -
818	28	54.9	67	2	D64513	archaeal histone,
819	28	54.9	72	2	D64513	ferredoxin 2[4Fe-4
820	28	54.9	72	2	S41699	hypothetical 8.1K
821	28	54.9	75	1	BVECKY	trialy protein - Bsc
822	28	54.9	75	2	C24544	trialy protein - Bsc
823	28	54.9	83	2	T03673	pil1 protein (clon
824	28	54.9	87	2	D82136	cell division topo
825	28	54.9	94	2	AP1403	ribosomal protein
826	28	54.9	94	2	AP1779	ribosomal protein
827	28	54.9	95	2	PH0865	Ig kappa chain V r
828	28	54.9	95	2	AB2014	hypothetical prote
829	28	54.9	98	2	PH1065	Ig kappa chain V r
830	28	54.9	99	2	T10554	hypothetical prote
831	28	54.9	101	2	S51384	hypothetical prote
832	28	54.9	103	2	S26332	Ig light chain V r

833	27	52.9	106	2	PL0262	Ig kappa chain V r	906	27	52.9	218	2	T36499	probable two-compo
834	27	52.9	106	2	H81852	HesB-like protein	907	27	52.9	219	2	G83137	riboflavin synthas
835	27	52.9	107	2	S24290	Ig kappa chain V r	908	27	52.9	219	2	T52088	glutathione transf
836	27	52.9	108	1	K1H0U	Ig kappa chain V-I	909	27	52.9	219	2	T52087	glutathione transf
837	27	52.9	108	1	K1H0KU	Ig kappa chain V-I	910	27	52.9	219	2	T52085	glutathione transf
838	27	52.9	108	1	K1H0RE	Ig kappa chain V-I	911	27	52.9	219	2	T52086	glutathione transf
839	27	52.9	108	2	S36277	Ig lambda chain V	912	27	52.9	224	2	G70119	hypothetical prote
840	27	52.9	108	2	I39154	Ig kappa chain (BR	913	27	52.9	227	2	B70438	hypothetical prote
841	27	52.9	108	4	P47271	nitrophenyl phosph	914	27	52.9	233	2	H84231	transcription repr
842	27	52.9	109	2	PH0888	Ig kappa chain V r	915	27	52.9	234	2	S14237	Ig kappa chain pre
843	27	52.9	109	2	B70037	hypothetical prote	916	27	52.9	237	2	S65313	probable membrane
844	27	52.9	109	4	S55848	Ig kappa chain V a	918	27	52.9	242	2	A86719	hypothetical prote
845	27	52.9	111	2	E53285	probable membrane	919	27	52.9	245	2	A81177	oxidoreductase yin
846	27	52.9	112	2	E95159	Ig kappa chain V a	920	27	52.9	245	2	C81929	phosphoribosylform
847	27	52.9	113	2	S61968	probable membrane	921	27	52.9	245	2	C83812	probable 1-(5-phos
848	27	52.9	114	2	D72552	hypothetical prote	922	27	52.9	246	1	R5D07	hypothetical prote
849	27	52.9	115	1	KVMSL6	Ig kappa chain pre	923	27	52.9	246	2	T46446	hypothetical prote
850	27	52.9	117	2	S24207	Ig kappa chain V r	924	27	52.9	247	2	T31140	hypothetical prote
851	27	52.9	125	2	T29941	hypothetical prote	925	27	52.9	248	2	T40415	cobalamin biosynth
852	27	52.9	126	2	H81089	HesB/Yadr/Yfhf fam	926	27	52.9	249	2	H64368	probable RING zinc
853	27	52.9	127	2	A23986	Ig kappa chain pre	927	27	52.9	249	2	C96775	hypothetical prote
854	27	52.9	128	2	PL0101	Ig kappa chain pre	928	27	52.9	249	1	T26482	homeotic protein H
855	27	52.9	128	2	D42524	A-ORF-H protein -	929	27	52.9	251	1	B60492	conserved hypothet
856	27	52.9	129	2	S52793	Ig kappa chain V r	930	27	52.9	251	2	C69046	transcription regu
857	27	52.9	135	2	S24320	hypothetical prote	931	27	52.9	252	2	C83877	ferritin precursor
858	27	52.9	143	2	F70727	Putative radC-like	932	27	52.9	253	2	S27358	hypothetical prote
859	27	52.9	148	2	A64965	hypothetical prote	933	27	52.9	253	2	D75193	ferritin heavy cha
860	27	52.9	156	2	T48047	hypothetical prote	934	27	52.9	254	1	FRFBH	hypothetical prote
861	27	52.9	157	2	B90574	probable DNA repai	935	27	52.9	254	2	E96535	proteasome endopep
862	27	52.9	158	2	C90979	hypothetical prote	936	27	52.9	254	2	B55904	hypothetical prote
863	27	52.9	159	2	T30445	probable transposa	937	27	52.9	254	2	E71225	probable ferritin
864	27	52.9	160	2	S31840	hypothetical prote	938	27	52.9	259	2	G84827	hypothetical prote
865	27	52.9	161	2	B97802	hypothetical prote	939	27	52.9	259	2	G75083	probable GDSL-mot
866	27	52.9	161	2	AF0536	conserved hypothet	940	27	52.9	261	2	G84453	glutathione S-tran
867	27	52.9	162	2	E71368	probable RNA polym	941	27	52.9	263	2	H84918	translation elonga
868	27	52.9	164	2	T17651	hypothetical prote	942	27	52.9	264	2	E75386	WD-repeat protein
869	27	52.9	164	2	A85063	hypothetical prote	943	27	52.9	265	2	AF1890	ORF4 protein - Chl
870	27	52.9	165	2	G81324	probable signal-tr	944	27	52.9	265	2	T18039	hypothetical prote
871	27	52.9	168	2	T14385	fatty acid elongas	945	27	52.9	268	2	C90321	oxidoreductase yne
872	27	52.9	168	2	T14434	probable beta-keto	946	27	52.9	270	2	B86788	hypothetical prote
873	27	52.9	169	2	T33949	hypothetical prote	947	27	52.9	270	2	F86897	probable drc prot
874	27	52.9	172	2	S23768	hypothetical prote	948	27	52.9	276	2	F70984	ribosomal protein
875	27	52.9	172	2	S26684	hypothetical prote	949	27	52.9	277	1	R5LV2	conserved hypothet
876	27	52.9	173	2	C84421	probable RING-H2 f	950	27	52.9	278	2	D82159	hypothetical prote
877	27	52.9	176	2	T22273	hypothetical prote	951	27	52.9	278	2	T26166	degv family protei
878	27	52.9	179	1	F64006	hypothetical prote	952	27	52.9	279	2	F95128	conserved hypothet
879	27	52.9	181	2	F70911	probable partial C	953	27	52.9	280	2	C97999	hypothetical prote
880	27	52.9	184	2	G85256	hypothetical prote	954	27	52.9	280	2	AF2558	dimethyladenosine
881	27	52.9	184	2	C85883	probable transcrip	955	27	52.9	281	2	E70173	hypothetical prote
882	27	52.9	184	2	A91039	probable transcrip	956	27	52.9	281	2	S62041	probable oxidoredu
883	27	52.9	186	2	F64157	hypothetical prote	957	27	52.9	282	2	T37144	hypothetical prote
884	27	52.9	191	2	B84890	hypothetical prote	958	27	52.9	283	2	T15964	hypothetical prote
885	27	52.9	192	2	E70167	ribosomal protein	959	27	52.9	284	2	T32281	hypothetical prote
886	27	52.9	195	2	B64359	endopeptidase Clp	960	27	52.9	287	2	S73160	probable N-acetyl
887	27	52.9	200	2	D70865	putative kinetoch	961	27	52.9	289	2	AG0812	N-acetylmutamoyl-1
888	27	52.9	200	2	T02710	hypothetical prote	962	27	52.9	289	2	B91042	N-acetylmutamoyl-1
889	27	52.9	200	2	C72332	conserved hypothet	963	27	52.9	289	2	A36964	hemp 5'-region hyp
890	27	52.9	201	2	E70163	hypothetical prote	964	27	52.9	289	2	B85886	probable aldolase
891	27	52.9	201	2	G72653	hypothetical prote	965	27	52.9	289	2	A53502	probable aldolase
892	27	52.9	201	2	T49213	competence protein	966	27	52.9	292	2	D91829	ribosomal protein
893	27	52.9	205	2	E70199	hypothetical prote	967	27	52.9	292	2	C86076	hypothetical prote
894	27	52.9	206	2	S76178	hypothetical prote	968	27	52.9	296	2	E71717	hypothetical prote
895	27	52.9	206	2	T01312	alpha-1-acid glyco	969	27	52.9	297	2	T13317	hypothetical prote
896	27	52.9	207	1	OMMS1	alpha-1-acid glyco	970	27	52.9	299	2	F72210	hypothetical prote
897	27	52.9	207	2	B35425	probable two-compo	971	27	52.9	299	2	T24086	hypothetical prote
898	27	52.9	208	2	F83265	hypothetical prote	972	27	52.9	300	2	T18796	DNA repair endo/ex
899	27	52.9	208	2	B89879	conserved hypothet	973	27	52.9	302	2	F90158	ornithine carbamoy
900	27	52.9	210	2	T40369	probable dna bindi	974	27	52.9	306	2	E70447	forminoglutamate
901	27	52.9	210	2	S51359	conserved hypothet	975	27	52.9	308	2	F84276	probable transcrip
902	27	52.9	215	2	H82830	DNA endonuclease (976	27	52.9	308	2	C83220	probable integrat
903	27	52.9	218	1	S14133	glutathione transf	977	27	52.9	308	2	F70917	probable transcrip
904	27	52.9	218	1	S36835		978	27	52.9	308	2	AF0809	

979 27 52.9 308 2 H65014
 980 27 52.9 311 2 AH3412
 981 27 52.9 312 2 AG2884
 982 27 52.9 312 2 D97660
 983 27 52.9 312 2 A46750
 984 27 52.9 318 2 T49167
 985 27 52.9 319 2 AE1443
 986 27 52.9 319 2 A11733
 987 27 52.9 320 1 G2BPSV
 988 27 52.9 320 2 S31172
 989 27 52.9 320 2 T28379
 990 27 52.9 323 2 T64186
 991 27 52.9 324 1 F69068
 992 27 52.9 325 2 T27688
 993 27 52.9 326 2 E64887
 994 27 52.9 327 2 D72503
 995 27 52.9 327 2 S33670
 996 27 52.9 327 2 T35322
 997 27 52.9 329 2 D64423
 998 27 52.9 331 2 G96785
 999 27 52.9 336 2 T09186
 1000 27 52.9 337 2 T31129

ALIGNMENTS

RESULT 1

PH1083
 Ig light chain V region (clone 111.67) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1083
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
 J:Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1083
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-98 <TIL>
 A:Cross-references: UNIPARC:UPI0000176ABF
 A:Experimental source: B cell, strain [NZB x NZW] F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.2%; Score 47; DB 2; Length 98;
 Best Local Similarity 90.9%; Pred. No. 0.056;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 |||||:|||||
 Db 24 RASKTISKYLA 34

RESULT 2

S26345
 Ig light chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
 C:Accession: S26345; S78447
 R:Stark, S.E.; Caton, A.J.
 J:Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421; PMID:1908510
 A:Accession: S26345
 A:Molecule type: mRNA
 A:Residues: 1-106 <STA>
 A:Cross-references: UNIPARC:UPI00001769B1; EMBL:X59177
 R:Caton, A.J.
 Submitted to the EMBL Data Library, April 1991
 A:Reference number: S78447

A:Accession: S78447
 A:Molecule type: mRNA
 A:Residues: 1-96, 'S', '98-106 <CAT>
 A:Cross-references: UNIPARC:UPI0000115F72; EMBL:X59177; NID:952307; PIDN:CAA41887.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.2%; Score 47; DB 2; Length 106;
 Best Local Similarity 90.9%; Pred. No. 0.06;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 |||||:|||||
 Db 24 RASKTISKYLA 34

RESULT 3

S04574
 Ig kappa chain precursor V region (MRL-RF24L) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
 C:Accession: S04574
 R:Kotler, R.; Noonan, D.J.; Strchal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
 Eur. J. Immunol. 17, 91-95, 1987
 A:Title: Molecular analysis of the murine lupus-associated anti-self response: involve
 A:Reference number: S04573; MUID:87133856; PMID:1102255
 A:Accession: S04574
 A:Molecule type: mRNA
 A:Residues: 1-127 <KOF>
 A:Cross-references: UNIPARC:UPI0000115DFF; EMBL:X14621; NID:952404; PIDN:CAA32774.1; PID
 A>Note: the authors translated the codon TAT for residue 30 as Thr
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-127/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 92.2%; Score 47; DB 2; Length 127;
 Best Local Similarity 90.9%; Pred. No. 0.071;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 |||||:|||||
 Db 44 RASKTISKYLA 54

RESULT 4

H30502
 Ig kappa chain V region (D42) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Nov-1988 #sequence_revision 03-Aug-1992 #text_change 21-Jan-2000
 C:Accession: H30502
 R:Belic, D.; Webster, D.M.; Rees, A.R.
 J:Immunol. 141, 1745-1753, 1988
 A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
 A:Reference number: A30502; MUID:88315787; PMID:2457627
 A:Accession: H30502
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-103 <EII>
 A:Cross-references: UNIPARC:UPI0000114DD4; GB:M21912; NID:9197077; PIDN:AAA38910.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 43; DB 2; Length 103;
 Best Local Similarity 81.8%; Pred. No. 0.36;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 |||||:|||||
 Db 21 RASKTISKYLA 31

RESULT 5

KIHUOU

Ig kappa chain V-I region (Ou) - human (tentative sequence)

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C/Accession: A01872

R/Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.

Science 169, 56-59, 1970

A/Title: Macroglobulin structure: variable sequence of light and heavy chains.

A/Reference number: A94242; MUID:70201507; PMID:5447531

A/Accession: A01872

A/Molecule type: protein

A/Residues: 1-108 <KOH>

A/Cross-references: UNIPROT:P01606; UNIPARC:UPI000012E149

A/Note: the sequence of the C region, which has the inv (3) marker, is also given

C/Comment: This chain was isolated from a Waldenstrom's macroglobulin.

C/Genetics:

A/Gene: GDB:IGKV1

A/Cross-references: GDB:136264

A/Map position: 2p12-2p12

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F/16-80/Domain: immunoglobulin homology <IMM>

F/23-88/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 74.5%; Score 38; DB 1; Length 108;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 10

Db 24 RASQSVSYLA 33

RESULT 6

S34102

Ig kappa chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999

C/Accession: S34102

R/Wagner, S.D.; Luzzatlo, L.

Eur. J. Immunol. 23, 391-397, 1993

A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A/Reference number: S34076; MUID:93170387; PMID:8436174

A/Accession: S34102

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-78 <WAG>

A/Cross-references: UNIPARC:UPI0000176B23; EMBL:X67186

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 78;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11

Db 15 RASQSVSYLA 25

RESULT 7

S16837

Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C/Accession: S16837

R/Blaison, G.; Kuntz, J.L.; Pasquali, J.L.

Eur. J. Immunol. 21, 1221-1227, 1991

A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa

A/Reference number: S16823; MUID:91243737; PMID:1903706

A/Accession: S16837

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-86 <BLA>

A/Cross-references: UNIPARC:UPI0000176DA6; EMBL:X54835

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-81/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 86;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11

Db 15 RASQSVSYLA 25

RESULT 8

S16830

Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C/Accession: S16830

R/Blaison, G.; Kuntz, J.L.; Pasquali, J.L.

Eur. J. Immunol. 21, 1221-1227, 1991

A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa

A/Reference number: S16823; MUID:91243737; PMID:1903706

A/Accession: S16830

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-86 <BLA>

A/Cross-references: UNIPARC:UPI0000176DA9; EMBL:X54828

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-81/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 86;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11

Db 15 RASQSVSYLA 25

RESULT 9

S16833

Ig kappa chain V-III region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C/Accession: S16833; S16838

R/Blaison, G.; Kuntz, J.L.; Pasquali, J.L.

Eur. J. Immunol. 21, 1221-1227, 1991

A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa

A/Reference number: S16823; MUID:91243737; PMID:1903706

A/Accession: S16833

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-86 <BLA>

A/Cross-references: UNIPARC:UPI0000176DA7; EMBL:X54831

A/Experimental source: clone dkv17

A/Accession: S16838

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-86 <BLM>

A/Cross-references: UNIPARC:UPI0000176DA7; EMBL:X54836

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/7-81/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 86;
Best Local Similarity 63.6%; Pred. No. 4.6;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||::|
Db 15 RASQSVSSYLA 25

RESULT 10
S16826

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S16826; S34101
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.

Eur. J. Immunol. 21, 1221-1227, 1991

A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706

A:Accession: S16826

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-86 <BLA>

A:Cross-references: UNIPARC:UPI0000115B92; EMBL:X54824; NID:g331653; PIDN:CAA38593.1; PID
R:Wagner, S.D.; Luzzatto, L.

Eur. J. Immunol. 23, 391-397, 1993

A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174

A:Accession: S34101

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-86 <WAG>

A:Cross-references: UNIPARC:UPI0000115B92; EMBL:X67185

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 86;
Best Local Similarity 63.6%; Pred. No. 4.6;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||::|
Db 15 RASQSVSSYLA 25

RESULT 11
S37506

Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37506

R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37506

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116576; EMBL:Z26606; NID:g405653; PIDN:CAA81359.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 72.5%; Score 37; DB 2; Length 92;
Best Local Similarity 63.6%; Pred. No. 4.9;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||::|
Db 7 RASQSVSSYLA 17

RESULT 12
S37512

Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37512

R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37512

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116576; EMBL:Z26622; NID:g405666; PIDN:CAA81353.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 72.5%; Score 37; DB 2; Length 92;
Best Local Similarity 63.6%; Pred. No. 4.9;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||::|
Db 7 RASQSVSSYLA 17

RESULT 13
S37522

Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37522

R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37522

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116586; EMBL:Z26622; NID:g405666; PIDN:CAA81375.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 72.5%; Score 37; DB 2; Length 92;
Best Local Similarity 63.6%; Pred. No. 4.9;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||::|
Db 7 RASQSVSSYLA 17

RESULT 14
S37516

Ig kappa chain V region (V-kappa 3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37516

R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+)IGD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37516

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116588; EMBL:Z26624; NID:g405674; PIDN:CAA81377.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 72.5%; Score 37; DB 2; Length 92;
Best Local Similarity 63.6%; Pred. No. 4.9;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
| | | | |
DB 7 RASQSVSYLA 17

RESULT 15

PC4282
Ig kappa chain (anti-Ss-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000

C/Accession: PC4282; PC4284

R/Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.

Biochem. Biophys. Res. Commun. 232, 101-106, 1997

A/Title: Molecular cloning of anti-Ss-A/Ro 60-KDa peptide fab fragments from infiltratin

A/Reference number: PC4279; PMID:97236289; PMID:9125110

A/Accession: PC4282

A/Molecule type: protein

A/Residues: 1-106 <SU2>

A/Cross-references: UNIPARC:UPI0000176B92

A/Note: E-42

A/Accession: PC4284

A/Molecule type: protein

A/Residues: 1-106 <SU2>

A/Cross-references: UNIPARC:UPI0000176B92

A/Note: E-56

C/Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjog

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/16-90/Domain: immunoglobulin homology <IMM>

QY 1 RASKTISKYLA 11
| | | | |
DB 22 RASQSVSYLA 32

RESULT 16

G44151
Ig kappa chain V region (IM-10) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

C/Accession: G44151

R/Rebedee, S.L.; Barbash, I.L.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.; Pya

Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992

A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.

A/Reference number: A44151; PMID:92228746; PMID:1373487

A/Accession: G44151

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-108 <ZEB>

A/Cross-references: UNIPARC:UPI00001139AC; GB:M88317; NID:G183968; PIDN:AAA35975.1; PID:

A/Note: nucleotide translation not given

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-89/Domain: immunoglobulin homology <IMM>

QY 1 RASKTISKYLA 11
| | | | |
DB 23 RASQSVSYLA 33

RESULT 17

S23628

Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S23628

R/Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gall, R.W.; Defcos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A/Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t

A/Reference number: S23623; PMID:92156804; PMID:1740665

A/Accession: S23628

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-111 <OLB>

A/Cross-references: UNIPARC:UPI0000115F96; EMBL:X59705; NID:G34022; PIDN:CAA42226.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

QY 1 RASKTISKYLA 11
| | | | |
DB 24 RASQSVSYLA 34

RESULT 18

S54905
Ig kappa chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C/Accession: S54905

R/Posito, G.; Traboni, C.

submitted to the EMBL Data Library, November 1994

A/Description: Cloning and sequencing of cDNA coding for the variable domains of a huma

A/Reference number: S54905

A/Accession: S54905

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-114 <ESP>

A/Cross-references: UNIPARC:UPI000011620A; EMBL:X82934; NID:G809554; PIDN:CAA58108.1; P

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-90/Domain: immunoglobulin homology <IMM>

QY 1 RASKTISKYLA 11
| | | | |
DB 24 RASQSVSYLA 34

RESULT 19

K3HUVG

Ig kappa chain precursor V-II region (Vg) - human

C/Species: Homo sapiens (man)

C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C/Accession: A01900

R/Pech, M.; Zachau, H.G.

Nucleic Acids Res. 12, 9229-9236, 1984

A/Title: Immunoglobulin genes of different subgroups are interdigitated within the V-K

A/Reference number: A93549; PMID:85087932; PMID:6440122

A/Accession: A01900

A/Molecule type: DNA

A/Residues: 1-115 <PEG>

A/Cross-references: UNIPROT:P04433; UNIPARC:UPI0000116D05; GB:X01668; GB:X02768; NID:G3

C/Note: the sequence was determined from the germline gene

C/Genetics:

A/Gene: GDB:IGKV3

A/Cross-references: GDB:136266

A/Map position: Zp12-Zp11

A:introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: Ig kappa chain V-III region (Vg) #status predicted <MAM>
F:21-43/Region: framework 1
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:55-69/Region: framework 2
F:70-76/Region: complementarity-determining 2
F:77-108/Region: framework 3
F:109-115/Region: complementarity-determining 3
F:43-108/Disulfide bonds: #status predicted

Query Match 72.5%; Score 37; DB 1; Length 115;
Best Local Similarity 63.6%; Pred. No. 6;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
||||:|
Db 44 RASQSVSYLA 54

RESULT 20
A56701
Ig kappa chain V region precursor (Hua) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: A56701
R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J Biol. Chem. 270, 12457-12465, 1995
A:Title: Human and mouse monoclonal antibodies to blood group A substance, which are new
A:Reference number: A56701; MUID:95279371; PMID:7759488
A:Accession: A56701
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <NIC>
A:Cross-references: UNIPARC:UPI0000113826; GB:141174; NID:6762823; PIDN:AA64877.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 128;
Best Local Similarity 63.6%; Pred. No. 6.7;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
||||:|
Db 44 RASQSVSYLA 54

RESULT 21
S40379
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40379
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40379
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: UNIPARC:UPI0000116181; EMBL:X72489; NID:9441446; PIDN:CAA51157.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 128;

Best Local Similarity 63.6%; Pred. No. 6.7;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
||||:|
Db 44 RASQSVSYLA 54

RESULT 22
S40363
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40363
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40363
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: UNIPARC:UPI0000116171; EMBL:X72473; NID:9441444; PIDN:CAA51141.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-109/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 37; DB 2; Length 129;
Best Local Similarity 63.6%; Pred. No. 6.7;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
||||:|
Db 43 RASQSVSYLA 53

RESULT 23
PL0106
Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma secr
A:Reference number: PL0106; MUID:89235583; PMID:2541221
A:Accession: PL0106
A:Molecule type: mRNA
A:Residues: 1-144 <SLI>
A:Cross-references: UNIPARC:UPI00001767A2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRB>

Query Match 72.5%; Score 37; DB 2; Length 144;
Best Local Similarity 63.6%; Pred. No. 7.4;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
||||:|
Db 44 RASQSVSYLA 54

RESULT 24
S57444
Ig kappa chain V-J region - human (fragment)

A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34082
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <WA2>
A:Cross-references: UNIPARC:UPI000011604F; EMBL:X66042; NID:G33318; PIDN:CAA46841.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 68.6%; Score 35; DB 2; Length 71;
Best Local Similarity 72.7%; Pred. No. 9.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||: |||
Db 17 RASQGISNYLA 27

RESULT 30
S34090
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34090
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34090
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <WA2>
A:Cross-references: UNIPROT:Q9UL79; UNIPARC:UPI00001160A2; EMBL:X67174
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 82;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||: |||
Db 15 RASQGISNYLA 25

RESULT 31
S16832
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16832
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(Kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16832
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI00001160D68; EMBL:X54830
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 86;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||: |||
Db 15 RASHSVSYLA 25

RESULT 32
S21523
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C:Accession: S34079; S21523
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <WA2>
A:Cross-references: UNIPARC:UPI000011604C; EMBL:X66039; NID:G333312; PIDN:CAA46838.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 87;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||: |||
Db 17 RASQGISNYLA 27

RESULT 33
S21525
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C:Accession: S34081; S21525
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34081
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <WA2>
A:Cross-references: UNIPARC:UPI000011604B; EMBL:X66041; NID:G333316; PIDN:CAA46840.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 88;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||: |||
Db 17 RASQGISNYLA 27

RESULT 34
S21520
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C:Accession: S34077; S21520
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34077
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <WA2>
A:Cross-references: UNIPARC:UPI000011604A; EMBL:X66037; NID:G333306; PIDN:CAA46836.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 88;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:||||
Db 17 RASQGISNYLA 27

RESULT 35

S34104
Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34104

R;Wagner, S.D.; Luzzatlo, L.

Eur. J. Immunol. 23, 391-397, 1993

A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A:Reference number: S34076; MUID:93170387; PMID:8436174

A:Accession: S34104

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-88 <MAG>

A:Cross-references: UNIPARC:UPI000011604B; EMBL:X66038; NID:933310; PIDN:CAA46837.1; PIR

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 88;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:||||
Db 17 RASQGISNYLA 27

RESULT 36

S21524
Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C:Accession: S34080; S21524

R;Wagner, S.D.; Luzzatlo, L.

Eur. J. Immunol. 23, 391-397, 1993

A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed

A:Reference number: S34076; MUID:93170387; PMID:8436174

A:Accession: S34080

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-88 <MA2>

A:Cross-references: UNIPARC:UPI000011604D; EMBL:X66040; NID:933314; PIDN:CAA46839.1; PIR

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 88;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:||||
Db 17 RASQGISNYLA 27

RESULT 37

PH0866

Ig kappa chain V region (anti-DNA, 1X7RG1) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000

C:Accession: PH0866

C:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype

A:Reference number: PH0862; MUID:92078875; PMID:1660528

A:Accession: PH0866

A:Molecule type: DNA

A:Residues: 1-95 <MAN>

A:Cross-references: UNIPARC:UPI0000176DA3

C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bear

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-95/Region: complementarity-determining 3

Query Match 68.6%; Score 35; DB 2; Length 95;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:||||
Db 24 RASQGISNYLA 34

RESULT 38

PH0863

Ig kappa chain V region (anti-DNA, III-2R) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 31-Dec-2004

C:Accession: PH0863

R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype

A:Reference number: PH0862; MUID:92078875; PMID:1660528

A:Accession: PH0863

A:Molecule type: DNA

A:Residues: 1-95 <MAN>

A:Cross-references: UNIPROT:Q9UL70; UNIPARC:UPI0000176DA0

C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bear

C:Superfamily: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:16-90/Domain: immunoglobulin homology <IMM>

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-95/Region: complementarity-determining 3

Query Match 68.6%; Score 35; DB 2; Length 95;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:||||
Db 24 RASQGISNYLA 34

RESULT 39

S44117

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C:Accession: S44117

R;Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

submitted to the EMBL Data Library, March 1994

A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable

```
A:Reference number: S44105
A:Accession: S44117
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <HAM>
A:Cross-references: UNIPARC:UPI0000116633; EMBL:Z1393; NID:g472971; PIDN:CAA83268.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-90/Domain: immunoglobulin homology <IMM>

Query Match      68.6%; Score 35; DB 2; Length 101;
Best Local Similarity 72.7%; Pred. No. 13;
Matches      8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
      |||: |||
      19 RASQGISNYLA 29

Db

RESULT 40
C33936
Ig kappa chain V region (VM13) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C:Accession: C33936
R:Meek, K.; Johanson, B.; Schuman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A:Reference number: A33936; MUID:89282831; PMID:2471975
A:Accession: C33936
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <MEB>
A:Cross-references: UNIPARC:UPI0000114884; GB:J04577; NID:9623187; PIDN:AAA60443.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      68.6%; Score 35; DB 2; Length 106;
Best Local Similarity 63.6%; Pred. No. 14;
Matches      7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
      |||: |||
      24 KASQDINKYLA 34

Db

RESULT 41
S36268
Ig lambda chain V region (clone alpha-THY-33) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36268
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36266; MUID:93178448; PMID:7679990
A:Accession: S36268
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: UNIPARC:UPI0000176CD6; EMBL:Z18837
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      68.6%; Score 35; DB 2; Length 107;
Best Local Similarity 63.6%; Pred. No. 14;
Matches      7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
      |||: |||
      24 RASQGISNYLA 34

Db
```

```
RESULT 42
S36275
Ig lambda chain V region (clone alpha-FOG1-A4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36275
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36275
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: UNIPARC:UPI0000118DED; EMBL:Z18827; NID:g33416; PIDN:CAA79279.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      68.6%; Score 35; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 14;
Matches      8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
      |||: |||
      24 RASQGISNYLA 34

Db

RESULT 43
S40366
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40366
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40366
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-107 <KLB>
A:Cross-references: UNIPARC:UPI0000116174; EMBL:X72476; NID:g441420; PIDN:CAA51144.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match      68.6%; Score 35; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 14;
Matches      8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
      |||: |||
      36 RASQGISNYLA 46

Db

RESULT 44
K1RHUHU
Ig kappa chain V-I region (Hau) - human
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C:Accession: A01868; S02574
R:Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970
A:Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg
A:Reference number: A01868; MUID:71032830; PMID:4097974
A:Accession: A01868
A:Molecule type: protein
A:Residues: 1-108 <MAT>
A:Cross-references: UNIPROT:P01600; UNIPARC:UPI000012E143
A>Note: the C region of this chain has the Inv (3) marker
```

R:Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987

A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A:Reference number: S02572; PMID:8600515; PMID:3115831

A:Contents: annotation
C:Comment: This is a Bence Jones protein.

C:Genetics:
A:Gene: GDB:IGKV1

A:Cross-references: GDB:136264

A:Map position: 2p12-2p12

C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into 16

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

F:23-88/Disulfide bonds: #status predicted

Query Match 68.6%; Score 35; DB 1; Length 108;

Best Local Similarity 63.6%; Pred. No. 14;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11

Db 24 RASQGISSTYLA 34

RESULT 45

S34007

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S34007

R:Marlette, X.; Tsapis, A.; Brunet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; PMID:93209281; PMID:7681398

A:Accession: S34007

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <MAR>

A:Cross-references: UNIPARC:UPI0000176CC8

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 108;

Best Local Similarity 72.7%; Pred. No. 14;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11

Db 24 RASQGISSTYLA 34

RESULT 46

S30521

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S30521

R:Marlette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30521

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <MAR>

A:Cross-references: UNIPARC:UPI0000176B26; EMBL:Z18327

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 108;

Best Local Similarity 72.7%; Pred. No. 14;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11

Db 24 RASQGISSTYLA 34

RESULT 47

C21056

Ig kappa chain precursor V region (HK137) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000

C:Accession: C21056

R:Bentley, D.L.; Rabbits, T.H.

Cell 32, 181-189, 1983

A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplica

A:Reference number: A21056; PMID:83129397; PMID:6402305

A:Accession: C21056

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-117 <BEN>

A:Cross-references: UNIPARC:UPI00001198E4; GB:J00248; NID:G185991; PIDN:AAA59094.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 117;

Best Local Similarity 72.7%; Pred. No. 15;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11

Db 46 RASQGISSTYLA 56

RESULT 48

S40318

Ig kappa chain V region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40318

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; PMID:94080891; PMID:8258341

A:Accession: S40318

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-124 <KLE>

A:Cross-references: UNIPARC:UPI0000116144; EMBL:X72428; NID:G441324; PIDN:CAA51096.1; P

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 35; DB 2; Length 124;

Best Local Similarity 72.7%; Pred. No. 16;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11

Db 40 RASQGISSTYLA 50

RESULT 49

S40336

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40336

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40336

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-124 <KLE>

A:Cross-references: UNIPARC:UPI0000116156; EMBL:X72446; NID:G441360; PIDN:CAA5114.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:31-105/Domain: immunoglobulin homology <IMM>

Query Match

68.6%; Score 35; DB 2; Length 124;

Best Local Similarity 72.7%; Pred. No. 16;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11

DB 39 RASQGISRWLA 49

RESULT 50

S11240

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S11240

R:Feigenhauer, M.; Kohl, J.; Rueker, F.

Nucleic Acids Res. 18, 4927, 1990

A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A:Reference number: S11239; MUID:90370490; PMID:1697678

A:Accession: S11240

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-127 <PEL>

A:Cross-references: UNIPARC:UPI0000113780; EMBL:X53612; NID:G23868; PIDN:CAA37674.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match

68.6%; Score 35; DB 2; Length 127;

Best Local Similarity 63.6%; Pred. No. 16;

Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11

DB 46 RASQGISRWLA 56

Search completed: January 17, 2006, 12:06:06
Job time : 22.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:47:28 ; Search time 62 Seconds
(without alignments)
125.174 Million cell updates/sec

Title: US-10-665-658-13
Perfect score: 51
Sequence: 1 RASKTISKYIA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	76.5	217	2	05A224 CANAL
2	39	76.5	569	2	08T203 DICDI
3	38	74.5	108	1	KVIN_HUMAN
4	37	72.5	115	1	KV31_HUMAN
5	37	72.5	479	2	Q961T5 DROME
6	37	72.5	1007	2	Q9V474 DROME
7	36	70.6	47	2	Q4L3Y6 STAHJ
8	36	70.6	236	2	Q7Z3Y4_HUMAN
9	36	70.6	384	2	Q6BUD5_DEBHA
10	36	70.6	421	2	Q9E200_GALPH
11	36	70.6	510	1	YD85_SCHPO
12	36	70.6	602	2	08S191_CLOPA
13	36	70.6	765	2	Q4WRT7_ASPTU
14	36	70.6	1981	2	Q5ZTT4_LEGPH
15	35	68.6	108	1	KV1H_HUMAN
16	35	68.6	108	2	Q9UL70_HUMAN
17	35	68.6	136	2	Q5FLS2_IACAC
18	35	68.6	208	1	RS8_SPOPR
19	35	68.6	208	2	Q6F475_PLUXY
20	35	68.6	236	2	Q6PIH7_HUMAN
21	35	68.6	252	2	Q9H61_SCADU
22	35	68.6	409	2	Q6BTH9_DEBHA
23	35	68.6	584	2	Q5EY37_AEDAE
24	35	68.6	749	2	Q7UR05_RHOBA
25	35	68.6	812	2	Q5PAZ8_AYAWM
26	35	68.6	853	1	TOP1_BUCAP
27	35	68.6	911	2	QANCY4_9MICC
28	34	66.7	107	2	Q9UL81_HUMAN
29	34	66.7	107	2	Q96SA9_HUMAN
30	34	66.7	108	2	Q9UL77_HUMAN
31	34	66.7	129	1	KV1W_HUMAN

32	34	66.7	200	2	Q5W550_9DIPT	05w550 polietina n
33	34	66.7	205	2	Q8YYN6_ANASP	08yyne anabaena sp
34	34	66.7	206	2	Q8ESJ5_OCBIRH	08esjs oceanobacill
35	34	66.7	208	2	Q5UAN6_BOWMO	05uan6 bombyx mori
36	34	66.7	220	2	Q74ZE2_ASHGO	074ze2 ashbya goss
37	34	66.7	234	1	GU33_RAT	03g33 ratcus norv
38	34	66.7	234	2	Q7Z473_HUMAN	07z473 homo sapien
39	34	66.7	253	2	Q57DQ0_BRUAB	057dq0 bruceella ab
40	34	66.7	253	2	Q8G165_BRUSU	08g165 bruceella su
41	34	66.7	253	2	Q8YGP8_BRUSU	08ygp8 bruceella me
42	34	66.7	271	2	Q59Z41_CANAL	059z41 candida alb
43	34	66.7	295	2	Q9KSM5_VIRCH	09kems vibrio chol
44	34	66.7	304	2	Q73HE3_MOLPM	073he3 wolbachia p
45	34	66.7	318	2	Q7WCJ1_BORPA	07wcj1 bordetella
46	34	66.7	318	2	Q7WCJ7_BORBR	07wcj7 bordetella
47	34	66.7	331	2	Q7TRF3_MOUSE	07trf3 mus musculu
48	34	66.7	334	2	Q4VIC2_BACCZ	04vic2 bacillus ce
49	34	66.7	379	2	Q8L7C4_ARATH	08l7c4 arabidopsis
50	34	66.7	390	2	Q6OPC2_CABER	06opc2 caenorhabd
51	34	66.7	391	2	Q8GYH4_ARATH	08gyh4 arabidopsis
52	34	66.7	406	2	Q8LG65_ARATH	08lg65 arabidopsis
53	34	66.7	406	2	Q9FN21_ARATH	09fn21 arabidopsis
54	34	66.7	415	2	Q04344_ARATH	004344 arabidopsis
55	34	66.7	417	2	Q9LJ77_ARATH	09lj77 arabidopsis
56	34	66.7	431	2	Q5LEF7_BACFN	05lef7 bacteroides
57	34	66.7	440	2	Q5H182_STAAC	05h182 staphylococ
58	34	66.7	440	2	Q6GJ74_STAHJ	06gj74 staphylococ
59	34	66.7	452	2	Q4ZLS8_PSESY	04zls8 pseudomonas
60	34	66.7	452	2	Q4K447_PSEPS	04k447 pseudomonas
61	34	66.7	452	2	Q87J18_PSSSM	087j18 pseudomonas
62	34	66.7	467	2	Q9WZRE_THEMEA	09wzre thermotoga
63	34	66.7	482	2	Q99W18_STAHJ	099w18 staphylococ
64	34	66.7	482	2	Q7A753_STAHJ	07a753 staphylococ
65	34	66.7	545	2	Q682S0_ARATH	0682s0 arabidopsis
66	34	66.7	593	2	Q93YA6_ARATH	093ya6 arabidopsis
67	34	66.7	593	2	Q9M6N8_ARATH	09m6n8 arabidopsis
68	34	66.7	613	2	Q6KIK8_MYCOK	06kik8 mycoplasma
69	34	66.7	635	2	Q7R030_GIALA	07r030 giardia lam
70	34	66.7	682	1	PAD16_MOUSE	0pad16 mus musculu
71	34	66.7	694	2	Q5A515_CANAL	05a515 candida alb
72	34	66.7	758	2	Q6KHJ6_MYCOK	06khj6 mycoplasma
73	34	66.7	770	2	Q54F34_DICDI	054f34 dictyosteli
74	34	66.7	779	2	Q611N7_CABER	0611n7 caenorhabd
75	34	66.7	784	2	Q5XWM4_SOLTR	05xwm4 solanum tub
76	34	66.7	856	2	Q4Y127_PLACH	04y127 plasmodium
77	34	66.7	878	2	Q613U1_SOLDE	0613u1 solanum dem
78	34	66.7	903	2	Q9NCX8_DROME	09ncx8 drosophila
79	34	66.7	903	2	Q9VZ19_DROME	09vz19 drosophila
80	34	66.7	912	2	Q95V83_DROME	095v83 drosophila
81	34	66.7	912	2	Q5LAW0_BACFN	05law0 bacteroides
82	34	66.7	912	2	Q6ARA7_BACFN	06ara7 bacteroides
83	34	66.7	920	2	Q7RJS2_ANOCA	07rjs2 anopheles g
84	34	66.7	932	2	Q6PUB4_ANOCA	06pub4 anopheles g
85	34	66.7	977	2	Q5VUY0_CRYNE	05vyu0 cryptococcu
86	34	66.7	977	2	Q5SQ96_CRYNE	05sq96 cryptococcu
87	34	66.7	977	2	Q5KFX1_CRYNE	05kfx1 cryptococcu
88	34	66.7	977	2	Q97349_9TRYP	097349 trypanosoma
89	34	66.7	1096	2	Q97350_9TRYP	097350 trypanosoma
90	34	66.7	1096	2	Q7RNM8_PLAIO	07rnm8 plasmodium
91	34	66.7	114	2	Q9RIJ2_STREY	09rij2 streptococ
92	34	66.7	114	2	Q03750_PASWU	003750 pasteurella
93	34	66.7	117	1	KV1J_HUMAN	001602 homo sapien
94	34	66.7	118	2	Q4FUD8_GCANM	04fud8 psychrobact
95	34	66.7	139	2	Q7VPE1_HABBU	07vpe1 haemophilus
96	34	66.7	157	2	Q971S0_SULTO	0971s0 sulfobius
97	34	66.7	160	2	Q88WU2_LACPL	088wu2 lactobacill
98	34	66.7	188	2	Q5E688_VIBEL	05e688 vibrio fisc
99	34	66.7	220	2	Q4K594_PSEBS	04k594 pseudomonas
100	34	66.7	221	2	Q88QH8_PSEBK	088qh8 pseudomonas
101	34	66.7	225	2	Q49597_MYCKA	049597 mycobacteri
102	34	66.7	236	2	Q6GMX9_HUMAN	06gmx9 homo sapien
103	34	66.7	241	2	Q921A6_MOUSE	0921a6 mus musculu
104	34	66.7	247	2	Q4T8A0_TETNG	04t8a0 tetraodon n

105	33	64.7	260	2	Q6N6T0_RHOPA	Q6n6t0 rhodopeau	178	32	62.7	236	2	Q4PC87_USTMA	Q4pc87 ustlago ma
106	33	64.7	289	2	Q55R16_CRYNE	Q55r16 cryptococcu	179	32	62.7	241	2	Q4X638_PLACH	Q4x638 plasmodium
107	33	64.7	289	2	Q5KTV1_CRYNE	Q5ktv1 cryptococcu	180	32	62.7	245	1	TPP1_SACMI	Q9net1 saccharomyc
108	33	64.7	296	2	Q5DM12_BPTS	Q5dm12 bacterioph	181	32	62.7	245	2	Q5OP04_ENTHI	Q5OP04 entamoeba h
109	33	64.7	296	2	Q66LU4_BPTS	Q66lu4 bacterioph	182	32	62.7	245	2	Q51408_ENTHI	Q51408 entamoeba h
110	33	64.7	296	2	Q6QGG6_BPTS	Q6qgg6 bacterioph	183	32	62.7	261	1	DEBA_BACCU	P39971 bacillus eu
111	33	64.7	296	2	Q5XCS2_STRP6	Q5xcs2 streptococc	184	32	62.7	277	2	Q7Y424_9CAUD	Q7Y424 enterobacte
112	33	64.7	296	2	Q8K7Y6_STRP6	Q8k7y6 streptococc	185	32	62.7	279	2	Q7MJC1_VIBVY	Q7mjcl vibrio vuln
113	33	64.7	296	2	Q8PIG3_STRP8	Q8pig3 streptococc	186	32	62.7	286	2	Q9XR71_VIBCH	Q9xr71 vibrio chol
114	33	64.7	296	2	Q8ADJ1_STRPY	Q8adj1 streptococc	187	32	62.7	287	2	Q7MJE7_VIBVY	Q7mje7 vibrio vuln
115	33	64.7	297	2	Q7QSP4_ANGPA	Q7qsp4 anophelies g	188	32	62.7	289	2	Q31286_9ENTR	Q31286 buchnera ap
116	33	64.7	332	2	Q7MRH1_WOLSU	Q7mrh1 wolinhella s	189	32	62.7	295	2	Q8RR58_9GAMM	Q8rr58 acinetobact
117	33	64.7	359	2	Q66660_9GAMA	Q66660 equid herpe	190	32	62.7	315	2	Q16934_9BILA	Q16934 anisocytro
118	33	64.7	388	2	Q986Y6_RHILU	Q986y6 rhizobium l	191	32	62.7	325	2	Q9L6K3_9GAMP	Q9L6K3 methylophag
119	33	64.7	389	2	Q6CIP3_KLUTA	Q6cip3 kluyveromyc	192	32	62.7	335	2	Q7VOL8_PROMP	Q7VOL8 prochloroco
120	33	64.7	391	2	Q73WP2_TREDE	Q73wp2 treponema d	193	32	62.7	338	2	Q73GC9_WOLPM	Q73gc9 wolbachia p
121	33	64.7	393	1	HEMH_YEAST	P16622 saccharomyc	194	32	62.7	340	2	Q8S7UO_ORYSA	Q8s7uo oryza sativ
122	33	64.7	431	1	Q6LX43_MERTMP	Q6lx43 methanococc	195	32	62.7	343	2	Q6WU11_MYCMS	Q6wu11 mycoplasma
123	33	64.7	434	1	GATX_METUA	Q58560 methanococc	196	32	62.7	347	2	Q5GTT1_WOLTR	Q5gtt1 wolbachia s
124	33	64.7	478	2	Q5CVI4_CRYPH	Q5cv14 cryptospori	197	32	62.7	348	2	Q4ID19_GIBZE	Q4id19 gibberella
125	33	64.7	491	2	Q5CMT4_CRYHO	Q5cmt4 cryptospori	198	32	62.7	354	1	RAD57_SCHPO	Q9u12 schizosacch
126	33	64.7	498	2	Q6LBB3_OLICA	Q6lbb3 oligotropha	199	32	62.7	358	2	Q5MKF3_BACSK	Q5mkf3 bacillus cl
127	33	64.7	498	2	Q4UVX5_XANCP	Q4uvx5 xanthomonas	200	32	62.7	378	2	Q4NMV6_9DELT	Q4nmv6 anaeromyxob
128	33	64.7	533	2	Q8P865_XANCP	Q8p865 xanthomonas	201	32	62.7	382	2	Q9UG58_HUMAN	Q9ug58 homo sapien
129	33	64.7	533	2	Q4NIX0_THEBA	Q4nix0 theileria p	202	32	62.7	389	1	INX6_CAEBL	Q9u34 caenorhabdi
130	33	64.7	533	2	Q4U977_THEAN	Q4u977 theileria a	203	32	62.7	397	1	ACKA2_VIBPA	Q8tj5 vibrio para
131	33	64.7	533	2	Q6MSM2_MYCMS	Q6msm2 mycoplasma	204	32	62.7	397	1	UT2_RABIT	Q28614 oryctolagus
132	33	64.7	553	2	Q8R8S8_THETN	Q8r8s8 thermoaer	205	32	62.7	399	1	KPR52_ORYSA	Q69xq6 oryza sativ
133	33	64.7	556	1	YMC3_YEAST	Q03718 saccharomyc	206	32	62.7	399	2	Q6NG05_CORDI	Q6ng05 corynebacte
134	33	64.7	563	1	Q5SFE7_DICDI	Q5sfe7 dictyostell	207	32	62.7	406	2	Q8Y4W1_CLOTE	Q8y4w1 clostridium
135	33	64.7	584	2	Q4SHY0_TETNG	Q4shy0 tetraodon n	208	32	62.7	427	2	Q4TLX2_9SPHN	Q4tlx2 erythrobact
136	33	64.7	584	2	Q4WJM3_ASPPU	Q4wjm3 aspergillus	209	32	62.7	432	1	YC31_YEAST	Q4tlx2 erythrobact
137	33	64.7	608	2	Q98G18_RHILU	Q98g18 rhizobium l	210	32	62.7	435	2	Q4TUY2_9SPHN	Q4tly2 erythrobact
138	33	64.7	656	1	DNLT_HELPY	Q92418 helicobacte	211	32	62.7	440	2	Q6GBP2_STANM	Q6gbp2 staphylococ
139	33	64.7	656	1	DNLT_HELPY	Q25336 helicobacte	212	32	62.7	440	2	Q8NXX9_STANM	Q8nxx9 staphylococ
140	33	64.7	731	2	Q4N264_THEBA	Q4n264 theileria p	213	32	62.7	443	2	Q8TPI6_DROME	Q8tip6 dirosophila
141	33	64.7	758	2	Q4N7W0_THEBA	Q4n7w0 theileria p	214	32	62.7	449	2	Q51ZM2_MAGGR	Q51zm2 magnaporthe
142	33	64.7	758	2	Q4U9G7_THEAN	Q4u9g7 theileria a	215	32	62.7	451	2	Q5NBP4_ORYSA	Q5nbp4 oryza sativ
143	33	64.7	768	2	Q7SELO_ASHGO	Q7selo ashbya goss	216	32	62.7	466	1	VATB_AERPE	Q9y3f6 aetopyrum p
144	33	64.7	816	2	Q5CTP5_WOLTR	Q5ctp5 wolbachia s	217	32	62.7	471	2	Q677Z3_9VIRU	Q677z3 lymphocyeti
145	33	64.7	861	2	Q8H6S8_PEA	Q8h6s8 plisum sattiv	218	32	62.7	474	1	VRK3_HUMAN	Q81f63 homo sapien
146	33	64.7	909	2	Q8IDR8_PLAF7	Q8idr8 plasmodium	219	32	62.7	474	1	Q9V048_PYPAB	Q9v048 pyrococcus
147	33	64.7	909	2	Q9Y007_PLAF7	Q9y007 plasmodium	220	32	62.7	474	2	Q502Y2_HUMAN	Q502y2 homo sapien
148	33	64.7	961	2	Q6FRK6_CANGA	Q6frk6 candida gla	221	32	62.7	475	1	ATXA_BACAN	Q4636 bacillus an
149	33	64.7	975	2	Q7Z291_CAEBL	Q7z291 caenorhabdi	222	32	62.7	475	2	Q4MKV3_BACCE	Q4mkv3 bacillus ce
150	33	64.7	1006	2	Q7QOU5_ANOGA	Q7qou5 anopheles g	223	32	62.7	476	2	Q4MW56_BACCE	Q4mw56 bacillus ce
151	33	64.7	1011	1	MY31D_DROME	Q23978 dirosophila	224	32	62.7	478	2	Q5FNP2_GLUOX	Q5fnp2 gluconobact
152	33	64.7	1020	2	Q8IU50_CAEBL	Q8iu50 caenorhabdi	225	32	62.7	478	2	Q5FNP2_GLUOX	Q5fnp2 gluconobact
153	33	64.7	1020	2	Q19204_CAEBL	Q19204 caenorhabdi	226	32	62.7	495	1	KCNM1_HUMAN	Q09470 homo sapien
154	33	64.7	1045	2	Q8GZX4_ORYSA	Q8gzx4 oryza sattiv	227	32	62.7	496	1	MYOTI_MOUSE	Q9ubf9 mus musculu
155	33	64.7	1134	2	Q6JPB0_9NUCL	Q6jpb0 neodipteron	228	32	62.7	498	2	Q5M1Q2_YEREN	Q5m1q2 yersinia en
156	33	64.7	1132	2	Q81YZ8_BACAN	Q81yz8 bacillus an	229	32	62.7	501	2	Q8DP48_VIBVU	Q8dp48 vibrio vuln
157	33	64.7	1207	2	Q4X1R2_ASPPU	Q4x1r2 aspergillus	230	32	62.7	502	2	Q5M1P6_YEREN	Q5m1p6 yersinia en
158	33	64.7	1267	2	Q4S3C8_TETNG	Q4s3c8 tetraodon n	231	32	62.7	502	2	Q6BW75_DEBHA	Q6bw75 debaryomyce
159	33	64.7	1616	1	SIAP_BACCI	P35824 bacillus ci	232	32	62.7	520	2	Q7NZW9_CHRYO	Q7nzw9 schizosacch
160	33	64.7	1667	2	Q4P5T4_USTMA	Q4p5t4 ustlago ma	233	32	62.7	532	2	Q6OLN3_CABRR	Q6oln3 caenorhabdi
161	33	64.7	1854	2	Q5B6B8_TEMNT	Q5b6b8 aspergillus	234	32	62.7	539	2	Q8ZX42_PYPAB	Q8zx42 pyrobaculum
162	33	64.7	2345	2	Q4WVX6_THEAN	Q4wvx6 theileria a	235	32	62.7	546	2	Q8ZX42_PYPAB	Q8zx42 pyrobaculum
163	33	64.7	2815	2	Q4WVW7_ASPPU	Q4wvw7 aspergillus	236	32	62.7	555	1	BGL10_CAEBL	Q49809 caenorhabdi
164	33	64.7	6973	2	Q6MDY2_PARUM	Q6mdy2 giardia lam	237	32	62.7	569	2	Q7VVM9_HABDU	Q7vvm9 haemophilus
165	33	64.7	67	2	Q90SH9_CAEV	Q90sh9 caprine art	238	32	62.7	575	2	Q4PEK3_USTMA	Q4pek3 ustlago ma
166	32	62.7	83	2	Q968T0_CAEBL	Q968t0 caenorhabdi	239	32	62.7	577	2	Q9RE16_ARTSP	Q9re16 arthroabacte
167	32	62.7	97	2	Q5E0V5_VITB1	Q5e0v5 vibrio fisc	240	32	62.7	598	2	Q27162_MERTH	Q27162 methanobact
168	32	62.7	100	2	Q5E0V5_VITB1	Q5e0v5 vibrio fisc	241	32	62.7	601	2	Q4ZUI5_PSSBY	Q4zui5 pseudomonas
169	32	62.7	104	2	Q4JFB4_STAUV	Q4jfb4 staphylococ	242	32	62.7	629	2	Q6GGW7_MOUSE	Q6ggw7 mus musculu
170	32	62.7	107	1	KVIL_HUMAN	P01596 homo sapien	243	32	62.7	641	1	PSO2_YEAST	Q74327 schizosacch
171	32	62.7	108	1	KVSK_MOUSE	P01644 mus musculu	244	32	62.7	661	1	Q5OV18_ENTHI	Q5ov18 entamoeba h
172	32	62.7	108	1	KVSM_MOUSE	P01666 mus musculu	245	32	62.7	757	2	Q4UHP6_THEAN	Q4uhp6 theileria a
173	32	62.7	108	1	KVSM_MOUSE	P01666 mus musculu	246	32	62.7	764	2	Q4UHP6_THEAN	Q4uhp6 theileria a
174	32	62.7	140	1	Q4YOB9_PLAAB	Q4yob9 plasmodium	247	32	62.7	776	1	TOP1_RICCN	Q921h1 rickettsia
175	32	62.7	193	1	COAB_FUSNN	Q8rh77 fusobacteri	248	32	62.7	776	1	TOP1_RICCN	Q9zdx2 rickettsia
176	32	62.7	193	1	Q7P8K6_FUSNV	Q7p8k6 fusobacteri	249	32	62.7	776	1	TOP1_RICCN	Q9zdx2 rickettsia
177	32	62.7	214	2	Q7RS57_PLAYO	Q7rs57 plasmodium	250	32	62.7	776	2	Q7P8H0_RICSI	Q7pbh0 rickettsia

251	32	62.7	776	2	Q4UM42_RICE	Q4um42_rickettsia	324	32	62.7	993	2	Q8BUV4_MOUSE	Q8buv4_mus musculus
252	32	62.7	779	2	Q68X45_RICTY	Q68x45_rickettsia	325	32	62.7	994	2	Q817Q2_DROME	Q817q2_drosophila
253	32	62.7	781	2	Q80661_ARATH	Q80661_arabidopsis	326	32	62.7	1007	2	Q4PB02_USTMA	Q4pb02_ustilago ma
254	32	62.7	799	2	Q8KGB3_CHLRE	Q8kgb3_chlorobium	327	32	62.7	1085	2	Q4XXA1_PLACH	Q4xxa1_placidium
255	32	62.7	814	2	Q8GCG0_9FUSO	Q8gcg0_fusobacteri	328	32	62.7	1185	2	Q8XJP0_CLOPE	Q8xjp0_clostridium
256	32	62.7	815	1	TOP1_XYLFA	Q9pev8_xylella fas	329	32	62.7	1224	2	Q63YR6_HUMAN	Q63yr6_homo sapien
257	32	62.7	815	1	TOP1_XYLFA	Q87aq6_xylella fas	330	32	62.7	1229	2	Q4Q4R4_LBIMA	Q4q4r4_leishmania
258	32	62.7	816	2	Q73G34_WOLPM	Q73g34_wolbachia p	331	32	62.7	1323	2	Q7Q0D6_MOUSE	Q7q0d6_mus musculus
259	32	62.7	828	2	Q89K08_BRAJA	Q89k08_bradyrhizob	332	32	62.7	1327	2	Q86W58_HUMAN	Q86w58_homo sapien
260	32	62.7	830	2	Q5HSD7_XANOR	Q5h5d7_xanthomonas	333	32	62.7	1327	2	Q60859_HUMAN	Q60859_homo sapien
261	32	62.7	830	2	Q8PG14_XANNC	Q8pg14_xanthomonas	334	32	62.7	1327	2	Q8Y114_MOUSE	Q8y114_mus musculus
262	32	62.7	831	2	Q4UQ08_XANCP	Q4uq08_xanthomonas	335	32	62.7	1332	2	Q8Y117_HUMAN	Q8y117_homo sapien
263	32	62.7	831	2	Q8P4F3_XANCP	Q8p4f3_xanthomonas	336	32	62.7	1365	2	Q5RDS0_PONPY	Q5rds0_pongo pygma
264	32	62.7	848	2	Q5AH87_CANAL	Q5ah87_candida alb	337	32	62.7	1488	2	Q4SDV0_TETNG	Q4sdv0_tetradodon n
265	32	62.7	848	2	Q5AH82_CANAL	Q5ah82_candida alb	338	32	62.7	1442	2	Q7NGZ7_GLOVI	Q7ngz7_gloeobacter
266	32	62.7	853	2	Q6FZS1_BAROU	Q6fz81_bartonella	339	32	62.7	1495	1	IQG1_YEAST	Q12280_saccharomyc
267	32	62.7	853	2	Q6G3F7_BABBE	Q6g3f7_bartonella	340	32	62.7	1607	2	Q6CFH7_YAALI	Q6cfh7_yarrowia li
268	32	62.7	853	2	Q4FIQ1_9RICK	Q4fiq1_candidatus	341	32	62.7	1628	2	Q7XKY1_ORESA	Q7xky1_oryza sativ
269	32	62.7	855	1	TOP1_ECOLI	P06612_escherichia	342	32	62.7	1737	2	Q9TW28_DICDI	Q9tw28_dicystoteli
270	32	62.7	855	1	TOP1_SALTI	P0a212_salmonella	343	32	62.7	1844	2	Q96Q83_HUMAN	Q96q83_homo sapien
271	32	62.7	865	1	TOP1_SALTY	P0a210_shigella fl	344	32	62.7	1869	2	Q5CK97_CRYHO	Q5ck97_cryptospori
272	32	62.7	865	1	TOP1_SALTY	P0a210_shigella fl	345	32	62.7	1871	2	Q5CWY0_CRYPV	Q5cwy0_cryptospori
273	32	62.7	865	2	Q57NU4_SALCH	Q57nu4_salmonella	346	32	62.7	1907	2	MYO3_CABER	Q601V4_caenorhadi
274	32	62.7	865	2	Q5PD10_SALPA	Q5pd10_salmonella	347	32	62.7	1969	2	Q601V4_CABER	P26676_h_large str
275	32	62.7	865	2	Q83LC4_SHIFL	Q83lc4_shigella fl	348	32	62.7	2262	1	Q4R4G3_PIZH	Q4r4g3_human para
276	32	62.7	865	2	Q8X7C5_ECOS7	Q8x7c5_escherichia	349	32	62.7	2263	2	Q81HV8_PLAF7	Q81hv8_plasmodium
277	32	62.7	866	2	Q7N4B4_PHOLL	Q7n4b4_photorhabd	350	32	62.7	2275	2	Q54LJ4_DICDI	Q54lj4_dicystoteli
278	32	62.7	866	2	Q6DAV4_ERMCT	Q6dav4_erwinia car	351	32	62.7	2563	2	Q6CMV9_HUMAN	Q6cmv9_homo sapien
279	32	62.7	867	2	Q7VIAN7_HABDU	Q7v1a7_haemophilus	352	32	62.7	235	2	Q8VIV1_HUMAN	Q8viv1_homo sapien
280	32	62.7	867	2	Q8EJW3_SHEON	Q8ej33_shewanelia	353	32	61.8	41.5	2	Q8VIV1_HUMAN	Q8viv1_homo sapien
281	32	62.7	868	1	TOP1_HAEMIN	P43012_haemophilus	354	31	60.8	61.8	2	Q7VCU5_PROMA	Q7vcu5_prochlocco
282	32	62.7	868	1	TOP1_PASMU	Q9cnc10_pasteurella	355	31	60.8	61.8	2	Q5NNW8_ZYMON	Q5nnw8_zymomonas m
283	32	62.7	868	1	TOP1_PSEAE	Q9hzi5_pseudomonas	356	31	60.8	61.8	2	Q90SG4_CAEV	Q9bvx4_homo sapien
284	32	62.7	868	2	Q4J2U4_AZOV1	Q4j2u4_azobacter	357	31	60.8	61.8	2	Q90SG4_CAEV	Q90sg5_captive art
285	32	62.7	868	2	Q4QK75_HAE18	Q4qk75_haemophilus	358	31	60.8	61.8	2	Q90SG5_CAEV	Q90sg7_captive art
286	32	62.7	868	2	Q65TK7_MANSM	Q65tk7_mannheimia	359	31	60.8	61.8	2	Q90SG7_CAEV	Q90sg7_captive art
287	32	62.7	869	2	Q88K29_PSEBK	Q88k29_pseudomonas	360	31	60.8	61.8	2	Q90SG8_CAEV	Q90sg9_captive art
288	32	62.7	869	2	Q87ZB5_PSESM	Q87zb5_pseudomonas	361	31	60.8	61.8	2	Q90SG8_CAEV	Q90sg9_captive art
289	32	62.7	870	2	Q4ZRA3_PSESY	Q4zra3_pseudomonas	362	31	60.8	61.8	2	Q90SH0_CAEV	Q90sh1_captive art
290	32	62.7	870	2	Q4KFC2_PSEBS	Q4kfc2_pseudomonas	363	31	60.8	61.8	2	Q90SH1_CAEV	Q90sh2_captive art
291	32	62.7	871	2	Q8ZEP4_YERPE	Q8zep4_yersinia pe	364	31	60.8	61.8	2	Q90SH2_CAEV	Q90sh3_captive art
292	32	62.7	871	2	Q66AJ0_YERPS	Q66aj0_yersinia ps	365	31	60.8	61.8	2	Q90SH3_CAEV	Q90sh4_captive art
293	32	62.7	872	2	Q5QWH4_IDILO	Q5qwh4_idiomarina	366	31	60.8	61.8	2	Q90SH4_CAEV	Q90sh5_captive art
294	32	62.7	873	2	Q98LX0_RHIL0	Q98lx0_rhizobium 1	367	31	60.8	61.8	2	Q90SH5_CAEV	Q90sh6_captive art
295	32	62.7	874	2	Q8DAR2_VIBVU	Q8dar2_vibrio vuln	368	31	60.8	61.8	2	Q90SH6_CAEV	Q90sh7_captive art
296	32	62.7	874	2	Q7MJ48_VIBVY	Q7mj48_vibrio chol	369	31	60.8	61.8	2	Q90SH7_CAEV	Q90sh8_captive art
297	32	62.7	876	1	TOP1_VIBCH	Q8kiz2_vibrio fisc	370	31	60.8	61.8	2	Q90SH8_CAEV	Q90sh9_captive art
298	32	62.7	876	2	Q5E600_VIBF1	Q5e600_vibrio fisc	371	31	60.8	61.8	2	Q90S10_CAEV	Q90s10_captive art
299	32	62.7	876	2	Q87QX7_VIBPA	Q87qx7_vibrio fisc	372	31	60.8	61.8	2	Q90S14_CAEV	Q90s14_captive art
300	32	62.7	877	2	Q578A3_BRUBA	Q578a3_brucella ab	373	31	60.8	61.8	2	Q90S14_CAEV	Q90s14_captive art
301	32	62.7	877	2	Q744V9_MYCPA	Q744v9_mycobacteri	374	31	60.8	61.8	2	Q8MEF7_9CAUD	Q8mef7_sinorhizobi
302	32	62.7	877	2	Q8FM60_BRUSU	Q8fm60_brucella su	375	31	60.8	61.8	2	Q83ENO_COXBU	Q83eno_coxiella bu
303	32	62.7	878	2	Q8EDN8_SHEON	Q8edn8_shewanelia	376	31	60.8	61.8	2	Q76M66_PROMM	Q76m66_prochlocco
304	32	62.7	879	2	Q8FHU9_ECOL6	Q8fhu9_escherichia	377	31	60.8	61.8	2	Q76M66_PROMM	Q76m66_synechococ
305	32	62.7	880	2	Q5LNX4_SILPO	Q5lnx4_silicibacte	378	31	60.8	61.8	2	Q7UB98_SYNPX	Q7ub98_homo sapien
306	32	62.7	881	2	Q6FEN8_ACIAD	Q6fen8_acinetobact	379	31	60.8	61.8	2	KVSP_MOUSE	P01636_mus musculu
307	32	62.7	883	1	Q6LIP7_PHOPR	Q6lip7_photobacter	380	31	60.8	61.8	1	KVSP_MOUSE	P01649_mus musculu
308	32	62.7	885	1	RSC3_YEAST	Q06619_saccharomyc	381	31	60.8	61.8	2	Q5RG57_9RICK	Q5rg57_rickettsia
309	32	62.7	892	2	Q7S0Q0_NEUCR	Q7s0q0_neurospora	382	31	60.8	61.8	2	Q4FPR6_9GAMM	Q4fpr6_psychrobact
310	32	62.7	892	2	Q4FR50_9GAMM	Q4fr50_psychrobact	383	31	60.8	61.8	2	Q6PYV7_SCHPA	Q6pyv7_schistosoma
311	32	62.7	892	2	Q8UFU3_AGR75	Q8ufu3_agrobacteri	384	31	60.8	61.8	2	Q4SH12_TETNG	Q4sh12_tetradodon n
312	32	62.7	898	2	Q5FRH2_GLUOX	Q5frh2_glucobact	385	31	60.8	61.8	2	Q5AR28_EMENT	Q5ar28_aspergillus
313	32	62.7	899	2	Q9A5I6_CAUCR	Q9a5i6_caulobact	386	31	60.8	61.8	2	Q7XO88_ORESA	Q7xw16_oryza sativ
314	32	62.7	900	2	Q92DL9_RHIME	Q92dl9_rhizobium m	387	31	60.8	61.8	2	Q7WY16_BACSH	Q7wyl6_bacillus sp
315	32	62.7	901	2	Q8YC66_BRUMS	Q8yc66_brucella me	388	31	60.8	61.8	2	Q8P3Q8_LEPNI	Q8p3q8_leptospira
316	32	62.7	911	2	Q7RJ02_PLAYO	Q7rj02_plasmodium	389	31	60.8	61.8	2	Q8F578_LEPNI	Q8f578_leptospira
317	32	62.7	911	2	Q6N559_RHOPA	Q6n559_rhodopseudo	390	31	60.8	61.8	2	Q8MP05_CAEEL	Q8mp05_caenorhadi
318	32	62.7	918	1	CARP_CORGL	Q93tm3_corynebacte	391	31	60.8	61.8	2	Q5DBP7_SCHPA	Q5dbp7_schistosoma
319	32	62.7	919	1	CARP_CORCT	Q6f5a7_corynebacte	392	31	60.8	61.8	2	Q98555_RHIL0	Q98555_rhizobium 1
320	32	62.7	920	2	Q6F5A7_CORGL	Q6f5a7_corynebacte	393	31	60.8	61.8	2	Q6MHP3_BDEBA	Q6mhp3_bdellovibri
321	32	62.7	921	2	Q6S113_ABGTA	Q6s113_aegilops ta	394	31	60.8	61.8	2	Q9C737_ARATH	Q9c737_arabidopsis
322	32	62.7	921	2	Q7G139_WHEAT	Q7g139_triticum ae	395	31	60.8	61.8	2		
323	32	62.7	928	2	Q6LJG6_PHOPR	Q6ljg6_photobacter	396	31	60.8	61.8	2		

397	31	60.8	199	2	061SR0_CABBR	061SR0_caenorhabdi	470	31	60.8	412	2	04J102_AZOVI	04J102_azotobacter
398	31	60.8	200	1	RISA_CHLPN	09sz20 chlamydia p	471	31	60.8	415	2	08T745_BRAFL	08T745_brancheiobes
399	31	60.8	206	1	069CU4_9ASCI	069cu4_heremania c	472	31	60.8	416	2	030211_ARCFU	030211_archoeglob
400	31	60.8	216	1	GSTR_STLCU	004522 silene cucu	473	31	60.8	425	2	05N201_AZOSE	05n201_azarcus sp
401	31	60.8	216	1	YLH3_CABEL	P34357 caenorhabdi	474	31	60.8	425	2	08BQJ9_MOUSE	08bqj9_mus musculu
402	31	60.8	216	1	061IW6_CABBR	061iw6_caenorhabdi	475	31	60.8	428	2	063H33_BACCZ	063h33_bacillus ce
403	31	60.8	217	2	07ANB2_NANEO	074nb2 nanoarchaeu	476	31	60.8	429	2	083D93_COXBU	083d93_coxiella bu
404	31	60.8	217	2	09PBY1_XYLEFA	09py1 xyella fas	477	31	60.8	433	2	04MH80_BACCE	04mh80_bacillus ce
405	31	60.8	226	2	048212_HAEIN	048212 haemophilus	478	31	60.8	441	2	05FRJ9_LACAC	05frj9_lactobacill
406	31	60.8	230	1	YF2A_STRAU	P03666 staphylococ	479	31	60.8	441	2	087D32_XYLEFT	087d32_xyella fas
407	31	60.8	233	1	04RIQ6_TETNG	04rix6 tetracodon n	480	31	60.8	441	2	09PC39_XYLEFA	09pc39_xyella fas
408	31	60.8	241	2	06BLF3_DEBHA	06blf3 debaryomyce	481	31	60.8	446	2	074111_LACUO	074111_lactobacill
409	31	60.8	241	2	05W542_9DIPT	05w542 phylorhiz b	482	31	60.8	446	2	005375_ATYAC	005375_actinobacil
410	31	60.8	244	1	FARG_BTUCAP	08k3j5 buchnera ap	483	31	60.8	447	2	08RZT1_PYRFA	08rzt1_pyrococcus
411	31	60.8	244	1	08KZG6_MOUSE	08kz6 mus musculu	484	31	60.8	451	2	04Q9E6_LEIMA	04q9e6_leishmania
412	31	60.8	246	2	051IH3_ENTHI	051ih3 entamoeba h	485	31	60.8	461	2	07PSK4_ANOGA	07psk4_anopheles g
413	31	60.8	249	2	074464_SCHPO	074464 schizosacch	486	31	60.8	468	1	NRAM_IASH2	08g7u4 bifidobacte
414	31	60.8	251	2	09CPA1_LACIA	09cpa1 lactococcus	487	31	60.8	470	2	080VE2_MOUSE	080ve2_mus musculu
415	31	60.8	253	2	050QY0_ENTHI	050qy0 entamoeba h	488	31	60.8	470	2	002697_PODAN	002697_podospora a
416	31	60.8	254	2	07KRX0_DROME	07krx0 drosophila	489	31	60.8	473	2	04INB7_GIBZE	04inb7_glibdrellia
417	31	60.8	255	2	0684A6_VIRIU	0684a6 sulfolobus	490	31	60.8	473	2	04UITV_THEAN	04uiv1 theileria a
418	31	60.8	263	2	08PX62_METMA	08px62 methanosarc	491	31	60.8	473	2	07WVB8_9STAP	07wvb8_staphylococ
419	31	60.8	263	2	014113_SCHPO	014113 schizosacch	492	31	60.8	492	2	07S3X3_NEOCR	07s3x3_neurospora
420	31	60.8	274	2	06AQ22_DESPS	06aq22 desulfotale	493	31	60.8	493	2	06ZAX2_BURMA	06zax2_burkholderi
421	31	60.8	275	2	07PZNS_FUSNV	07pzn5 fuscobacteri	494	31	60.8	494	1	TERF2_MOUSE	035144 mus musculu
422	31	60.8	275	2	08R5Y2_FUSNM	08r5y2 fuscobacteri	495	31	60.8	495	1	08GE07_HEILMO	08ge07_heliobacill
423	31	60.8	276	2	09PKR8_CHIMU	09pk8 chlamydia m	496	31	60.8	503	2	08DSA9_STREPCOC	08dsa9_streptococc
424	31	60.8	285	1	UPPS2_STRAW	08285 streptomyce	497	31	60.8	503	2	09DA18_MOUSE	09da18_mus musculu
425	31	60.8	285	2	04QPR9_LEIMA	04qtr9 leishmania	498	31	60.8	510	2	09DA18_MOUSE	09da18_mus musculu
426	31	60.8	290	2	081G88_DROME	081g88 drosophila	499	31	60.8	515	1	C76C3_ARATH	064638 arabidopsis
427	31	60.8	301	2	08RDF9_THEAN	08rfd9 thermococci	500	31	60.8	517	2	083E28_COXBU	083e28_coxiella bu
428	31	60.8	303	2	0741Y9_LACIO	0741y9 lactobacill	501	31	60.8	518	2	08JUM3_9CLOS	08jum3_sweet potat
429	31	60.8	313	2	06BXE3_DEBHA	06bx3 debaryomyce	502	31	60.8	528	2	063K00_BURPS	063k00_burkholderi
430	31	60.8	318	2	07VZM0_BORPE	07vzwo bordetella	503	31	60.8	534	2	055KJ9_CRYNE	055kj9_cryptococcu
431	31	60.8	320	2	08GN62_VIBU	08gn62 vibrio vuln	504	31	60.8	534	2	05KAX2_CRYNE	05kax2_cryptococcu
432	31	60.8	320	2	081YMS_BACAN	081yms bacillus an	505	31	60.8	537	2	050TV3_ENTHI	050tv3_entamoeba h
433	31	60.8	329	2	087166_VIBPA	087166 vibrio para	506	31	60.8	539	2	07ZWM3_LEPIC	07zwm3_leptospira
434	31	60.8	335	2	06BTK3_DEBHA	06btk3 debaryomyce	507	31	60.8	548	2	08F982_LEBIN	08f982_leptospira
435	31	60.8	337	2	07MTX1_PORGI	07mtx1 porphyromon	508	31	60.8	548	2	09CAJ9_ARATH	09caj9_arabidopsis
436	31	60.8	338	2	04K3Q1_PSEPS	04kq1 pseudomonas	509	31	60.8	557	2	0640T6_XENTR	0640t6_xenopus tro
437	31	60.8	343	2	05BQ14_ARATH	05bq14 arabidopsis	510	31	60.8	561	2	09XDC2_HERSE	09xdc2_herbaspirill
438	31	60.8	344	2	061KL8_CABBR	061kl8 caenorhabdi	511	31	60.8	562	2	06F3Q6_XENTR	06f3q6_xenopus tro
439	31	60.8	346	2	09G8M4_CALIA	09g8m4 calcarinus l	512	31	60.8	563	2	073659_XYLEA	073659_oryzias lac
440	31	60.8	349	1	YHHT_ECOLI	P37622 escherichia	513	31	60.8	568	2	06GM54_XENLA	06gm54_xenopus lae
441	31	60.8	349	2	07PNK4_ANOGA	07pnk4 anopheles g	514	31	60.8	573	2	0694V6_ANOST	0694v6_anopheles s
442	31	60.8	349	2	061AM3_BACAN	061am3 bacillus an	515	31	60.8	580	2	04IK95_GIBZE	04ik95_glibdrellia
443	31	60.8	349	2	0571P5_SALCH	0571p5 salmonella	516	31	60.8	581	1	PCMU_BROIN	09nmx2 bromus iner
444	31	60.8	349	2	05PUN3_SALPA	05pun3 salmonella	517	31	60.8	587	2	052L41_XENLA	052l41_xenopus lae
445	31	60.8	349	2	082258_SALTI	082258 salmonella	518	31	60.8	600	2	059PAS_CAVAL	059pas_candida alb
446	31	60.8	349	2	08ZLRS3_SALTY	08zls3 salmonella	519	31	60.8	603	2	0899F0_CLOTE	0899f0_clostridium
447	31	60.8	349	2	083J80_SHIFL	083j80 shigella fl	520	31	60.8	616	2	04HSN4_9DEIO	04hsn4_deinococcus
448	31	60.8	353	1	Y1698_HAEIN	005083 haemophilus	521	31	60.8	627	2	065380_ARATH	065380_arabidopsis
449	31	60.8	353	2	04QTP3_HAE18	04qtp3 haemophilus	522	31	60.8	628	2	06KACA_ORYSA	06kaca_oryza sativ
450	31	60.8	354	2	09BMB8_LYMDI	09bmb8 lymphotria d	523	31	60.8	631	2	04P641_USTMA	04p641_usellago ma
451	31	60.8	354	2	08XK37_CLOPE	08xk37 clostridium	524	31	60.8	632	2	04WU86_PLABE	04wu86_aspergillus
452	31	60.8	359	2	016389_CABEL	016389 caenorhabdi	525	31	60.8	646	2	04YAU6_PLABE	04yau6_plasmodium
453	31	60.8	364	2	050M46_ENTHI	050m46 entamoeba h	526	31	60.8	651	2	04XW27_PLACH	04xw27_usellago ma
454	31	60.8	364	2	068573_STRNU	068573 streptococc	527	31	60.8	658	2	04PIR0_USTMA	04pir0_ustima
455	31	60.8	369	2	080FX3_AGRYS	08ufx3 agrobacteri	528	31	60.8	685	1	IF2_CLOTE	0895f8 clostridium
456	31	60.8	371	2	06SKD0_BACID	06skd0 bacillus il	529	31	60.8	689	2	04LSV2_STAHU	04lsv2_staphylococ
457	31	60.8	376	2	08FCN4_ECOL6	08fcn4 escherichia	530	31	60.8	689	2	06G9W3_STVAS	06g9w3_staphylococ
458	31	60.8	377	2	04NSFI_9DELT	04nsfi anaeromonas	531	31	60.8	689	2	06GH15_STMAR	06gh15_staphylococ
459	31	60.8	384	1	DPO4_THETN	P5865 thermomacrob	532	31	60.8	689	2	05HPU2_STMAR	05hpu2_staphylococ
460	31	60.8	387	2	071F53_9RICK	071f53 rickettsia	533	31	60.8	689	2	05HG12_STYAC	05hg12_staphylococ
461	31	60.8	390	2	09AVL8_CAUCR	09avl8 caulobacter	534	31	60.8	689	2	07A5Y5_STMAN	07a5y5_staphylococ
462	31	60.8	392	2	05AS11_EBENT	05aas11 aspergillus	535	31	60.8	689	2	09YUM1_STMAN	09yum1_staphylococ
463	31	60.8	390	2	08FES9_ECOL6	08fes9 escherichia	536	31	60.8	689	2	08CSU3_STAP	08csu3_staphylococ
464	31	60.8	396	2	05VZH1_HALMA	05vzh1 haloarcula	537	31	60.8	690	1	TOP1_BACD	09kx23 bacillus ha
465	31	60.8	396	2	0896S3_CLOTE	0896s3 clostridium	538	31	60.8	690	2	05WPF7_BACSA	05wfp7_bacillus cl
466	31	60.8	400	2	05HQB4_STAEQ	05hqb4 staphylococ	539	31	60.8	692	2	08NWZ9_STAPW	08nwz9_staphylococ
467	31	60.8	400	2	08CP00_STAP	08cp00 staphylococ	540	31	60.8	692	2	04MGV8_BACCE	04mgv8_bacillus ce
468	31	60.8	411	2	07XWMS_ORYSA	07xwms oryza sativ	541	31	60.8	692	2	06HEI2_BACH	06hey2_bacillus th
469	31	60.8	412	2	04IH14_GIBZE	04ih14 gibdrellia	542	31	60.8	692	2	0720E6_LISMF	0720e6_listeria mo

543	31	60.8	692	2	Q732N7_BACCI	Q732n7_bacillus ce	616	31	60.8	1315	2	Q852D0_ORYSA	Q852d0_oryza sativ
544	31	60.8	692	2	Q834K0_ENTRA	Q834k0_enterococcu	617	31	60.8	1340	2	Q69YQ8_HUMAN	Q69yq8_homo sapien
545	31	60.8	692	2	Q8Y7K2_LISMO	Q8y7k2_listeria mo	618	31	60.8	1351	2	Q8MT65_DROME	Q8mt65_drosophila
546	31	60.8	692	2	Q92C77_LISIN	Q92c77_listeria in	619	31	60.8	1351	2	Q9GP62_DROME	Q9gp62_drosophila
547	31	60.8	692	2	Q636J3_BACCE	Q636j3_bacillus ce	620	31	60.8	1351	2	Q9VRS3_DROME	Q9vrs3_drosophila
548	31	60.8	692	2	Q81WK2_BACCA	Q81wk2_bacillus an	621	31	60.8	1438	2	Q65JJO_BACDI	Q65jjo_bacillus li
549	31	60.8	693	2	Q74JY9_IACCO	Q74jy9_lactobacilli	622	31	60.8	1495	2	Q61H02_CABER	Q61h02_caenorhabdi
550	31	60.8	694	2	Q8R9Y1_THERM	Q8r9y1_thermoanaer	623	31	60.8	1572	2	Q7RE86_GIALA	Q7re86_giardia lam
551	31	60.8	696	2	Q895L4_CLOTE	Q895l4_clostridium	624	31	60.8	1614	2	Q69YQ9_HUMAN	Q69yq9_homo sapien
552	31	60.8	697	2	Q97168_CLOAB	Q97168_clostridium	625	31	60.8	1643	2	Q81486_CHARE	Q81486_chlamydomon
553	31	60.8	699	2	Q97QF3_STREP	Q97qf3_streptococc	626	31	60.8	1676	2	Q7R139_PLAYO	Q7r139_plasmodium
554	31	60.8	700	2	Q8XUQ4_CLOPE	Q8xuq4_clostridium	627	31	60.8	1864	2	Q4RPN5_GIBZE	Q4rpn5_gibberella
555	31	60.8	700	2	Q8DP19_STRR6	Q8dp19_streptococc	628	31	60.8	2066	2	Q914X1_PACTO	Q914x1_aspergillus
556	31	60.8	702	2	Q6FWJ9_CANGA	Q6fwj9_candida gla	629	31	60.8	2489	2	Q5AWV8_EMENT	Q5awv8_plasmodium
557	31	60.8	705	2	Q5FKE2_IACAC	Q5fke2_lactobacilli	630	31	60.8	4811	2	Q4YV05_PLABE	Q4yv05_plasmodium
558	31	60.8	706	2	Q8DUZ2_STRAS	Q8duz2_streptococc	631	31	60.8	5432	2	Q7RXP5_PLAYO	Q7rpx5_gibberella
559	31	60.8	706	2	Q8E5T9_STRAJ	Q8e5t9_streptococc	632	31	60.8	9579	2	Q4HWM4_GIBRE	Q4hwm4_gibberella
561	31	60.8	709	2	Q5XC47_STRP6	Q5xc47_streptococc	633	31	60.8	17903	2	Q7RTL4_DROME	Q7rtl4_drosophila
562	31	60.8	709	2	Q99ZM4_STRPY	Q99zm4_streptococc	634	30.5	59.8	166	2	Q4MNY1_BACCE	Q4mny1_bacillus ce
563	31	60.8	709	2	Q8P107_STRP8	Q8p107_streptococc	636	30.5	59.8	266	2	Q5KX17_GEOXA	Q5kx17_geobacillus
564	31	60.8	709	2	Q8K7G5_STRP3	Q8k7g5_streptococc	637	30.5	59.8	269	2	Q5KX17_GEOXA	Q5kx17_geobacillus
565	31	60.8	710	1	TOP1_LACLA	Q8cg90_lactococcus	638	30.5	59.8	270	1	Y137J3_BACHD	Q05337_staphylococ
566	31	60.8	713	2	Q88V78_IACEPL	Q88v78_lactobacilli	639	30.5	59.8	270	1	Y4376_BACCI	Q9k466_bacillus ha
567	31	60.8	714	2	Q5M018_STRT1	Q5m018_streptococc	640	30.5	59.8	270	1	Y4376_BACCI	Q81262_bacillus ce
568	31	60.8	714	2	Q5M4N3_STRT2	Q5m4n3_streptococc	641	30.5	59.8	270	1	Y4376_BACCI	Q73J0P0_bacillus ce
569	31	60.8	715	2	Q88W22_IACPL	Q88w22_lactobacilli	642	30.5	59.8	270	1	Y4376_BACCI	Q81l1l_bacillus an
570	31	60.8	721	2	Q73NFS_TREDB	Q73nfs_treponema d	643	30.5	59.8	270	2	Q6HDM4_BACIK	P54470_bacillus su
571	31	60.8	721	2	Q63R07_BURPS	Q63r07_burkholderi	644	30.5	59.8	270	2	Q634P4_BACCE	Q6hdm4_bacillus th
572	31	60.8	758	2	Q6PYV9_OSTTA	Q6pyv9_ostreococcu	645	30.5	59.8	270	2	Q65H78_BACDI	Q65h78_bacillus ce
573	31	60.8	759	2	Q5WTK2_LEGPA	Q5wtk2_legionella	646	30.5	59.8	271	2	Y1946_OCEIH	Q8epx4_oceanobacti
574	31	60.8	759	2	Q5X1U1_LEGPA	Q5x1u1_legionella	647	30.5	59.8	271	2	Q416R3_STAYU	Q416r3_staphylococ
575	31	60.8	759	2	Q5ZSC0_LEGPH	Q5zsc0_legionella	648	30.5	59.8	271	2	Q5WHD3_BACSK	Q5whd3_bacillus cl
576	31	60.8	764	2	Q5NGD9_TRARTT	Q5ngd9_francisella	649	30.5	59.8	272	1	Y1250_STAEP	Q8cs67_staphylococ
577	31	60.8	765	2	Q83AAS_COXBU	Q83aas_coxiella bu	650	30.5	59.8	272	1	Y1392_STANP	P67200_staphylococ
578	31	60.8	768	2	Q7N1Z2_PHOHL	Q7n1z2_photorhabdu	651	30.5	59.8	272	1	Y1501_STAAS	Q6g993_staphylococ
579	31	60.8	778	2	P91136_CABEL	P91136_caenorhabdi	652	30.5	59.8	272	1	Y1563_STAMM	P67201_staphylococ
580	31	60.8	780	2	Q36411_9GAMA	Q36411_alcelaphine	653	30.5	59.8	272	1	Y1563_STAMM	Q67199_staphylococ
581	31	60.8	789	2	Q54LK8_DICDI	Q54lk8_dicyostelei	654	30.5	59.8	272	2	Q5HNY5_STAOK	Q5hny5_staphylococ
582	31	60.8	800	2	Q74FH3_BROSL	Q74fh3_geobacter s	655	30.5	59.8	272	2	Q5HJ77_STAMC	Q5hjf7_staphylococ
583	31	60.8	819	2	Q5FHL9_EHRRG	Q5fhl9_ehrlichia r	656	30.5	59.8	273	2	Q67RX3_SYMTH	Q67rx3_symbiobacte
584	31	60.8	819	2	Q5HBJ0_EHRRW	Q5hbj0_ehrlichia r	657	30.5	59.8	274	1	Y1457_LISMO	Q67195_listeria mo
585	31	60.8	831	2	Q4NPG0_9DELFT	Q4npg0_aeromonas xob	658	30.5	59.8	274	1	Y1476_LISMF	Q7123_listeria mo
586	31	60.8	845	2	Q4TMC3_9SPHN	Q4tmc3_erythrobact	659	30.5	59.8	274	1	Y1494_LISIN	Q67163_listeria in
587	31	60.8	858	2	Q6MON7_BDEBA	Q6mon7_bdellovibri	660	30	58.8	277	2	Q37212_9HEPC	Q37212_hepatitis c
588	31	60.8	875	2	Q758X4_ASHGO	Q758x4_aebhya goss	661	30	58.8	36	2	Q9NGN1_STRPU	Q9ngn1_streptyloce
589	31	60.8	881	2	Q55J59_CRYNE	Q55j59_cryptococcu	662	30	58.8	56	2	Q5BRJ8_SCHUA	Q5brj8_christosoma
590	31	60.8	881	2	Q5K9S2_CRYNE	Q5k9s2_cryptococcu	663	30	58.8	62	2	Q31220_CHRYI	Q31220_chromatium
591	31	60.8	885	2	Q4T2D7_TETNG	Q4t2d7_tetradodon n	664	30	58.8	65	2	Q592S2_LYMST	Q592s2_lymbaea sta
592	31	60.8	906	2	Q4J789_SULAC	Q4j789_sulfolobus	665	30	58.8	67	2	Q8YXN0_ANASP	Q8yxno_anabena sp
593	31	60.8	912	2	Q4N6X0_THERPA	Q4n6x0_thelilleria p	666	30	58.8	80	2	Q4MKZ3_BACCE	Q4mkz3_bacillus ce
594	31	60.8	929	2	Q6CBH9_TARLI	Q6cbh9_yarrowia li	667	30	58.8	87	1	MINE_VIBVU	Q8df62_vibrio vuln
595	31	60.8	929	2	Q4UIP2_THEAN	Q4uip2_thelilleria a	668	30	58.8	87	1	MINE_VIBVU	Q7mm12_vibrio vuln
596	31	60.8	951	2	Q54SX1_DICDI	Q54sx1_dicyostelei	669	30	58.8	89	2	Q5ISV5_NOCRA	Q5isv5_nocardia fa
597	31	60.8	964	2	Q4HCK6_9DEIO	Q4hck6_deinococcus	670	30	58.8	96	1	Y4356_SHEON	Q8ebd9_shewanella
598	31	60.8	965	2	Q5RBMX_PONPY	Q5rbmx_pongo pygma	671	30	58.8	96	1	Y4356_SHEON	Q8ebd9_vibrio chol
599	31	60.8	987	2	Q93Y59_ARATH	Q93y59_arabidopsis	672	30	58.8	101	2	Q6F7S5_ACIND	Q6f7s5_acinetobact
600	31	60.8	1015	2	Q753K8_ASHGO	Q753k8_aebhya goss	673	30	58.8	102	2	Q59MR6_CANAL	Q59mr6_candida alb
601	31	60.8	1016	2	Q60UJ7_CABER	Q60uj7_caenorhabdi	674	30	58.8	108	1	KV1S_HUMAN	Q9ul17_homo sapien
602	31	60.8	1017	2	Q27328_CABEL	Q27328_caenorhabdi	675	30	58.8	108	2	Q9UT79_HUMAN	Q9ut79_homo sapien
603	31	60.8	1020	2	Q73YI1_MYCPA	Q73yi1_mycobacteri	676	30	58.8	109	1	RL22_WOLSU	Q9aw18_wolliella s
604	31	60.8	1021	2	Q9RUI0_DEIRA	Q9rui0_deinococcus	677	30	58.8	109	2	Q59V61_CANAL	Q59v61_candida alb
605	31	60.8	1021	2	Q5A5B7_CANAL	Q5a5b7_candida alb	678	30	58.8	111	2	Q9AW18_GUTHH	Q9aw18_guillardia
606	31	60.8	1120	2	Q966P9_CABEL	Q966p9_caenorhabdi	679	30	58.8	112	1	FLIN_AOUAE	Q67495_aquifex aeo
607	31	60.8	1123	2	Q9M2T1_ARATH	Q9m2t1_arabidopsi	680	30	58.8	117	1	KV10_RABIT	P01691_oryctolagus
608	31	60.8	1148	2	Q966Q0_CABEL	Q966q0_caenorhabdi	681	30	58.8	122	2	Q5ZNU7_VIRIU	Q5znu7_cocciia con
609	31	60.8	1217	1	TOP1_ZYMMO	Q966q0_zymonas m	682	30	58.8	122	2	Q537D8_VIRIEU	Q537d8_cocciia plu
610	31	60.8	1234	2	Q84FA2_MYXXA	Q84fa2_myxococcus	683	30	58.8	123	2	Q8Z5E8_YEREP	Q8z5e8_yersinia pe
611	31	60.8	1251	2	Q9DPT9_BARE	Q9dpt9_brychydanio	684	30	58.8	123	2	Q66A87_YERPS	Q66a87_yersinia ps
612	31	60.8	1264	2	Q4XV87_PLACH	Q4xv87_plasmodium	685	30	58.8	126	2	Q64CP4_9AROH	Q64cp4_uncultured
613	31	60.8	1286	2	Q6WL99_9DIPF	Q6wl99_opercia nigr	686	30	58.8	128	2	Q9G903_OCHON	Q9g903_chromonas
614	31	60.8	1293	2	Q6WL96_9ASIL	Q6wl96_platybalpus	687	30	58.8	129	1	LYSCI_CANPA	Q9g903_chromonas
615	31	60.8	1310	2	Q6FJ98_CANGA	Q6fj98_candida gla	688	30	58.8	130	2	Q7QY14_GIALA	Q7qy14_giardia lam

689	30	58.8	135	2	088BB8_PSESM	088db8_pseudomonas	762	30	58.8	251	1	HIS4_BURML	0845u8_burkholderi
690	30	58.8	136	2	088ZNT_LACPL	088znt_lactobacilli	763	30	58.8	251	1	HIS4_BURPS	063q91_burkholderi
691	30	58.8	149	2	04V3S8_DROME	04v3s8_drosophila	764	30	58.8	251	1	04WE88_ASFPU	04we88_aspergillus
692	30	58.8	151	1	PAB2_BORR	07v183_bordetella	765	30	58.8	251	2	09ZFO0_GENTR	09zfo0_buchnera ap
693	30	58.8	151	1	PAB2_BORR	07v183_bordetella	766	30	58.8	251	2	04LM49_GENTR	04lm49_burkholderi
694	30	58.8	151	1	Q9X2M8_STACA	09x2m8_staphylococ	767	30	58.8	254	2	05ZKS9_CHICK	05zks9_gallus gall
695	30	58.8	151	2	06FC80_ACIAD	06fc80_actinobact	768	30	58.8	257	2	0675P5_JDMOC	0675p5_oligoptera
696	30	58.8	154	2	05ACR4_DICDI	05acr4_dictyostell	769	30	58.8	259	2	07IAR9_9DPT	07iar9_antisa sp.
697	30	58.8	159	2	07UGH8_RHOBA	07ugh8_rhodopirell	770	30	58.8	262	2	09HR73_HALSA	09hr73_haloacteri
698	30	58.8	159	2	07XOD9_ACIAD	07xod9_rhodopirell	771	30	58.8	263	2	098SC9_GUITH	098sc9_guillardia
699	30	58.8	167	2	04YTB5_PLABE	04ytb5_actinobact	772	30	58.8	264	1	Y1573_SYNY3	098sc9_guillardia
700	30	58.8	169	2	073DC6_BACCI	073dc6_bacillus ce	773	30	58.8	264	1	05I2F8_PHTIN	05i2f8_phtothor
701	30	58.8	171	2	09SGP9_ARATH	09sgp9_arabidopsis	774	30	58.8	269	2	05A2E34_MAGGR	05a2e34_magnaporthe
702	30	58.8	171	2	06ZM44_BRARE	06zm44_brachydanio	775	30	58.8	269	2	05A2H6_EUMNI	05a2h6_aspergillus
703	30	58.8	174	2	05Z6I7_MAGGR	05z6i7_magnaporthe	776	30	58.8	269	2	07RYX7_NEUCR	07ryx7_neurospora
704	30	58.8	174	2	081HR9_BACCR	081hr9_bacillus ce	777	30	58.8	270	2	05FKD3_LACAC	05fkd3_lactobacilli
705	30	58.8	176	2	04IZR0_AZOV1	04izr0_azotobacter	778	30	58.8	271	2	04I676_GIBZE	04i676_gibberella
706	30	58.8	177	2	08EDJ9_SHEON	08edj9_shevanella	779	30	58.8	271	2	08YB66_BROME	08ybe6_brucella me
707	30	58.8	181	2	07UEN8_RHOBA	07uen8_rhodopirell	780	30	58.8	272	1	GSPEC1_ERWCH	P31698_erwinia chr
708	30	58.8	185	1	RRF_EHRG	05f666_ehrlichia r	781	30	58.8	272	1	GSPEC2_ERWCH	001564_erwinia chr
709	30	58.8	185	1	RRF_EHRG	05f666_ehrlichia r	782	30	58.8	278	2	09EZK5_ENTFC	09ezk5_eterococcu
710	30	58.8	187	2	08ND01_HUMAN	08nd01_homo sapien	783	30	58.8	281	2	06BS29_DEBHA	06bs29_debaryomyce
711	30	58.8	198	2	00O6I8_HUMAN	00o6i8_homo sapien	784	30	58.8	281	2	038690_AMPCA	038690_amphidinium
712	30	58.8	201	2	066IJ0_BORGA	066ij0_bordetella ga	785	30	58.8	282	2	08EW91_MYCPE	08ew91_mycoplasma
713	30	58.8	207	2	04H3D6_CIOIN	04h3d6_ciona intes	786	30	58.8	283	2	072LX6_LEBPC	072lx6_leptospira
714	30	58.8	207	2	08BDI6_PSEBK	08bd16_pseudomonas	787	30	58.8	283	2	06A5M2_PROAC	06a5m2_propionibac
715	30	58.8	211	2	04PNG6_9BACT	04png6_uncultured	788	30	58.8	285	2	096X64_SULTO	096x64_sulfolobus
716	30	58.8	211	2	07J3N8_BORPA	07j3n8_bordetella	789	30	58.8	285	2	04MMT7_BACCE	04mmt7_bacillus ce
717	30	58.8	211	2	07WF14_BORR	07wf14_bordetella	790	30	58.8	285	2	08DPA1_VIBVU	08dpa1_vibrio vuln
718	30	58.8	216	2	09RYO0_DEIRA	09ryo0_deinococcus	791	30	58.8	285	2	06ZM63_BRARE	06zm63_brachydanio
719	30	58.8	216	2	096XB6_SULTO	096xb6_sulfolobus	792	30	58.8	287	2	05J3M6_BRARE	05j3m6_rattus norv
720	30	58.8	220	2	04ZMY1_PSESY	04zmy1_pseudomonas	793	30	58.8	287	2	08X3G0_RAT	08x3g0_candida alb
721	30	58.8	220	2	088908_PSESM	088908_pseudomonas	794	30	58.8	288	2	05S9S9_CANAL	05s9s9_saccharomyc
722	30	58.8	222	2	06TW94_BPD1	06tw94_bacterioph	795	30	58.8	289	2	008237_YEAST	008237_cryptococcu
723	30	58.8	223	2	06OE57_ORYSA	06oe57_oryzaectiv	796	30	58.8	291	2	05SL61_CRYNE	05sl61_cryptococcu
724	30	58.8	227	2	097EP7_CIOAB	097ep7_clostridium	797	30	58.8	291	2	05KAC0_CRYNE	05kac0_aeropyrum p
725	30	58.8	228	2	04P356_USTWA	04p356_ustilago ma	798	30	58.8	294	2	09YCF2_AERPE	09ycf2_bacillus th
726	30	58.8	228	2	07M0G9_BORPE	07m0g9_bordetella	799	30	58.8	296	2	06HE77_BACHX	06he77_bacillus ce
727	30	58.8	228	2	08D3N6_VIBVU	08d3n6_vibrio vuln	800	30	58.8	296	2	073IK8_BACCI	073ik8_bacillus ce
728	30	58.8	228	2	07MF56_VIBVY	07mf56_vibrio vuln	801	30	58.8	296	2	081827_BACCR	081827_bacillus ce
729	30	58.8	230	1	RACX_BACSU	p32960_bacillus su	802	30	58.8	296	2	081MD8_BACAN	081md8_bacillus an
730	30	58.8	230	1	04JEM9_ADEO7	04jem9_human adeno	803	30	58.8	296	2	0635U1_BACDZ	0635u1_bacillus ce
731	30	58.8	233	2	09K0U6_NEIMA	09k0u6_neisseria m	804	30	58.8	297	2	0803S3_BRARE	0803s3_brachydanio
732	30	58.8	236	2	026332_METTH	026332_methanobact	805	30	58.8	300	2	08S8F2_ENCCU	08s8f2_encephalito
733	30	58.8	236	2	06GMX0_HUMAN	06gmx0_homo sapien	806	30	58.8	308	2	04RPZ9_TENNG	04rpz9_tetrahodon n
734	30	58.8	236	2	06GMX8_HUMAN	06gmx8_homo sapien	807	30	58.8	309	2	06C6G1_YARLI	06c6g1_yarrowia ii
735	30	58.8	236	2	05W543_9DIP1	05w543_helina lasti	808	30	58.8	309	2	04HDL9_CAMCO	04hdl9_campylobact
736	30	58.8	237	2	057DU7_BRUB	057du7_brucella ab	809	30	58.8	309	2	04HR25_CAMLA	04hr25_campylobact
737	30	58.8	237	2	08G1B3_BRUBU	08g1b3_brucella su	810	30	58.8	310	2	04HRS1_CAMUP	04hrs1_candidatus
738	30	58.8	237	2	08Y6K4_BRUME	08y6k4_brucella me	811	30	58.8	310	2	04PEP1_GRICK	p27126_escherichia
739	30	58.8	240	2	05W541_9DIP1	05w541_phaeonia tug	812	30	58.8	311	2	0577B0_BRUB	0577b0_brucella ab
740	30	58.8	241	2	05W539_9DIP1	05w539_hylemyia sp.	813	30	58.8	311	2	08FWZ7_BRUB	08fwz7_brucella su
741	30	58.8	241	2	092F03_GENTR	092f03_buchnera ap	814	30	58.8	311	2	06WZD6_RHISN	06wzd6_rhizobium s
742	30	58.8	243	2	097687_SULTO	097687_sulfolobus	815	30	58.8	312	2	06LTV9_PHOPR	06ltv9_photobacter
743	30	58.8	244	2	051345_PSEAE	051345_pseudomonas	816	30	58.8	313	2	08TLVX3_MRTAC	08tlvx3_methanobact
744	30	58.8	245	2	0817L6_CAEEL	0817l6_caenorhabdi	817	30	58.8	315	2	08LTVX3_MRTAC	08ltvx3_methanobact
745	30	58.8	245	2	05F6C8_NEICL	05f6c8_neisseria g	818	30	58.8	317	2	TNFI1_HUMAN	014788_h tumor nec
746	30	58.8	245	2	054677_STRPH	054677_streptomyce	819	30	58.8	317	2	05T9Y4_HUMAN	05t9y4_homo sapien
747	30	58.8	245	2	09JUT2_NEIMA	09jut2_neisseria m	820	30	58.8	320	1	HEMH_YERPE	08zcg8_yersinia ps
748	30	58.8	246	2	04R7S3_MACPA	04r7s3_macaca fasc	821	30	58.8	320	1	HEMH_YERPS	08zcg8_yersinia ps
749	30	58.8	246	2	092VZ3_RHIME	092vz3_rhizobium m	822	30	58.8	320	1	09AL18_VIBPA	09al18_vibrio para
750	30	58.8	248	1	Y089_LACPL	089047_lactobacilli	823	30	58.8	330	2	087NK3_VIBPA	087nk3_vibrio para
751	30	58.8	248	2	04MG50_BACCE	04mg50_bacillus ce	824	30	58.8	330	2	08YMC3_ANASP	08ymc3_anabaena sp
752	30	58.8	248	2	063H68_BACCC	063h68_bacillus ce	825	30	58.8	331	2	06UNW3_9BIVA	06unw3_pichia anu
753	30	58.8	248	2	06HPN6_BACHK	06hpn6_bacillus th	826	30	58.8	332	2	06Y198_PICAN	06y198_pichia angu
754	30	58.8	248	2	073F74_BACCI	073f74_bacillus ce	827	30	58.8	332	2	060S01_CAEER	060s01_caenorhabdi
755	30	58.8	248	2	081J21_BACCR	081j21_bacillus ce	828	30	58.8	333	1	PCP3_AMPCA	p37682_escherichia
756	30	58.8	248	2	081V08_BACAN	081v08_bacillus an	829	30	58.8	334	1	Y1AU_ECOLI	07q372_anopheles g
757	30	58.8	249	2	0530I8_GENTR	0530i8_buchnera ap	830	30	58.8	334	2	07Q372_ANOEA	07q372_anopheles g
758	30	58.8	249	2	09ZEY6_GENTR	09zey6_buchnera ap	831	30	58.8	334	2	08XDK3_ECOS7	08xdk3_escherichia
759	30	58.8	250	1	09ZE28_GENTR	09ze28_buchnera ap	832	30	58.8	330	2	P72608_SYNY3	p72608_synchoocyst
760	30	58.8	250	1	REPA2_BUCAI	09zey9_burkholderi	833	30	58.8	330	2	08CCZ6_MOUSE	08ccz6_mus musculu
761	30	58.8	251	1	HIS4_BURMA	06zge4_burkholderi	834	30	58.8	334	2	09Z914_CHLBN	09z914_chlamydia p

835	30	58.8	340	2	05UP40_MIMIV	05up40 mimivirus.	908	30	58.8	422	2	091B15_NPVST	091b15 spodopozera
836	30	58.8	347	2	08QUP4_GVIRU	08qup4 infectious	909	30	58.8	423	2	089TG9_BRUJA	089tg9 bradyrhizob
837	30	58.8	351	2	08W7Y7_9TELE	08w7y7 astyanax ae	910	30	58.8	424	2	087UB4_PSESN	087ub4 pseudomonas
838	30	58.8	351	2	08M8B7_ASTPA	08m8b7 astyanax fa	911	30	58.8	430	2	08R196_FUSNN	08r196 fusbacteri
839	30	58.8	351	2	08M8A7_ASTPA	08m8a7 astyanax ae	912	30	58.8	433	2	064D71_9ARCH	064d71 uncultured
840	30	58.8	351	2	08M8Q0_9TELE	08m8q0 astyanax ae	913	30	58.8	433	2	08YCP3_BRUME	08ycp3 bruceella me
841	30	58.8	351	2	08M8S7_ASTPA	08m8s7 astyanax fa	914	30	58.8	436	2	06AM91_HUMAN	06am91 homo sapien
842	30	58.8	351	2	08M8V6_9TELE	08m8v6 astyanax ae	915	30	58.8	443	2	07R3Z8_GIALA	07r3z8 giardia lam
843	30	58.8	351	2	08MFC1_ASTPA	08mfc1 astyanax fa	916	30	58.8	445	2	09XH05_BRAJA	09xh05 bradyrhizob
844	30	58.8	351	2	08MFC2_ASTPA	08mfc2 astyanax fa	917	30	58.8	447	2	07AB62_ECO57	07ab62 escherichia
845	30	58.8	351	2	08MFC3_ASTPA	08mfc3 astyanax fa	918	30	58.8	447	2	083QC4_SHIFL	083qc4 shigella fl
846	30	58.8	351	2	08MFC4_ASTPA	08mfc4 astyanax fa	919	30	58.8	447	2	08X6P1_ECO57	08x6p1 escherichia
847	30	58.8	351	2	08MFC5_ASTPA	08mfc5 astyanax fa	920	30	58.8	449	2	07S237_NEUCR	07s237 neurospora
848	30	58.8	351	2	08MFC6_ASTPA	08mfc6 astyanax fa	921	30	58.8	450	2	05ORF0_ENTHI	05orf0 entamoeba h
849	30	58.8	351	2	08MFC7_ASTPA	08mfc7 astyanax fa	922	30	58.8	450	2	06D2X2_ERWCT	06d2x2 erwinia car
850	30	58.8	351	2	08MFC8_ASTPA	08mfc8 astyanax fa	923	30	58.8	453	2	0567W2_BRARE	0567w2 brachydanio
851	30	58.8	351	2	08MFC9_ASTPA	08mfc9 astyanax fa	924	30	58.8	453	2	06GQ39_XENLA	06gq39 xenopus lae
852	30	58.8	351	2	08MFD0_ASTPA	08mfd0 astyanax fa	925	30	58.8	457	2	08A1G3_9SPHN	08a1g3 sphingomona
853	30	58.8	351	2	08MFD1_9TELE	08mfd1 astyanax ae	926	30	58.8	458	2	086UB9_HUMAN	086ub9 homo sapien
854	30	58.8	351	2	08MFD2_9TELE	08mfd2 astyanax ae	927	30	58.8	458	2	05O4F4_RAT	05o4f4 rattus norv
855	30	58.8	352	2	08MFD3_9TELE	08mfd3 astyanax bi	928	30	58.8	458	2	08CE78_MOUSE	08ce78 mus musculus
856	30	58.8	352	2	08EGF5_SHEON	08egf5 shevanella	929	30	58.8	458	2	08BSY5_MOUSE	08bsy5 mus musculus
857	30	58.8	354	2	08ZT15_PYRAE	08zty5 pyrobaculum	930	30	58.8	458	2	09CYV5_MOUSE	09cyv5 mus musculus
858	30	58.8	354	2	09H6M3_HUMAN	09h6m3 homo sapien	931	30	58.8	459	1	UTMP_BOVIN	utmp bos taurus
859	30	58.8	354	2	097MG1_CLOAB	097mg1 clostridium	932	30	58.8	460	2	07W0B1_9THEM	07w0b1 thermocoga
860	30	58.8	356	2	097JUB_CLOAB	097j18 clostridium	933	30	58.8	460	2	08GB10_THENE	08gb10 thermocoga
861	30	58.8	359	2	04YX12_PLAAB	04yx12 plasmodium	934	30	58.8	460	2	08KX31_SYNP2	08kx31 synectococc
862	30	58.8	362	2	09U416_BRABE	09u416 brachylosto	935	30	58.8	461	2	04MZ08_TREPA	04mz08 thelaxia p
863	30	58.8	363	2	084AR2_SALTU	084ar2 salmonella	936	30	58.8	462	2	073RK7_TREDE	073rk7 treponema d
864	30	58.8	364	2	09NCP9_BRATL	09ncp9 brachylosto	937	30	58.8	469	2	06C0Z2_YARLI	06c0z2 yarrowia ll
865	30	58.8	367	2	07MOT2_WOLNU	07mot2 wolfinella s	938	30	58.8	473	2	04Q0U7_LBTMA	04q0u7 leishmania
866	30	58.8	370	2	04TKK8_9SPHN	04tkk8 erythrobaet	939	30	58.8	483	2	0732Q4_BACCI	0732q4 bacillus ce
867	30	58.8	371	2	08CAG3_MOUSE	08cag3 mus musculu	940	30	58.8	487	2	069924_PSTRON	069924 streptomyce
868	30	58.8	373	2	08BUO6_MOUSE	08buo6 mus musculu	941	30	58.8	490	2	04ZP76_PSRSSY	04zpf6 pseudomonas
869	30	58.8	374	2	07NKM6_CHRVO	07nkm6 chromobacte	942	30	58.8	490	2	087X76_PSRSSY	087x76 pseudomonas
870	30	58.8	377	2	0649B2_9ARCH	0649b2 uncultured	943	30	58.8	492	2	08XRG0_MOUSE	08xrg0 mus musculu
871	30	58.8	379	2	04TZP6_LEIME	04tzp6 leishmania	944	30	58.8	492	2	08KSF2_RALSO	08ksf2 ralestonia s
872	30	58.8	385	2	08SZR4_DROME	08szr4 drosophilla	945	30	58.8	495	2	068YT0_CRIPE	068yt0 crinipellis
873	30	58.8	385	2	09V8R0_DROME	09v8r0 drosophilla	946	30	58.8	496	2	075BR9_ASHGO	075br9 ashbya goss
874	30	58.8	385	2	05E7M9_VITB1	05e7m9 vibrio fisc	947	30	58.8	498	2	05GZY0_XANOR	05gzy0 xanthomonas
875	30	58.8	388	2	07PKJ9_ANOGA	07pkj9 anophelies g	948	30	58.8	498	2	08P1L4_XANAC	08p1l4 xanthomonas
876	30	58.8	390	2	05HRJ3_STAOG	05hrj3 staphylococc	949	30	58.8	506	2	09D0U1_MOUSE	09d0u1 mus musculu
877	30	58.8	390	2	08CQZ0_STAEP	08cqz0 staphylococc	950	30	58.8	507	2	07RNT7_PLAYO	07rnt7 plasmodium
878	30	58.8	392	2	05HNS1_STAEP	05hns1 staphylococc	951	30	58.8	508	2	0977R9_9CRBN	0977r9 uncultured
879	30	58.8	392	2	08CND0_STAEP	08cnd0 staphylococc	952	30	58.8	508	2	0560K0_CRYVE	0560k0 cryptococcu
880	30	58.8	396	1	KBL_BACAN	081105 bacillus an	953	30	58.8	508	2	05KRP6_CRYVE	05krp6 cryptococcu
881	30	58.8	396	1	KBL_BACCR	081105 bacillus ce	954	30	58.8	514	2	050065_ARATH	050065 arabidopsis
882	30	58.8	396	1	PMEL_RALSO	081105 bacillus ce	955	30	58.8	514	2	0578T2_BRUAB	0578t2 bruceella ab
883	30	58.8	396	2	05IHG5_MAGGR	05ihg5 magnaporthe	956	30	58.8	514	2	08FVW8_BRUSU	08fvw8 bruceella su
884	30	58.8	396	2	04MNE7_BACCE	04mne7 bacillus ce	957	30	58.8	516	2	086A25_DICDI	086a25 dicystosell
885	30	58.8	396	2	07JDM4_BACCI	07jdm4 bacillus ce	958	30	58.8	521	2	05BCN9_EMENT	05bcn9 aspergillius
886	30	58.8	396	2	06HNU4_BACCK	06hnu4 bacillus th	959	30	58.8	524	2	08UBM9_AGRIS	08ubm9 agrobacteri
887	30	58.8	396	2	063G26_BACCC	063g26 bacillus ce	960	30	58.8	524	2	08UBM9_AGRIS	08ubm9 agrobacteri
888	30	58.8	399	2	08E844_SHEON	08e844 shevanella	961	30	58.8	530	2	09GPF0_DICDI	09gpf0 dictyosgeli
889	30	58.8	400	2	Y1038_HABIN	044039 haemophilus	962	30	58.8	533	2	08ZG37_YERPE	08zgz37 yersinia pe
890	30	58.8	400	2	04OLP2_HAB18	04qlz2 haemophilus	963	30	58.8	533	2	066CA7_YERPS	066ca7 arabidopsis
891	30	58.8	401	2	06LZ32_METMP	06lzz2 methanococc	964	30	58.8	534	1	APG_ARATH	apg arabidopsis
892	30	58.8	403	1	T230_CASBL	009474 caenorhabdi	965	30	58.8	534	1	04F10_GIBBE	04f10 gibberella
893	30	58.8	409	2	08SUT8_ENCCU	08sut8 encephalito	966	30	58.8	536	2	04QY42_LEIMA	04qy42 leishmania
894	30	58.8	412	2	0617D3_STAAN	0617d3 etaphylococ	967	30	58.8	536	2	06DHU1_BRARE	06dhu1 brachydanio
895	30	58.8	413	2	08PVA6_METMA	08pva6 methanocarc	968	30	58.8	539	2	06CQP1_KLUTA	06cqp1 kluyveromyc
896	30	58.8	415	2	06IA59_HUMAN	06ias9 homo sapien	969	30	58.8	541	2	08EBE2_SHEON	08ebe2 shevanella
897	30	58.8	415	2	09H974_HUMAN	09h974 homo sapien	970	30	58.8	546	2	09H289_HUMAN	09h289 homo sapien
898	30	58.8	415	2	05R998_PONPY	05r998 pongo pygma	971	30	58.8	547	2	05OVI0_ENTHA	05ovi0 entamoeba h
899	30	58.8	416	2	04MHW9_ASPFU	04mhw9 aspergillius	972	30	58.8	552	1	PYRG_WIGBR	pyrg wigglewort
900	30	58.8	417	1	AMIC_ECOLI6	033884 escherichia	973	30	58.8	553	2	04R851_MACRA	04r851 macaca fasc
901	30	58.8	417	1	AMIC_ECOLI	057kc7 salmonella	974	30	58.8	553	2	09WG32_NPVHC	09wg32 hyphantia
902	30	58.8	417	2	057KCT_SALCH	057kc7 salmonella	975	30	58.8	555	2	07SE10_ASHOC	07se10 ashbya goss
903	30	58.8	417	2	05PEN1_SALPA	05pen1 salmonella	976	30	58.8	555	2	07PH63_ANOGA	07ph63 anophelies g
904	30	58.8	417	2	08Z422_SALTU	08z422 salmonella	977	30	58.8	555	2	09ZOM3_POPPR	09zom3 populus tri
905	30	58.8	421	2	08ZMB9_SALTU	08zmb9 salmonella	978	30	58.8	555	2	09PSC9_POPPR	09psc9 populus tri
906	30	58.8	421	2	064BH3_9ARCH	064bh3 uncultured	979	30	58.8	555	2	08BKU8_MOUSE	08bku8 mus musculu
907	30	58.8	421	2	050G69_ENTHI	050g69 entamoeba h	980	30	58.8	562	2	06CLH6_KLUTA	06clh6 kluyveromyc

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981 30 58.8 563 1 YX13 CABEL
982 30 58.8 566 2 09SR12 ARATH
983 30 58.8 566 2 070VC5 GIATA
984 30 58.8 566 2 09X1E2 THEM4
985 30 58.8 568 2 05ZPA0 CHICK
986 30 58.8 574 2 073MU5 TREDE
987 30 58.8 581 2 08LTH0 9CAUD
988 30 58.8 584 2 04V706 DROME
989 30 58.8 594 2 05ZVY2 LEPGH
990 30 58.8 596 2 0875G7 CANGA
991 30 58.8 598 2 06FK45 CANGA
992 30 58.8 602 2 07QAP4 ANOGA
993 30 58.8 601 2 05YK19 PICAN
994 30 58.8 610 2 074GF0 GEOSL
995 30 58.8 610 2 06J180 9VIRU
996 30 58.8 610 2 09Y1C1 9VIRU
997 30 58.8 611 2 05L6Z0 CHLAB
998 30 58.8 614 1 ADIP HUMAN
999 30 58.8 615 2 04UBX4 THEAN
1000 30 58.8 631 2 05SP41_CRYNE
05SP41 cryptococcu

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ALIGNMENTS

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RESULT 1
Q5A224 CANAL PRELIMINARY; PRT; 217 AA.
ID Q5A224 CANAL PRELIMINARY; PRT; 217 AA.
AC 05A224;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Caol5.10337, Caol9.2819;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Pederspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RL "The diploid genome sequence of Candida albicans";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dunagan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Pearson K., Donnelly S., Favoretto S., Truong K.-W.,
RA Jones T., Scherer S., Agabian N.;
RL "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AACQ01000080; EAK96736.1; -; Genomic DNA.
DR EMBL; AACQ01000079; EAK96787.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 217 AA; 25474 MW; CF640A3257839131 CRC64;

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Query Match 76.5%; Score 39; DB 2; Length 217;
 Best local Similarity 72.7%; Pred. No. 24;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 RASKTISKYIA 11
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   : |||||
Db 6 KLSKTSKYPA 16

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RESULT 2
Q8T2Q3 D1C1D1
ID Q8T2Q3 D1C1D1 PRELIMINARY; PRT; 569 AA.
AC Q8T2Q3;

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DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DD80167502;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.E., Gulgo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and Analysis of Chromosome 2 of Dictyostelium.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugang R., Bertram M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Fairbrother P., Desany B., Just E., Morio T., Roet R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Moutier T., Pain A., Lu M., Harper D., Lindner R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchsieser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Louissege H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitz E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward G., Rosenthal A., Cox E.C.,
RA Shaulsky G., Schleicher M., Weinrock G., Rosenthal A., Cox E.C.,
RA Williams R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA Williams J., Dear P.R., Noegel A.A., Barrett B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
DR EMBL; AC116305; AML92254.1; -; Genomic DNA.
DR EMBL; AAF101000028; EAL69851.1; -; Genomic DNA.
DR InterPro; IPR012979; DUF_NUC189_C.
DR InterPro; IPR003301; Viral_VD10.
DR InterPro; IPR001680; WD40.
DR Pfam; PF08162; NUC189; 1.
DR Pfam; PF00400; WD40; 2.
DR PRINTS; PR01364; VD10PROTEIN.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 569 AA; 64664 MW; 5F8BE9F349EBA711 CRC64;

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Query Match 76.5%; Score 39; DB 2; Length 569;
 Best local Similarity 70.0%; Pred. No. 63;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RASKTISKYL 10
   : |||||
   : |||||
Db 238 RASKTIVTYL 247

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RESULT 3
KV1N HUMAN STANDARD; PRT; 108 AA.
ID KV1N HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.

```

OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy chains";
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenström's macroglobulin.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC removed.
CC -----
CC PIR; A01872; K1HU0U.
DR HSSP; A01607; 1BMW.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11779 MW; 8283DA24105827E CRC64;

Query Match 74.5%; Score 38; DB 1; Length 108;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKITSKY 10
DB 24 RASKITSKY 33

RESULT 4
KV31_HUMAN STANDARD; PRT; 115 AA.
ID KV31_HUMAN
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=5087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated within the Vκ locus";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X01668; -; NOT_ANNOTATED_CDS; Genomic DNA.
DR PIR; A01900; K3HU0G.
DR HSSP; P01625; 1EEQ.
DR SMR; P04433; 21-115.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR003556; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 Ig kappa chain V-II region VG.
FT REGION 21 43 Framework-1.
FT REGION 44 54 Complementarity-determining-1.
FT REGION 55 69 Framework-2.
FT REGION 70 76 Complementarity-determining-2.
FT REGION 77 108 Framework-3.
FT REGION 109 115 Complementarity-determining-3.
FT DISULFID 43 108 By similarity.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 72.5%; Score 37; DB 1; Length 115;
Best Local Similarity 63.6%; Pred. No. 32;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKITSKY 11
DB 44 RASKITSKY 54

RESULT 5
O961T5 DROME PRELIMINARY; PRT; 479 AA.
ID O961T5 DROME
AC O961T5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GH08783p.
GN Name=dbf; Synonym=BeDNA; ID26519;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Garxin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Munoz J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.B., Rubin G.M., Celisner S.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY047576; AAK77308.1; -; mRNA.
DR FlyBase; FBgn0067779; dbf.
DR GO; GO:0005771; C:multivesicular body; IDA.
SQ SEQUENCE 479 AA; 53170 MW; D71305553E1967C CRC64;

Query Match 72.5%; Score 37; DB 2; Length 479;
Best Local Similarity 77.8%; Pred. No. 1,3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKITSKY 9
DB 451 RASKITSKY 459


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RESULT 6
OJv474 DROME PRELIMINARY; PRT; 1007 AA.
ID OJv474 DROME PRELIMINARY; PRT; 1007 AA.
AC OJv474_
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE CG11371-PB (BGDNA.ID26519).
GN Name=chr; Synonym=BGDNA.ID26519; ORFNames=CG11371;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Morten J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiri J.F., Agoyani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher S., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Guan P., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Chame M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Munz D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodeggen E.J.,
RA Svitskas R., Taber P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svitskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;

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RT "The transposable elements of the Drosophila melanogaster euchromatic
genome perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacle J., Park S., Svitskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tang G.,
RA Agbayani A., Arcalata T.T., Baxter E., Blazek R.G., Butenoff C.,
RA Chame M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA Houston K.A., Hummel S.R., Kim E., Li P., Moshrefi M., Pacle J.M.,
RA Park S., Sequeira A., Sethi H., Sitr E., Svitskas R.R., Weinburg T.,
RA Celniker S.E.;
RT "Full Length Drosophila melanogaster cDNA database.";
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AE003590; AAF51565.1; -; genomic_DNA.
DR EMBL; AF184228; AAD55739.1; -; mRNA.
DR Ensembl; CG11371; Drosophila melanogaster.
DR FlyBase; FBgn0067779; CG11371.
DR FlyBase; FBgn0067779; dbi.
DR GO; GO:0005771; C:multivesicular body; IDA.
SQ SEQUENCE 1007 AA; 110580 MW; 0579DA2441F412D2 CRC64;
Query Match 72.5%; Score 37; DB 2; Length 1007;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 RASKITSKY 9
DB 979 RITSKITSKY 987

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RESULT 7
OJ43Y6 STAHU PRELIMINARY; PRT; 47 AA.
ID OJ43Y6 STAHU PRELIMINARY; PRT; 47 AA.
AC OJ43Y6_
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Mercuric reductase homologue.
GN ORFNames=SH2332;
OS Staphylococcus haemolyticus (strain JSC1435).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcaceae.
OX NCBI TaxID=279808;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=JSC1435;
RA Takeuchi F., Matanabe S., Baba T., Yuzawa H., Ito T., Cui L.,
RA Morimoto Y., Kuroda W., Takahashi W., Anai A., Baba S., Fukui S.,

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RA Lee J.C., Hiramatsu K.;
 RT "whole genome sequencing of *Staphylococcus haemolyticus* uncovers
 extreme plasticity of its genome and dynamics in the evolution of
 human-colonizing staphylococcal species."; Genomic DNA.
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB006716; BAE05641.1; -; Genomic DNA.
 SQ SEQUENCE 47 AA; 4998 MW; 968077070BE7B10A CRC64;

Query Match 70.6%; Score 36; DB 2; Length 47;
 Best Local Similarity 54.5%; Pred. No. 21;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
 ID 0723Y4_HUMAN PRELIMINARY; PRT; 236 AA.
 AC Q723Y4;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]

RESULT 8
 ID 0723Y4_HUMAN PRELIMINARY; PRT; 236 AA.
 AC Q723Y4;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skletal Muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ugin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skletal Muscle;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005332; AAH05332.1; -; mRNA.
 DR HSSP; P01834; IHEZ.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; CI-set; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN; 1.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 236 AA; 25702 MW; 7BFBFAED23084BC6 CRC64;

Query Match 70.6%; Score 36; DB 2; Length 236;
 Best Local Similarity 72.7%; Pred. No. 1e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
 ID 06BDU5; DEBHA PRELIMINARY; PRT; 384 AA.
 AC Q6BDU5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to gp1006178 *Saccharomyces cerevisiae* YLR328w.
 GN OrderedLocNames=DEHA0C126397;
 OS *Saccharomyces Hansenii* (Yeast) (Torulasporea hansenii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 NCBI_TaxID=4959;
 [1]

RESULT 9
 ID 06BDU5; DEBHA PRELIMINARY; PRT; 384 AA.
 AC Q6BDU5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to gp1006178 *Saccharomyces cerevisiae* YLR328w.
 GN OrderedLocNames=DEHA0C126397;
 OS *Saccharomyces Hansenii* (Yeast) (Torulasporea hansenii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 NCBI_TaxID=4959;
 [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 36239 / CBS 767;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrans P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neugebäude V., Babour A., Barbe V.,
 RA Goffard N., Frangoul L., Aigle M., Anthonard N., Beyne E., Bleykaeren C.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykaeren C.,
 RA Boissière A., Boyer J., Catilico L., Confantollet H., Groppi A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., de Druar A.,
 RA Hantreya F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Müller H.,
 RA Nicard J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pelenz S., Potier S., Richard G.-F., Straub M.-L., Sileau A.,
 RA Swennen D., Tekala F., Wesolowski-Jouvet M., Weisnot E., Wirth B.,
 RA Zenlou-Weyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallard C., Weisenbach J.,
 RA Winkler P., Souciet J.-L.;
 RT "Genome evolution in yeasts."; Nature 430:35-44(2004).
 RL EMBL; CR82135; CAG86260.1; -; Genomic DNA.
 DR GO; GO:0016779; F:nuclcleotidyltransferase activity; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR GO; GO:0009435; P:NAD biosynthesis; IEA.
 DR InterPro; IPR004820; Cytidylyltransf.
 DR InterPro; IPR005248; NAMN adrnsmfrase.
 DR Pfam; PF01467; CTP transf 2; 1.
 DR TIGRFAMs; TIGR00482; NAMN_adrnsmfrase; 1.
 KW Complete proteome.
 SQ SEQUENCE 384 AA; 43456 MW; FAF5107C8FBF179F CRC64;

Query Match 70.6%; Score 36; DB 2; Length 384;
 Best Local Similarity 70.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASKTISKYL 10
 ID 09E200_9ALPH PRELIMINARY; PRT; 421 AA.
 AC Q9E200;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Cercopithecine herpesvirus 9 (Simian varicella virus).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

RESULT 10
 ID 09E200_9ALPH PRELIMINARY; PRT; 421 AA.
 AC Q9E200;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Cercopithecine herpesvirus 9 (Simian varicella virus).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

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OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=35246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2151382; PubMed=11352673; DOI=10.1006/viro.2001.0912;
RA Gray W.L., Starnes B., White M.W., Mahalingam R.;
RT "The DNA sequence of the simian varicella virus genome.";
RL Virology 284:123-130(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
RT "Complete sequence of the Simian Varicella Virus Genome.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275348; AAG27188.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0019033; C:viral tegument; IEA.
DR InterPro; IPR007764; Herpes_UL43.
DR Pfam; PF05072; Herpes_UL43; 1.
DR Hypothetical protein.
SQ SEQUENCE 421 AA; 47270 MW; 7C2F33937883041C CRC64;

Query Match 70.6%; Score 36; DB 2; Length 421;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKTISKYLA 11
Db 405 NKTISKYLS 413

RESULT 11
YD85 SCHPO STANDARD; PRT; 510 AA.
ID 010410;
AC 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 13-SEP-2005 (rel. 48, Last annotation update)
DE Hypothetical protein C1F3.05 in chromosome 1.
GN ORFNames=SPAC1F3.05;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouras J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hiderago J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moutle S., Mungall K.L., Murphy L.D., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M.N., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Voiclaert G., Aert R., Robben J., Grymopier B.,
RA Welfens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrsach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wandt R., Fumelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucet M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
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RL Nature 415:871-880(2002).
CC -!- FUNCTION: May play a role in the regulation of membrane traffic
CC through the trans-Golgi network (By similarity).
CC -!- SIMILARITY: Contains 1 GAB domain.
CC -!- SIMILARITY: Contains 1 GAT domain.
CC -!- SIMILARITY: Contains 1 VHS domain.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z70690; CA94623.1; -; Genomic_DNA.
CC PIR; T38076; T38076.
DR HSSP; Q960X8; 1DVP.
DR GenDB_Spombe; SPAC1F3.05; -.
DR InterPro; IPR008152; A/G_adapt_C.
DR InterPro; IPR008153; Gamma_adaptin_C.
DR InterPro; IPR002014; GAT.
DR Pfam; PF02883; Alpha_adaptinC2; 1.
DR Pfam; PF00790; VHS; 1.
DR ProDom; PD003686; VHS; 1.
DR SMART; SM00288; VHS; 1.
DR PROSITE; PS50180; GAE; 1.
DR PROSITE; PS50909; GAT; 1.
DR PROSITE; PS50179; VHS; 1.
KM Coiled coil; Complete proteome; Golgi stack; Hypothetical protein;
KW Membrane; Protein transport; Transport.
FT DOMAIN 14 150
FT DOMAIN 177 301
FT DOMAIN 391 510
FT GAE.
SQ SEQUENCE 510 AA; 56789 MW; D039C8976BFC6C6 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 510;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
Db 2 RSKQTSKYL 11

RESULT 12
085191 CLOPA PRELIMINARY; PRT; 602 AA.
ID 085191;
AC 085191;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 525;
RX MEDLINE=98340497; PubMed=9675846;
RA Macis L., Daniel R., Gottschalk G.;
RT "Properties and sequence of the coenzyme B12-dependent glycerol
RT dehydratase of Clostridium pasteurianum.";
RL FEWS Microbiol. Lett. 164:21-26(1998).
DR EMBL; AF051373; AAC27925.1; -; Genomic_DNA.
DR HSSP; Q59474; INEW.
DR InterPro; IPR009191; DdrA_PduG.
DR PIRSF; PIRSF011502; DdrA_PduG; 1.
KM Hypothetical protein.
SQ SEQUENCE 602 AA; 64506 MW; DDE0741FB1C339BE CRC64;

Query Match 70.6%; Score 36; DB 2; Length 602;
Best Local Similarity 77.8%; Pred. No. 2.6e+02;
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KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KM Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A61608D0618 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 76;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
DB 24 RASQGISNYLA 34

RESULT 16
Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9827139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;
RA Xu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype."
RL J. Exp. Med. 174:1639-1652(1991).
DR EMBL; AF035044; AAD56280.1; -, mRNA.
DR PIR; PH0863; PH0863.
DR HSSP; P01607; 1BMW.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 68.6%; Score 35; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 76;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
DB 24 RASQGISNYLA 34

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RESULT 17
Q5FLS2 LACAC PRELIMINARY; PRT; 136 AA.
ID Q5FLS2;
AC Q5FLS2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Putative nudix family protein.
DE Name=mutT; OrderedLocustNames=LSA0465;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
NCBI_TaxID=1579;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCFM;
RX PubMed=15671160; DOI=10.1073/pnas.0409188102;
RA Altermann E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
RA Buck B.L., McAlliffe O., Souther N., Dobson A., Duong T., Callanan M.,
RA Lick S., Hamrick A., Cano R., Kleenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium
RT Lactobacillus acidophilus NCFM."
RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
CC 1- SIMILARITY: Belongs to the Nudix hydrolase family.
DR EMBL; CP000033; AAV42352.1; -, Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00293; NUDIX; 1.
DR PRINTS; PR00502; NUDIXFAMILY.
DR PROSITE; PS00893; NUDIX; UNKNOWN_1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 136 AA; 16061 MW; DABBF354C22991D CRC64;

Query Match 68.6%; Score 35; DB 2; Length 136;
Best Local Similarity 63.6%; Pred. No. 95;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
DB 78 RSKTIVTYLA 88

RESULT 18
RS8 SPOFR STANDARD; PRT; 208 AA.
ID RS8;
AC Q8W015;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 40S ribosomal protein S8.
GN Name=Rps8;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictysta; Noctuoidea;
OC Noctuidae; Amphipyritinae; Spodoptera.
NCBI_TaxID=7108;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Landais I., Ogliastro M., Mita K., Nohata J., Lopez-Ferber M.,
RA Duonier-Cerutti M., Fournier P., Devauchelle G.;
RT "Full-length ribosomal protein sequence from an EST library of
RT Spodoptera frugiperda cells (Sf9)."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to the ribosomal protein S8e family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AY072291; AAL62472.1; -, mRNA.
DR InterPro; IPR01047; Ribosomal_S8e.

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DR Pfam; PF01201; Ribosomal_S8e; 1.
 DR TIGRPFAM; TIGR00307; S8e; 1.
 DR PROSITE; PS01193; RIBOSOMAL_S8E; 1.
 KW Ribonucleoprotein; Ribosomal protein.
 SQ SEQUENCE 208 AA; 23792 MW; E4C7268DE96D086E CRC64;

Query Match 68.6%; Score 35; DB 1; Length 208;
 Best Local Similarity 63.6%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 ID 141 RSKKTAKKYLA 151

RESULT 19
 Q6F475_PLUXY
 ID Q6F475_PLUXY PRELIMINARY; PRT; 208 AA.

AC Q6F475;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, last sequence update)
 DE 25-OCT-2004 (TReMBLrel. 28, last annotation update)
 DE Ribosomal protein S8.
 OS Plutella xylostella (Diamondback moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Yponomeutoidea; Plutellidae; Plutella.
 OC NCBI_TaxID=51655;

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;
 RA Bum J.H., Yoe S.M., Seo Y.R., Kang S.W., Han S.S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

RN [2]
 RC TISSUE=Whole body.

RA Bum J., Yoe S., Seo Y., Kang S., Han S.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB180415; BAD26559.1; -, mRNA.
 DR GO; GO:0005622; C:intracellular; IEA.

DR GO; GO:0005840; C:ribosome; IEA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

DR GO; GO:0006412; P:protein biosynthesis; IEA.

DR InterPro; IPR001047; Ribosomal_S8E.

DR Pfam; PF01201; Ribosomal_S8e; 1.

DR TIGRPFAM; TIGR00307; S8e; 1.

DR PROSITE; PS01193; RIBOSOMAL_S8E; 1.

KW Ribosomal protein.
 SQ SEQUENCE 208 AA; 23712 MW; 9D9135ED5535E9EB CRC64;

Query Match 68.6%; Score 35; DB 2; Length 208;
 Best Local Similarity 63.6%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 ID 141 RSKKTAKKYLA 151

RESULT 20
 Q6PIH7_HUMAN
 ID Q6PIH7_HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6PIH7;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)

DT 05-JUL-2004 (TReMBLrel. 27, last sequence update)

DT 05-JUL-2004 (TReMBLrel. 27, last annotation update)

DE ICKC protein.

GN Name=ICKC;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OX NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC NIT MGC Project;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC034141; AAH34141.1; -, mRNA.

DR HSSP; P01607; IAR2.

DR SWR; Q6PIH7; 23-236.

DR Ensembl; ENSG00000163245; Homo sapiens.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_C1.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF07654; C1-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGC1; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.

KW Ribosomal protein.
 SQ SEQUENCE 236 AA; 25603 MW; 8BC56110661213F CRC64;

Query Match 68.6%; Score 35; DB 2; Length 236;
 Best Local Similarity 72.7%; Pred. No. 1.7e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 ID 46 RASQGISYLA 56

RESULT 21
 Q9HH61_9CAUD
 ID Q9HH61_9CAUD PRELIMINARY; PRT; 252 AA.

AC Q9HH61;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)

DE Hypothetical protein ORF8.

GN Name=ORF8;

OS Methanothermobacter wolfeii prophage psim100.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.

OC NCBI_TaxID=173824;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=21429258; PubMed=11544247;

RX DOI=10.1126/JB.183.19.5788-5792.2001;

RA Luo Y., Pfister P., Heisinger T., Wasserrfallen A.;

RT "The genome of archaeal prophage psiM100 encodes the lytic enzyme responsible for autolysis of *Methanothermobacter wolfeii*.";
 RL J. Bacteriol. 183:5788-5792(2001).
 DR EMBL; AF301375; AAC39950.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 252 AA; 29207 MW; C282D651A8CDE365 CRC64;

Query Match 68.6%; Score 35; DB 2; Length 252;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
 ||| |||||
 DB 55 RASPEISKYL 64

RESULT 22
 Q6BTH9_DEBHA PRELIMINARY; PRT; 409 AA.
 ID Q6BTH9 DEBHA PRELIMINARY;
 AC Q6BTH9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Similar to tr|Q9P8B4|Agaricus bisporus Glucanase.
 GN OrderedLocustNames=DEHA0D008039;
 OS Debaryomyces hansenii (Yeast) (Torula spora hansenii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
 NC NCB1_Taxid=4959;
 RN 11
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 36239 / CBS 767;
 RX PubMed=15239592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Latouche I., de Montigny J., Marck C., Neveglisse C., Talla E.,
 RA Goffard N., Frangoul L., Aigle M., Anthonard V., Babour A., Barbe V.,
 RA Barnay S., Blanchun S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Catolico L., Confantolero F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Janiaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.-M., Nikolaki M., Oztas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudon B., Scarpelli C., Gallard J., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 DR EMBL; CR382136; CAG86594.1; -; Genomic DNA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR010905; Glyco_Hydro_88.
 DR Pfam; PF07470; Glyco_Hydro_88; 1.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 409 AA; 46841 MW; 5199FE1BDC5CD9A CRC64;

Query Match 68.6%; Score 35; DB 2; Length 409;
 Best Local Similarity 87.5%; Pred. No. 2.9e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASKTISKY 9
 ||| |||||
 DB 274 AKKTISKY 281

RESULT 23
 OSEY37_AEDAE PRELIMINARY; PRT; 584 AA.
 ID OSEY37_AEDAE PRELIMINARY;
 AC OSEY37;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Leucokinin receptor protein.
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Culicinae; Culicini; Aedes; Stegomyia.
 NC NCB1_Taxid=7159;
 RN 11

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Rockefeller;
 RX PubMed=15663775; DOI=10.1111/j.1365-2583.2004.00531.x;
 RA Pietrantoni P.V., Jagger C., Taneja-Bagehwar S., Nachman R.J.,
 RA Barnoud R.;
 RT "The mosquito *Aedes aegypti* (L.) leucokinin receptor is a multiligand receptor for the three *Aedes* kinins."
 RL Insect Mol. Biol. 14:55-67(2005).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; AY596453; AAT95982.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PR01012; NRPEPTIDEYR.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 584 AA; 65202 MW; D63CF9D9C21634D CRC64;

Query Match 68.6%; Score 35; DB 2; Length 584;
 Best Local Similarity 70.0%; Pred. No. 4.1e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
 ||| |||||
 DB 148 RASKTISKYV 157

RESULT 24
 Q7UR05_RHOBA PRELIMINARY; PRT; 749 AA.
 ID Q7UR05_RHOBA PRELIMINARY;
 AC Q7UR05;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ATP-dependent DNA helicase RecQ (EC 3.6.1.-).
 GN Name=RecQ; OrderedLocustNames=RB5969;
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 NC NCB1_Taxid=117;
 RN 11
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lomardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Hellmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete *Pirellula* sp. strain 1."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294143; CAD74537.1; -; Genomic_DNA.
 DR HSSP; P15043; 10YY.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004003; F:ATP-dependent DNA helicase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.

DR GO; GO:0009432; P:SOS response; IEA.
 DR InterPro: IPR006293; ATP RecQ.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR002121; HRDC.
 DR InterPro: IPR004589; RecQ.
 DR InterPro: IPR010916; TONB_Box_N.
 DR Pfam: PF002270; DEAD; 1.
 DR Pfam: PF002271; Helicase_C; 1.
 DR Pfam: PF00570; HRDC; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 DR SMART: SM00341; HRDC; 1.
 DR TIGRFAMs: TIGR01389; recQ; 1.
 DR TIGRFAMs: TIGR00614; recQ_fam; 1.
 DR PROSITE: PS50967; HRDC; 1.
 DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
 DR PROSITE: PS00430; Helicase; Hydrolase.
 KW Complete proteome; Helicase; 749 AA; 82680 MW; 36414408DB9FEIC CRC64;
 SQ SEQUENCE

Query Match 68.6%; Score 35; DB 2; Length 749;
 Best Local Similarity 54.5%; Pred. No. 5.3e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RASKISKYLA 11
 DB 671 RASTVANKILS 681

RESULT 25
 QSPAZ8 ANAMM
 ID QSPAZ8 ANAMM PRELIMINARY; PRT; 812 AA.
 AC QSPAZ8;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE DNA topoisomerase (EC 5.99.1.2).
 GN Name=topA; OrderedlocusNames=AM502;
 OS Anaplasma marginale (strain St. Maries).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Anaplasma.
 OX NCBI_TaxID=234826;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA PubMed:15618402; DOI=10.1073/pnas.040656102;
 RA Brayton K.A., Kappey L.S., Herndon D.R., Dark M.J., Tibbals D.L.,
 RA Palmer G.H., McGuire T.C., Knowles D.P. Jr.;
 RT "Complete genome sequencing of Anaplasma marginale reveals that the
 RT surface is skewed to two superfamilies of outer membrane proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 102:844-849(2005).
 RL EMBL: CP000030; AAY8532.1; -, Genomic_DNA.
 DR GO; GO:0005694; C:Chromosome; IEA.
 DR GO; GO:0003917; F:DNA topoisomerase type I activity; IEA.
 DR GO; GO:0006304; P:DNA modification; IEA.
 DR GO; GO:0006265; P:DNA topological change; IEA.
 DR GO; GO:0006268; P:DNA unwinding; IEA.
 DR InterPro: IPR003601; DNATopI_ATP_bind.
 DR InterPro: IPR003602; DNATopI_DNA_bind.
 DR InterPro: IPR005733; DNA_topI_bact.
 DR InterPro: IPR000380; DNA_topI_bact.
 DR InterPro: IPR006171; Toprim_dom.
 DR InterPro: IPR006154; Toprim_sub.
 DR Pfam: PF01131; Topoisom_bac; 1.
 DR Pfam: PF01131; Topoisom_bac; 1.
 DR Pfam: PF01751; Toprim; 1.
 DR Pfam: PF01396; zf-C4_TopoIsm; 1.
 DR PRINTS: PR00417; PRTPISMRASE1.
 DR SMART: SM00437; TOP1AC; 1.
 DR SMART: SM00436; TOP1BC; 1.
 DR SMART: SM00493; TOP1RM; 1.
 DR TIGRFAMs: TIGR01051; topA_bact; 1.
 DR PROSITE: PS00396; TOPOISOMERASE_I_PROK; 1.
 KW Complete proteome; Isomerase.

SQ SEQUENCE 812 AA; 90799 MW; 0A592D4C7DFDEC38 CRC64;
 Query Match 68.6%; Score 35; DB 2; Length 812;
 Best Local Similarity 87.5%; Pred. No. 5.7e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 SKTISKYL 10
 DB 12 AKTISKYL 19

RESULT 26
 TOP1_BUCAP
 ID TOP1_BUCAP STANDARD; PRT; 853 AA.
 AC 08K9B7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
 DE (unwinding enzyme) (Swivelase).
 GN Name=topA; OrderedlocusNames=BUSg273;
 OS Buchera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=22084549; PubMed=12089438; DOI=10.1126/science.1071278;
 RA Tamas I., Klason L., Canback B., Naeslund A.K., Eriksson A.-S.,
 RA Wernegren J.U., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria.";
 RT Science 296:2376-2379(2002).
 CC -1- FUNCTION: The reaction catalyzed by topoisomerases leads to the
 CC conversion of one topological isomer of DNA to another.
 CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
 CC DNA, followed by passage and rejoining.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA
 CC backbone bond, it simultaneously forms a protein-DNA link, in
 CC which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
 CC at one end of the enzyme-severed DNA strand.
 CC -1- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
 CC family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AE014103; AAM67831.1; -, Genomic_DNA.
 DR HSP: P06612; IECL.
 DR InterPro: IPR003601; DNA_topI_ATP_bd.
 DR InterPro: IPR005733; DNA_topI_bact.
 DR InterPro: IPR003602; DNA_topI_DNA_bd.
 DR InterPro: IPR000380; DNA_topI_bact.
 DR InterPro: IPR006171; Toprim_dom.
 DR InterPro: IPR006154; Toprim_sub.
 DR PANTHER: PTHR11390; DNA_topIsmrase; 2.
 DR Pfam: PF01131; Topoisom_bac; 1.
 DR Pfam: PF01751; Toprim; 1.
 DR Pfam: PF01396; zf-C4_TopoIsm; 2.
 DR PRINTS: PR00417; PRTPISMRASE1.
 DR SMART: SM00437; TOP1AC; 1.
 DR SMART: SM00436; TOP1BC; 1.
 DR SMART: SM00493; TOP1RM; 1.
 DR TIGRFAMs: TIGR01051; topA_bact; 1.
 DR PROSITE: PS00396; TOPOISOMERASE_I_PROK; 1.
 KW Complete proteome; DNA-binding; Isomerase; Metal-binding; Repeat;
 KW Topoisomerase; Zinc; Zinc-finger.
 FT ZN_FING 589 621 C4-type 1.
 FT ZN_FING 649 676 C4-type 2.
 FT ZN_FING 699 724 C4-type 3.

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FT ACT SITE 313 313 DNA cleavage (By similarity).
SQ SEQUENCE 853 AA; 98816 MW; 99854AB78AC6D1B CRC64;

Query Match
Best Local Similarity 68.6%; Score 35; DB 1; Length 853;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKTISKYL 10
   :|||||
Db 14 AKTISKYL 21

RESULT 27
Q4NCN4_9M1CC PRELIMINARY; PRT; 911 AA.
ID Q4NCN4_9M1CC PRELIMINARY; PRT; 911 AA.
AC Q4NCN4;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE DNA topoisomerase I (EC 5.99.1.2).
GN ORFName=ArthRBART_1202;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Istrati S., Plutnick S., Richardson P.;
RA "Sequencing of the draft genome assembly of Arthrobacter sp. FB24."
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (PGF-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Arthrobacter sp. FB24."
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AHS01000015; EAL95016.1; -; Genomic_DNA.
KW Isomerase.
SQ SEQUENCE 911 AA; 99526 MW; A45C77432A9A63D3 CRC64;

Query Match
Best Local Similarity 87.5%; Score 35; DB 2; Length 911;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKTISKYL 10
   :|||||
Db 20 SKTIAYKL 27

RESULT 28
Q9UL81_HUMAN PRELIMINARY; PRT; 107 AA.
ID Q9UL81_HUMAN PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX

```

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RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -; mRNA.
DR HSSP; P01607; 1BWV.
DR SMR; Q9UL81; 1-107.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 2; Length 107;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAKTISKYL 10
   :|||||
Db 24 RASQISINYL 33

RESULT 29
Q96SA9_HUMAN PRELIMINARY; PRT; 107 AA.
ID Q96SA9_HUMAN PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglycosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal antigenic autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene
RT segments associated with the autoimmune repertoire."
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pilling M., Ghosesein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiootype."
RL J. Exp. Med. 174:1639-1652(1991).
RN [5]

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RP NUCLEOTIDE SEQUENCE.
RX PubMed=1903706;
RA Blaison G., Kuntz J.L., Pasquali J.L.;
RT "Molecular analysis of V kappa III variable regions of polyclonal
RT rheumatoid factors during rheumatoid arthritis.";
RL Eur. J. Immunol. 21:1221-1227(1991).
DR EMBL; U96396; AAB68785.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BMW.
DR SMR; Q96SA9; 1-107.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_Like; 1.
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577P16 CRC64;

Query Match
Best Local Similarity 70.0%; Score 34; DB 2; Length 107;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKITSKYL 10
DB 24 RASQISSYL 33

RESULT 30
ID Q9UL77 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
CX [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Bernay S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal strictional autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene
RT segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Iuzza L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RL EMBL; AF035037; AAD56273.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.

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DR HSSP; P01607; 1BMW.
DR SMR; Q9UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_Like; 1.
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match
Best Local Similarity 70.0%; Score 34; DB 2; Length 108;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKITSKYL 10
DB 24 RASQISSYL 33

RESULT 31
ID KY1W HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
CX [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM; Genomic_DNA.
DR PIR; A01883; K1JHWK.
DR HSSP; P01607; 1BMW.
DR SMR; P04431; 23-129.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_Like; 1.
DR Immunoglobulin domain; Immunoglobulin V region; Signal.
KW IMUNOGLOBULIN DOMAIN; IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1
FT CHAIN 23
FT REGION 23 129
FT REGION 23 45
FT REGION 46 56
FT REGION 57 71
FT REGION 72 78
FT REGION 79 110
FT REGION 111 119
FT REGION 120 129
FT REGION 120 129
FT DISULFID 45
FT NON_TER 129
FT SEQUENCE 129 AA; 14069 MW; F941PA07DAFC2P9 CRC64;

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Query Match          66.7%; Score 34; DB 1; Length 129;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYL 10
      |||:|:|:|
      46 RASQISINYL 55

Db

RESULT 32
Q5W550_9D1PT PRELIMINARY; PRT; 200 AA.
ID Q5W550;
AC Q5W550;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE CAD protein (Fragment).
GN Namecad;
OS Polletina nigra.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
OC Muscidae; Polletina.
OX NCBI_TaxID=253337;
RN [1]
NP NUCLEOTIDE SEQUENCE.
RA Schenli G.S., Carvalho C.J.B.D., Wiegmann B.M.;
RT "Regarding the taxonomic status of Ophyra, 1830 Robineau-Desvoidy
RT (Diptera: Muscidae): A molecular approach.";
RL Zootaxa 712:1-12(2004).
CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
CC phosphate + L-glutamate + carbamoyl phosphate.
EMBL: AF605048; CA53246.1; -; Genomic_DNA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004086; P:carbamoyl-phosphate synthase activity; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0006807; P:nitrogen compound metabolism; IEA.
DR InterPro: IPR006220; Anth_synthII.
DR InterPro: IPR001317; CP_synthGATase.
DR InterPro: IPR002474; CP_synthsmall.
DR InterPro: IPR011702; GATase.
DR InterPro: IPR000991; GATase_1.
DR Pfam: PF00988; CPSase_sm_chain; 1.
DR Pfam: PF00117; GATase_1.
DR PRINTS; PR00097; ANTSYNTHASEIT.
DR PRINTS; PR00099; CPSGATASE.
DR PRINTS; PR00096; GATASE.
DR PROSITE; PS00442; GATASE_TYPE_1; 1.
FT NON_TER 1
FT NON_TER 200
FT SEQUENCE 200 AA; 21830 MW; 331AFD463B308EB1 CRC64;

SQ

Query Match          66.7%; Score 34; DB 2; Length 200;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYL 11
      |||:|:|:|
      17 RAKETLSKXMA 27

Db

RESULT 33
Q8YVNG_ANASP PRELIMINARY; PRT; 205 AA.
ID Q8YVNG;
AC Q8YVNG;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transcriptional regulator.
GN Anabaena sp. (strain PCC 7120).
OS Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OC NCBI_TaxID=103690;

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RN [1]
NP NUCLEOTIDE SEQUENCE.
RP MEDLINE=21595285; PubMed=11759840;
RX Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Itiguchi M., Ishikawa A., Kawashina K., Kimura T.,
RA Kishida Y., Kohara M., Matsuno M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; BA000019; BAB72767.1; -; Genomic_DNA.
DR PIR; A1907; A11907.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR012287; Homeodomain-rel.
DR InterPro: IPR01647; HTH_Tetr.
DR Pfam; PF0440; Tetr_N; 1.
DR PRINTS; PR00455; HTHTETR.
DR PROSITE; PS01081; HTH_TETR_1; 1.
DR PROSITE; PS09377; HTH_TETR_2; 1.
KW Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 205 AA; 22717 MW; 5E29812783E5826 CRC64;

QY      2 ASKTISKYL 11
      |||:|:|:|
      139 ALETISKYL 148

Db

RESULT 34
Q8ESU5_OCEIH PRELIMINARY; PRT; 206 AA.
ID Q8ESU5;
AC Q8ESU5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical conserved protein.
GN OrderedLocustNames=OB0639;
OS Oceanobacillus thelyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
NP NUCLEOTIDE SEQUENCE.
RP STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkt526;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus thelyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935(2002).
DR EMBL; BA000028; BAC12595.1; -; Genomic_DNA.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro: IPR000073; A/b_hydrolase.
DR InterPro: IPR003089; AB_hydrolase.
DR InterPro: IPR001173; GAP_dhdrogenase.
DR InterPro: IPR000379; Ser_ester.
DR Pfam: PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
DR PROSITE; PS00071; GAPDH; UNKNOWN_1.
KW Complete proteome; Hydrolase; Hypothetical protein.
SQ SEQUENCE 206 AA; 23292 MW; AA969D20DFFC71A CRC64;

QY      1 RASKTISKYL 10
      |||:|:|:|
      6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Query Match          66.7%; Score 34; DB 2; Length 206;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Db 164 RASKRLAKYI 173

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RESULT 35
OSUNAN6_BOMMO
ID OSUNAN6_
AC OSUNAN6_
DT 01-FEB-2005 (Tremblrel. 29, Created)
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
DE Ribosomal protein S8.
GN Name=Rps8;
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OC NCBI_TaxID=7091;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=P50;
RA Heckel D.G., Morgan M., Shimada T., Mita K.;
RT "Ribosomal proteins of Bombyx mori."
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=P50;
RA Shimada T., Mita K.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY769322; AAV34864.1; -, mRNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR01047; Ribosomal_S8E.
DR Pfam; PF01201; Ribosomal_S8E; 1.
DR Prodom; PD005658; Ribosomal_S8E; 1.
DR TIGRFAMs; TIGR00307; S8e; 1.
DR PROSITE; PS01193; RIBOSOMAL_S8E; 1.
KW Ribosomal protein.
SQ SEQUENCE 208 AA; 23791 MW; EPEC66EFFF1D198CA CRC64;

Query Match 66.7%; Score 34; DB 2; Length 208;
Best Local Similarity 63.6%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
Db 141 RSOQTARKYLA 151

RESULT 36
Q74ZE2_ASHGO
ID Q74ZE2_ASHGO PRELIMINARY; PRT; 220 AA.
AC Q74ZE2;
DT 05-JUN-2004 (Tremblrel. 27, Created)
DT 05-JUN-2004 (Tremblrel. 27, Last sequence update)
DE 05-JUN-2004 (Tremblrel. 27, Last annotation update)
DE AGS257CP.
GN Name=AGR257C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OC NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegelé S., Bricaut S., Ierch A., Gates K., Steiner S.,
RA Moir C., Poehlmann R., Luedi F., Choi S., Wing K.A., Flavier A.,
RA Gaffney T.D., Philippesen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
Saccharomyces cerevisiae genome."

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RL Science 304:304-307(2004).
DR EMBL; AE016820; AAS54747.1; -, Genomic_DNA.
DR HSSP; P10114; IKA0.
DR AGD; AGR257C; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR003579; GTPase_Rab.
DR InterPro; IPR003577; GTPase_Ras.
DR InterPro; IPR003578; GTPase_Rho.
DR InterPro; IPR002041; RAN_tnsfmng.
DR InterPro; IPR001806; Ras_tnsfmng.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; Ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR SMART; SM00175; RAB; 1.
DR SMART; SM00176; RAN; 1.
DR SMART; SM00173; RAS; 1.
DR SMART; SM00174; RHO; 1.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR Cell cycle; Cell division; Complete proteome; GTP-binding;
KW Nucleotide-binding.
SQ SEQUENCE 220 AA; 24572 MW; C098B1758AFF9F47 CRC64;

Query Match 66.7%; Score 34; DB 2; Length 220;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKY 9
Db 5 RTNKTKISKY 13

RESULT 37
GU33_RAT
ID GU33_RAT STANDARD; PRT; 234 AA.
AC P35896;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Possible gustatory receptor clone PTEB3 (fragment).
DE Rattus norvegicus (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Fischer; TISSUE=Lingual epithelium;
RX MEDLINE=9318133; PubMed=8380780; DOI=10.1016/0014-5793(93)81302-G;
RA Abe K., Kusakabe Y., Tanemura K., Emori Y., Arai S.;
RT "Multiple genes for G-protein-coupled receptors and their expression
in lingual epithelia."
RL FEBS Lett. 316:253-256(1993).
CC -1- FUNCTION: Possible taste receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Tongue specific.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; S28998; S28998.
CC DR Ensembl; ENSRNOG0000033934; Rattus norvegicus.
CC DR InterPro; IPR000276; GPCR_Rhodopsn.
CC DR InterPro; IPR000725; Olfact_receptor.
CC DR PANTHER; PTHR11398; Olfact_receptor; 1.
CC Pfam; PF00001; 7tm_1; 1.
CC DR PRINTS; PR00237; GPCR_RHODOPSIN.
CC DR PRINTS; PR00245; OLFACTORR.

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DR PROSITE; P500237; G. PROTEIN RECEPTOR; FALSE_NEG.
DR PROSITE; P550262; G. PROTEIN RECEPTOR; 2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
KW Transmembrane.
FT TRANSMEM 11 2 (Potential).
FT TOPO_DOM 12 42 Extracellular (Potential).
FT TRANSMEM 43 62 3 (Potential).
FT TOPO_DOM 63 84 Cytoplasmic (Potential).
FT TRANSMEM 85 105 4 (Potential).
FT TOPO_DOM 106 138 Extracellular (Potential).
FT TRANSMEM 139 160 5 (Potential).
FT TOPO_DOM 161 182 Cytoplasmic (Potential).
FT TRANSMEM 183 202 6 (Potential).
FT TOPO_DOM 203 212 Extracellular (Potential).
FT TRANSMEM 213 234 7 (Potential).
FT CARBOHYD 109 109 N-linked (GlcNAc... ) (Potential).
FT DISULFID 39 121 By similarity.
FT NON_TER 1 1
FT NON_TER 234 234
SQ SEQUENCE 234 AA; 26686 MW; 937E9098B982924 CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 1; Length 234;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
DB 169 RMSSTVSKYKA 179

RESULT 38
Q72473 HUMAN PRELIMINARY; PRT; 234 AA.
ID Q72473
AC Q72473
DT 01-OCT-2003 (TRMBLrel. 25, Created)
DT 01-OCT-2003 (TRMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
DE IGKC protein.
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.D., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grummond J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalms D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RG NIH GGC Project;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC056256; AAHS6256.1; -, mRNA.
DR HSSP; P01834; 1HE2.
DR SMR; Q72473; 22-234.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; P550835; IG_LIKE; 2.
DR PROSITE; P500290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
KW PROSITE; P500290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BA51BC0F CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 2; Length 234;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
DB 44 RASQSIGSYLA 54

RESULT 39
Q57D00 BRUAB PRELIMINARY; PRT; 253 AA.
ID Q57D00
AC Q57D00;
DT 10-MAY-2005 (TRMBLrel. 30, Created)
DT 10-MAY-2005 (TRMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRMBLrel. 30, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
GN Ordered locus names=Brub1_0868;
OS Brucella abortus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=9-941 / Biovar 1;
RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuercher R.L.,
RA Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.,
RT "Completion of the genome sequence of Brucella abortus and comparison
to the highly similar genomes of Brucella melitensis and Brucella
rt suis."
RT J. Bacteriol. 187:2715-2726(2005).
DR EMBL; AE017223; AAX74234.1; -, Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 253 AA; 26517 MW; 384A8E4611586F3 CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 2; Length 253;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
DB 96 RAKTILQKILA 106

RESULT 40
Q8G165 BRUSU PRELIMINARY; PRT; 253 AA.
ID Q8G165
AC Q8G165;
DT 01-MAR-2003 (TRMBLrel. 23, Created)
DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
GN Ordered locus names=BR0856;
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;

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RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=1330 / Biorxiv 1;
 RX MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
 RA Van Aken S.E., Richmond S., Tettelin H., Gill S.R., White O.,
 RA Salzberg S.L., Hoover D.L., Lindler L.B., Halling S.M., Boyle S.M.,
 RA Frazer C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
 DR EMBL; AE014291; AAN29785.1; -; Genomic_DNA.
 DR PIR; AH3390; AH3390.
 DR TIGR; BK0856; -;
 DR InterPro; IPR008565; DUF847.
 DR Pfam; PF05838; DUF847; 1.
 KM Complete proteome: Hypothetical protein.
 SQ SEQUENCE 253 AA; 26517 MW; 384ABE6111586F3 CRC64;

Query Match 66.7%; Score 34; DB 2; Length 253;
 Best Local Similarity 63.6%; Pred. No. 2.8e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 DB 96 RAAKTILOKILA 106

RESULT 41
 ID Q8YGP8_BRUME PRELIMINARY; PRT; 253 AA.
 AC Q8YGP8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SECRETION ACTIVATOR PROTEIN.
 GN OrderedLocustNames=BME11110;
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [Large Scale Genomic DNA].
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX PubMed=11756688; DOI=10.1073/pnas.221575398; Patra G., Mujer C., Los T.,
 RA DelVecchio V.G., Kaparatil V., Redkar R.J., Patra G., Mujer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonksi L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,
 RA Selkov E., Elizer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyriades N.C., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
 DR EMBL; AE009550; AA52291.1; -; Genomic_DNA.
 DR PIR; AH3390; AH3390.
 DR InterPro; IPR008565; DUF847.
 DR Pfam; PF05838; DUF847; 1.
 KM Complete proteome.
 SQ SEQUENCE 253 AA; 26517 MW; 384ABE6111586F3 CRC64;

Query Match 66.7%; Score 34; DB 2; Length 253;
 Best Local Similarity 63.6%; Pred. No. 2.8e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 DB 96 RAAKTILOKILA 106

RESULT 42

Q59241_CANAL
 ID Q59241 CANAL PRELIMINARY; PRT; 271 AA.
 AC Q59241;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Potential mitochondrial ribosomal protein (B. coli L9).
 GN ORFNames=CaO19.2259, CaO19.9799;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
 RA Jones T., Federopiel N.A., Chihana H., Dungan J., Kalman S.,
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.;
 RT "The diploid genome sequence of Candida albicans.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SC5314;
 RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegoke O.,
 RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
 RA Jones T., Scherer S., Agabian N.;
 RT "Annotation of the genome of Candida albicans.";
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AAC001000096; EAK5744.1; -; Genomic_DNA.
 DR EMBL; AAC001000095; EAK5808.1; -; Genomic_DNA.
 KM Ribosomal protein.
 SQ SEQUENCE 271 AA; 30423 MW; 6220C3D1F867E79F CRC64;

Query Match 66.7%; Score 34; DB 2; Length 271;
 Best Local Similarity 60.0%; Pred. No. 3e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 10
 DB 28 RPKTISKYLA 37

RESULT 43
 ID Q9KSM5_VIBCH PRELIMINARY; PRT; 295 AA.
 AC Q9KSM5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytidine deaminase.
 GN OrderedLocustNames=VC1231;
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=El Tor N16961 / Serotype O1.
 RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000; Gwin M.L.,
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
 RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
 RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
 RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
 RA Mekalanos J.J., Venter J.C., Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483 (2000).
 DR EMBL; AE004202; AAF94390.1; -; Genomic_DNA.
 DR PIR; G82226; G82226.
 DR HSP; P13652; ICTT.

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DR TIGR; VC1231; -.
DR GO; GO:0004126; F:cyclidine deaminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0046087; F:cyclidine metabolism; IEA.
DR InterPro; IPR006263; Cyt_deam_dimer.
DR Pfam; PF00383; dCMP_cyt_deam; 1.
DR TIGRFAMs; TIGR01355; cyt_deam_dimer; 1.
DR PROSITE; PS00903; Cyt_dCMP_DEAMINASES; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 295 AA; 31955 MW; 7AA76021089D736 CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 2; Length 295;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 10
Db 152 RAAKTLQEXYL 161

RESULT 44
Q73HE3_WOLPM PRELIMINARY; PRT; 304 AA.
ID Q73HE3;
AC Q73HE3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Membrane protein, putative.
OS OrderedLocustNames=WD0621;
OC Wolbachia pipiensis wMel.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachieae; Wolbachia.
OX NCBI_Taxid=66077;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15024419; DOI=10.1371/journal.pbio.0020069;
Wu M., Sun L.V., Vamathavan J.J., Riegler M., DeBoy R.T.,
Brownlie J.C., McGraw E.A., Martin W., Esser C., Almadhinej N.,
Wiegand C., Madupu R., Beaman M.J., Brinkac L.M., Daugherty S.C.,
Durkin A.S., Kolman J.F., Nelson W.C., Monod Y., Lee P.,
Berry K.J., Young M.B., Utterback T.R., Weidman W.C.,
Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Bisen J.A.,
"Phylogenomics of the reproductive parasite Wolbachia pipiensis wMel:
a streamlined genome overrun by mobile genetic elements.";
RL PLOS Biol. 2:327-341(2004).
DR EMBL; A5017258; AAS14322.1; -; Genomic_DNA.
DR TIGR; WD0621; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000620; DUF6.TM.
DR InterPro; IPR001236; Flavodoxin.
DR Pfam; PF00892; DUF6; 2.
DR PROSITE; PS00201; FLAVODOXIN; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 304 AA; 34477 MW; 0D06322B2B1D112A CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 2; Length 304;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASKTISKYLA 11
Db 24 ANDTISKYLS 33

RESULT 45
Q7WCJ1_BORPA PRELIMINARY; PRT; 318 AA.
ID Q7WCJ1;
AC Q7WCJ1;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

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DE Putative exported protein.
GN OrderedLocustNames=BPF0332;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_Taxid=519;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
Achman M., Atkin R., Baker S., Basham A., Bason N., Chervach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640438; CAE35915.1; -; Genomic_DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR InterPro; IPR005064; UPF0065.
PFam; PF03401; Bug; 1.
SQ SEQUENCE 318 AA; 33894 MW; 8FC5AF07910F80B CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 2; Length 318;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 KTSISKYLA 11
Db 2 KTSISKYLA 9

RESULT 46
Q7WQJ7_BORBR PRELIMINARY; PRT; 318 AA.
ID Q7WQJ7;
AC Q7WQJ7;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative exported protein.
GN OrderedLocustNames=BB0335;
OS Bordetella bronchiseptica.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_Taxid=518;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
Achman M., Atkin R., Baker S., Basham A., Bason N., Chervach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640438; CAE35915.1; -; Genomic_DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR InterPro; IPR005064; UPF0065.
PFam; PF03401; Bug; 1.

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KW Complete proteome.
SQ SEQUENCE 318 AA; 33836 MW; BFC5AB407910F692 CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 2; Length 318;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KTISKYLA 11
|:|||||
2 KSISKYLA 9

Db 227 RMSSTVSKYKA 237

RESULT 47
Q7TRF3_MOUSE PRELIMINARY; PRT; 331 AA.

AC Q7TRF3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Olfactory receptor OlfR67.
GN Name=OlfR67; (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22974002; PubMed=14611657; DOI=10.1186/gb-2003-4-11-r71;
RA Young J.M., Shykind B.M., Lane R.P., Tonnes-Priddy L., Rose J.A.,
Walker M., Williams E.M., Trask B.J.;
RT "Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and unequal
expression levels.";
RT Genome Biol. 4:R71-R71(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sanders K.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY318045; AAP71342.1; -, Genomic_DNA.
DR Ensemble; ENSMUSG0000004454; Mus musculus.
DR MGI; MGI:3030701; OlfR67.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004984; F:olfactory receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR InterPro; IPR000725; Olfact_receptor.
DR PANTHER; PTHR11398; Olfact_receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00245; OLFACTORXR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 331 AA; 37660 MW; E5897320AE55C10 CRC64;

Query Match
Best Local Similarity 66.7%; Score 34; DB 2; Length 311;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|:|||||
Db 227 RMSSTVSKYKA 237

RESULT 48
Q4V1C2_BACCCZ
ID Q4V1C2_BACCCZ PRELIMINARY; PRT; 334 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 2-dehydro-3-deoxygluconokinase (EC 2.7.1.45).
GN Name=kdgK; ORFNames=PB331466_0342;
OS Bacillus cereus (strain ZX).
OC Bacillus cereus (strain ZX).
OC Bacillus cereus (strain ZX).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PB331;
RG Joint Genome Institute Microbial Sequencing, Finishing and Annotation
RG Team;
RT "Complete genome sequence of Bacillus cereus E33L.";
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PB331;
RG Joint Genome Institute Microbial Sequencing, Finishing and Annotation
RG Team;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000040; AAY60485.1; -, Genomic_DNA.
KW Kinase; Plasmid; Transposase.
SQ SEQUENCE 334 AA; 37738 MW; 87A27B83FF9A7F50 CRC64;

Query Match
Best Local Similarity 70.0%; Score 34; DB 2; Length 334;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
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Db 177 RASKTINKYL 186

RESULT 49
Q8L7C4_ARATH
ID Q8L7C4_ARATH PRELIMINARY; PRT; 379 AA.

AC Q8L7C4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At5g67290.
GN Name=At5g67290;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
Cerninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.U., Sakurai T., Satou M.,
Seki M., Shimada P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,
Wu H.C., Yamada K., Yu G., Yuan S., Shinzaki K., Becker J.,
RA Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Cerninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shimada P., Yamada K., Shinzaki K.,
Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY136344; AAM97010.1; -, mRNA.
DR EMBL; BT000169; AAN15488.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0008152; P:metabolism; IEA.

DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR006076; Fcd oxrd.
DR InterPro: IPR003042; Rng_moxygcnase.
DR Pfam: PF01266; DNO: 1
DR PRINTS: PR00420; RNMGNOXGNASE.
DR Hypothetical protein.
KW SEQUENCE 3/9 AA; 40207 MW; 44399D69519C378 CRC64

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Query Match      66.7%; Score 34; DB 2; Length 379;
Best Local Similarity 60.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      1 RAKTISKYL 10
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Db      289 RAKTVSSYL 298
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RESULT 50

Q60PC2_CAEBR
ID Q60PC2_CAEBR PRELIMINARY; PRT; 390 AA.

AC Q60PC2;
DT 25-OCT-2004 (TREMBlere1. 28, Created)

DT	25-OCT-2004 (Tremblere1. 28, last sequence update)
DT	25-OCT-2004 (Tremblere1. 28, last annotation update)

DE Hypothetical protein CBG22306.
GN Name=CBG22306;
OS Caenorhabditis briggsae.

0C Eukaryota; Metazoa; Nematoda; Chromadorea
0C Rhabditidae; Peloderinae; Caenorhabditis.
0X NCBI_TaxID=6238;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases

CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; CAAC01000130; CAE74550.1; -; Genomic_DNA.

DR GO; GO:0005921; C:gap junction; IEA

DR InterPro; IPR000990; Immexin

DR Pfam; PF00876; Innexin; 1.

DR PRINTS; PR01262; INNEXIN.

DR PROSITE; PS51013; PANNEXIN; 1..

KW Hypothetical protein.

SQ SEQUENCE 390 AA; 45027 MW; C51C644BBBB434BF7 CRC64;

Query Match	66.7%;	Score 34;	DB 2;	Length 390;
Best Local Similarity	63.6%;	Pred. No. 4.4e+02;		
Matches	7;	Conservative	1;	Mismatches 3;
			Indels	0;
			Gaps	0

QY	1	RASKTISKYLA	11
	:		
Db	307	KAOKTIRNYLA	317

Search completed: January 17, 2006, 12:06:13
Job time : 93 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 17, 2006, 11:50:24 : Search time 19 Seconds
(without alignments)
47.865 Million cell updates/sec

Title: US-10-665-658-13
Perfect score: 51
Sequence: 1 RASKTISKXYLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5/COMB.pep: *
2: /cgn2_6/prodata/1/iaa/6/COMB.pep: *
3: /cgn2_6/prodata/1/iaa/H/COMB.pep: *
4: /cgn2_6/prodata/1/iaa/PC/COMB.pep: *
5: /cgn2_6/prodata/1/iaa/R/COMB.pep: *
6: /cgn2_6/prodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	11	2	US-08-974-899-13
2	51	100.0	11	2	US-09-795-798-13
3	51	100.0	108	2	US-08-974-899-1
4	51	100.0	108	2	US-08-974-899-2
5	51	100.0	108	2	US-09-795-798-1
6	51	100.0	108	2	US-09-795-798-2
7	51	100.0	109	2	US-09-027-449-47
8	51	100.0	109	2	US-08-804-444A-47
9	51	100.0	109	2	US-09-026-985-47
10	51	100.0	109	2	US-09-121-952A-47
11	51	100.0	109	2	US-09-234-340A-47
12	51	100.0	109	2	US-09-355-014-47
13	39	76.5	11	1	US-08-182-067-4
14	39	76.5	11	1	US-08-465-313-4
15	39	76.5	11	1	US-09-809-739-10
16	39	76.5	11	2	US-09-378-967-4
17	39	76.5	88	2	US-09-905-243-32
18	39	76.5	105	2	US-08-635-109-6
19	39	76.5	105	2	US-08-844-215-9
20	39	76.5	125	1	US-08-039-198B-12
21	39	76.5	125	1	US-08-182-067-2
22	39	76.5	125	1	US-08-465-313-2
23	39	76.5	125	2	US-09-809-739-1
24	39	76.5	125	2	US-09-378-967-2
25	39	76.5	127	2	US-09-809-739-10
26	39	76.5	234	2	US-09-848-832-4
27	38	74.5	104	1	US-08-276-852-106

28	38	74.5	104	1	US-08-899-575-106	Sequence 106, App
29	38	74.5	104	1	US-08-899-575-106	Sequence 106, App
30	38	74.5	104	4	PCR-US95-08743-106	Sequence 106, App
31	38	74.5	107	1	US-07-934-373C-18	Sequence 18, Appl
32	38	74.5	107	2	US-08-437-642B-18	Sequence 18, Appl
33	38	74.5	107	2	US-08-146-206C-18	Sequence 18, Appl
34	38	74.5	107	2	US-09-648-067A-14	Sequence 18, Appl
35	38	74.5	107	2	US-09-705-392A-18	Sequence 18, Appl
36	38	74.5	107	2	US-09-705-392A-18	Sequence 18, Appl
37	38	74.5	107	2	US-09-602-812A-5	Sequence 18, Appl
38	38	74.5	107	2	PCR-US93-07832-18	Sequence 18, Appl
39	38	74.5	108	4	US-08-974-899-3	Sequence 3, Appl1
40	38	74.5	108	2	US-09-795-798-3	Sequence 12, Appl
41	38	74.5	108	2	US-08-908-469-12	Sequence 3, Appl1
42	38	74.5	109	2	US-09-157-370-3	Sequence 86, Appl
43	38	74.5	95	2	US-10-194-975-86	Sequence 14, Appl
44	37	72.5	100	2	US-09-899-896-4	Sequence 14, Appl
45	37	72.5	107	1	US-08-107-669D-14	Sequence 14, Appl
46	37	72.5	107	1	US-08-472-788A-14	Sequence 14, Appl
47	37	72.5	107	1	US-08-477-531B-14	Sequence 14, Appl
48	37	72.5	107	1	US-08-082-842A-14	Sequence 14, Appl
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50	37	72.5	107	2	US-09-438-954-38	Sequence 14, Appl
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53	37	72.5	107	2	US-09-438-954-40	Sequence 14, Appl
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55	37	72.5	115	1	US-08-053-131-179	Sequence 14, Appl
56	37	72.5	115	1	US-08-096-762-179	Sequence 14, Appl
57	37	72.5	115	2	US-09-042-353-42	Sequence 14, Appl
58	37	72.5	115	2	US-08-758-417A-307	Sequence 14, Appl
59	37	72.5	139	2	US-09-472-087-16	Sequence 14, Appl
60	37	72.5	139	2	US-09-472-087-91	Sequence 14, Appl
61	37	72.5	142	2	US-09-472-087-91	Sequence 14, Appl
62	37	72.5	146	2	US-09-472-087-21	Sequence 14, Appl
63	37	72.5	146	2	US-09-472-087-93	Sequence 14, Appl
64	37	72.5	224	2	US-09-456-090A-46	Sequence 14, Appl
65	37	72.5	224	2	US-09-456-090A-82	Sequence 14, Appl
66	37	72.5	224	2	US-09-456-090A-84	Sequence 14, Appl
67	37	72.5	224	2	US-09-456-090A-88	Sequence 14, Appl
68	37	72.5	224	2	US-09-456-090A-90	Sequence 14, Appl
69	37	72.5	224	2	US-09-453-234-46	Sequence 14, Appl
70	37	72.5	224	2	US-09-453-234-82	Sequence 14, Appl
71	37	72.5	224	2	US-09-453-234-84	Sequence 14, Appl
72	37	72.5	224	2	US-09-453-234-88	Sequence 14, Appl
73	37	72.5	224	2	US-09-453-234-90	Sequence 14, Appl
74	37	72.5	234	2	US-09-472-087-17	Sequence 14, Appl
75	37	72.5	234	2	US-09-472-087-69	Sequence 14, Appl
76	37	72.5	241	2	US-09-270-767-61433	Sequence 14, Appl
77	37	72.5	663	2	US-09-270-767-45897	Sequence 14, Appl
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79	36	70.6	107	2	US-09-240-574-169	Sequence 14, Appl
80	36	70.6	107	2	US-09-848-798-169	Sequence 14, Appl
81	36	70.6	107	2	US-09-848-798-169	Sequence 14, Appl
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83	36	70.6	108	1	US-08-379-057-28	Sequence 14, Appl
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88	36	70.6	111	1	US-07-942-245-518	Sequence 14, Appl
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93	35	68.6	95	2	US-08-627-896B-27	Sequence 14, Appl
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98	35	68.6	95	2	US-09-339-596A-42	Sequence 14, Appl
99	35	68.6	95	2	US-10-330-613A-63	Sequence 14, Appl
100	35	68.6	106	2	US-09-232-290-5	Sequence 14, Appl

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103	35	68.6	107	1	US-08-276-852-84	Sequence 84, App1	176	34	66.7	103	2	US-09-848-798-42	Sequence 42, App1
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105	35	68.6	107	1	US-08-899-575-84	Sequence 84, App1	178	34	66.7	107	1	US-08-276-852-105	Sequence 105, App
106	35	68.6	107	1	US-08-899-575-82	Sequence 82, App1	179	34	66.7	107	1	US-08-899-575-104	Sequence 104, App
107	35	68.6	107	1	US-08-899-575-84	Sequence 84, App1	180	34	66.7	107	1	US-08-899-575-105	Sequence 105, App
108	35	68.6	107	4	US-08-899-575-84	Sequence 84, App1	181	34	66.7	107	1	US-08-899-575-104	Sequence 104, App
109	35	68.6	107	4	PCT-US95-08743-82	Sequence 82, App1	182	34	66.7	107	1	US-08-899-575-105	Sequence 105, App
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114	35	68.6	109	1	US-07-934-373C-3	Sequence 3, App11	187	34	66.7	107	2	US-09-240-274-37	Sequence 37, App1
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117	35	68.6	109	2	US-09-025-769B-43	Sequence 28, App1	190	34	66.7	107	2	US-09-240-274-40	Sequence 40, App1
118	35	68.6	109	2	US-08-146-206C-3	Sequence 43, App1	191	34	66.7	107	2	US-09-240-274-156	Sequence 156, App
119	35	68.6	109	2	US-09-705-686-3	Sequence 3, App11	192	34	66.7	107	2	US-09-240-274-158	Sequence 158, App
120	35	68.6	109	2	US-09-490-070A-28	Sequence 28, App1	193	34	66.7	107	2	US-09-240-274-168	Sequence 168, App
121	35	68.6	109	2	US-09-490-070A-43	Sequence 43, App1	194	34	66.7	107	2	US-09-240-274-173	Sequence 173, App
122	35	68.6	109	2	US-09-490-153-28	Sequence 28, App1	195	34	66.7	107	2	US-09-240-274-175	Sequence 175, App
123	35	68.6	109	2	US-09-490-153-43	Sequence 43, App1	196	34	66.7	107	2	US-09-240-274-176	Sequence 176, App
124	35	68.6	109	2	US-09-705-392A-3	Sequence 3, App11	197	34	66.7	107	2	US-09-848-798-33	Sequence 33, App1
125	35	68.6	109	2	US-09-705-398-3	Sequence 3, App11	198	34	66.7	107	2	US-09-848-798-37	Sequence 37, App1
126	35	68.6	109	2	US-09-490-324-28	Sequence 28, App1	199	34	66.7	107	2	US-09-848-798-38	Sequence 38, App1
127	35	68.6	109	2	US-09-490-324-43	Sequence 43, App1	200	34	66.7	107	2	US-09-848-798-39	Sequence 39, App1
128	35	68.6	109	4	PCT-US93-07832-3	Sequence 3, App11	201	34	66.7	107	2	US-09-848-798-40	Sequence 40, App1
129	35	68.6	134	2	US-09-472-087-23	Sequence 23, App1	202	34	66.7	107	2	US-09-848-798-156	Sequence 156, App
130	35	68.6	134	2	US-09-472-087-97	Sequence 97, App1	203	34	66.7	107	2	US-09-848-798-158	Sequence 158, App
131	35	68.6	159	2	US-09-270-767-38167	Sequence 538167, A	204	34	66.7	107	2	US-09-848-798-168	Sequence 168, App
132	35	68.6	159	2	US-09-270-767-53384	Sequence 53384, A	205	34	66.7	107	2	US-09-848-798-173	Sequence 173, App
133	35	68.6	235	2	US-08-812-586-16	Sequence 16, App1	206	34	66.7	107	2	US-09-848-798-175	Sequence 175, App
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136	34	66.7	11	2	US-09-511-939-10	Sequence 10, App1	209	34	66.7	107	4	PCT-US95-08743-104	Sequence 104, App
137	34	66.7	11	2	US-09-511-939-16	Sequence 16, App1	210	34	66.7	107	4	PCT-US95-08743-105	Sequence 105, App
138	34	66.7	11	2	US-09-511-939-22	Sequence 22, App1	211	34	66.7	108	1	US-08-276-852-102	Sequence 102, App
139	34	66.7	11	2	US-09-511-939-28	Sequence 28, App1	212	34	66.7	108	1	US-08-899-575-102	Sequence 102, App
140	34	66.7	11	2	US-09-511-939-34	Sequence 34, App1	213	34	66.7	108	1	US-08-899-575-102	Sequence 102, App
141	34	66.7	11	2	US-09-511-939-40	Sequence 40, App1	214	34	66.7	108	1	US-08-379-057-29	Sequence 29, App1
142	34	66.7	11	2	US-09-511-939-46	Sequence 46, App1	215	34	66.7	108	1	US-08-378-939-30	Sequence 30, App1
143	34	66.7	11	2	US-09-511-939-52	Sequence 52, App1	216	34	66.7	108	2	US-08-983-607-29	Sequence 29, App1
144	34	66.7	11	2	US-09-511-939-64	Sequence 64, App1	217	34	66.7	108	2	US-08-983-607-37	Sequence 37, App1
145	34	66.7	11	2	US-09-511-939-100	Sequence 100, App	218	34	66.7	108	2	US-09-240-274-32	Sequence 32, App1
146	34	66.7	11	2	US-09-511-939-106	Sequence 106, App	219	34	66.7	108	2	US-09-240-274-43	Sequence 43, App1
147	34	66.7	11	2	US-09-511-939-112	Sequence 112, App	220	34	66.7	108	2	US-09-240-274-163	Sequence 163, App
148	34	66.7	11	2	US-09-511-939-118	Sequence 118, App	221	34	66.7	108	2	US-09-240-274-167	Sequence 167, App
149	34	66.7	11	2	US-09-511-939-124	Sequence 124, App	222	34	66.7	108	2	US-09-025-769B-14	Sequence 14, App1
150	34	66.7	11	2	US-09-511-939-136	Sequence 136, App	223	34	66.7	108	2	US-09-490-070A-14	Sequence 14, App1
151	34	66.7	11	2	US-09-511-939-154	Sequence 154, App	224	34	66.7	108	2	US-09-490-153-14	Sequence 14, App1
152	34	66.7	11	2	US-09-511-939-160	Sequence 160, App	225	34	66.7	108	2	US-09-490-324-14	Sequence 14, App1
153	34	66.7	11	2	US-09-511-939-166	Sequence 166, App	226	34	66.7	108	2	US-09-848-798-32	Sequence 32, App1
154	34	66.7	11	2	US-09-511-939-172	Sequence 172, App	227	34	66.7	108	2	US-09-848-798-43	Sequence 43, App1
155	34	66.7	11	2	US-09-511-939-178	Sequence 178, App	228	34	66.7	108	2	US-09-848-798-163	Sequence 163, App
156	34	66.7	11	2	US-09-511-939-202	Sequence 202, App	229	34	66.7	108	2	US-09-848-798-167	Sequence 167, App
157	34	66.7	11	2	US-09-511-939-208	Sequence 208, App	230	34	66.7	108	4	PCT-US95-08743-102	Sequence 102, App
158	34	66.7	11	2	US-09-511-939-226	Sequence 226, App	231	34	66.7	109	2	US-10-330-613A-10	Sequence 10, App1
159	34	66.7	11	2	US-09-511-939-232	Sequence 232, App	232	34	66.7	115	1	US-08-053-1131-181	Sequence 181, App
160	34	66.7	11	2	US-09-511-939-244	Sequence 244, App	233	34	66.7	115	1	US-08-096-762-181	Sequence 181, App
161	34	66.7	11	2	US-09-511-939-250	Sequence 250, App	234	34	66.7	115	1	US-09-042-353-44	Sequence 44, App1
162	34	66.7	11	2	US-09-511-939-256	Sequence 256, App	235	34	66.7	115	2	US-08-758-417A-309	Sequence 309, App1
163	34	66.7	11	2	US-09-511-939-280	Sequence 280, App	236	34	66.7	127	2	US-10-268-883-5	Sequence 5, App11
164	34	66.7	11	2	US-09-511-939-292	Sequence 292, App	237	34	66.7	137	2	US-09-582-337-24	Sequence 24, App1
165	34	66.7	11	2	US-09-511-939-304	Sequence 304, App	238	34	66.7	162	2	US-09-248-796A-14407	Sequence 14407, A
166	34	66.7	50	2	US-09-270-767-61844	Sequence 61844, A	239	34	66.7	224	2	US-09-456-090A-36	Sequence 36, App1
167	34	66.7	76	2	US-08-851-362D-21	Sequence 21, App1	240	34	66.7	224	2	US-09-456-090A-48	Sequence 48, App1
168	34	66.7	95	2	US-09-472-087-94	Sequence 94, App1	241	34	66.7	224	2	US-09-453-234-36	Sequence 36, App1
169	34	66.7	95	2	US-10-194-975-54	Sequence 54, App1	242	34	66.7	240	2	US-09-453-234-48	Sequence 48, App1
170	34	66.7	95	2	US-10-194-975-55	Sequence 55, App1	243	34	66.7	240	2	US-09-192-854-2	Sequence 2, App11
171	34	66.7	95	2	US-10-194-975-87	Sequence 87, App1	244	34	66.7	240	2	US-09-511-939-2	Sequence 2, App11
172	34	66.7	95	2	US-10-330-613A-43	Sequence 43, App1	245	34	66.7	340	2	US-09-270-767-46274	Sequence 46274, A
173	34	66.7	102	2	US-09-726-219A-173	Sequence 173, App1	246	34	66.7	664	2	US-10-181-612-2	Sequence 2, App11

247	33	64.7	72	2	US-09-270-767-36860	Sequence 36860, A	320	32	62.7	107	2	US-09-610-838-149	Sequence 149, App
248	33	64.7	72	2	US-09-270-767-52077	Sequence 52077, A	321	32	62.7	107	2	US-09-711-465-149	Sequence 149, App
249	33	64.7	95	1	US-08-290-592E-19	Sequence 19, Appl	322	32	62.7	107	4	PCT-US95-11235-66	Sequence 66, Appl
250	33	64.7	95	1	US-08-290-592E-33	Sequence 33, Appl	323	32	62.7	108	2	US-09-065-059-3	Sequence 3, Appl1
251	33	64.7	95	2	US-10-194-975-72	Sequence 72, Appl	324	32	62.7	108	2	US-09-240-274-31	Sequence 31, Appl1
252	33	64.7	95	4	PCT-US95-10053-16	Sequence 16, Appl	325	32	62.7	108	2	US-09-232-280-21	Sequence 21, Appl
253	33	64.7	95	4	PCT-US95-10053-30	Sequence 30, Appl	326	32	62.7	108	2	US-09-848-798-31	Sequence 31, Appl1
254	33	64.7	95	4	PCT-US96-09448-19	Sequence 19, Appl	327	32	62.7	108	2	US-08-913-555-33	Sequence 33, Appl1
255	33	64.7	95	4	PCT-US96-09448-33	Sequence 33, Appl	328	32	62.7	108	2	US-08-913-555-21	Sequence 21, Appl1
256	33	64.7	96	1	US-08-737-560A-9	Sequence 9, Appl1	329	32	62.7	109	1	US-07-942-245-10	Sequence 10, Appl1
257	33	64.7	107	1	US-08-888-366-22	Sequence 22, Appl	330	32	62.7	109	2	US-09-905-243-67	Sequence 67, Appl1
258	33	64.7	107	2	US-09-240-274-162	Sequence 162, App	331	32	62.7	110	1	US-08-300-386A-70	Sequence 70, Appl1
259	33	64.7	107	2	US-09-247-352-8	Sequence 8, Appl1	332	32	62.7	110	2	US-08-931-645-70	Sequence 70, Appl1
260	33	64.7	107	2	US-09-247-352-12	Sequence 12, Appl1	333	32	62.7	110	4	PCT-US95-11235-70	Sequence 67, Appl1
261	33	64.7	107	2	US-09-438-954-3	Sequence 3, Appl1	334	32	62.7	111	1	US-08-137-117D-67	Sequence 67, Appl1
262	33	64.7	107	2	US-09-434-870-1	Sequence 1, Appl1	335	32	62.7	111	1	US-08-436-717-67	Sequence 67, Appl1
263	33	64.7	107	2	US-09-848-798-162	Sequence 162, App	336	32	62.7	126	1	US-08-137-117D-71	Sequence 71, Appl1
264	33	64.7	108	2	US-09-240-274-41	Sequence 41, Appl1	337	32	62.7	126	1	US-08-436-717-71	Sequence 71, Appl1
265	33	64.7	108	2	US-09-157-370-4	Sequence 4, Appl1	338	32	62.7	127	1	US-08-137-117D-29	Sequence 29, Appl1
266	33	64.7	108	2	US-09-247-352-1	Sequence 1, Appl1	339	32	62.7	127	1	US-08-436-717-29	Sequence 29, Appl1
267	33	64.7	108	2	US-09-466-635-1	Sequence 1, Appl1	340	32	62.7	127	1	US-08-436-717-37	Sequence 37, Appl1
268	33	64.7	108	2	US-09-848-798-41	Sequence 41, Appl1	341	32	62.7	127	1	US-08-648-100-17	Sequence 17, Appl1
269	33	64.7	112	2	US-09-615-192A-276	Sequence 276, App	342	32	62.7	127	2	US-08-649-100-33	Sequence 33, Appl1
270	33	64.7	113	2	US-10-114-716A-48	Sequence 48, Appl1	343	32	62.7	127	2	US-08-236-520-2	Sequence 2, Appl1
271	33	64.7	127	1	US-08-574-699A-2	Sequence 2, Appl1	344	32	62.7	131	1	PCT-US95-05262-2	Sequence 2, Appl1
272	33	64.7	128	1	US-08-339-582-4	Sequence 4, Appl1	345	32	62.7	131	4	US-08-235-838-11	Sequence 11, Appl1
273	33	64.7	133	2	US-09-615-192A-277	Sequence 277, App	346	32	62.7	241	1	US-08-465-473B-11	Sequence 11, Appl1
274	33	64.7	214	2	US-09-247-352-4	Sequence 4, Appl1	347	32	62.7	241	1	US-08-465-473B-11	Sequence 11, Appl1
275	33	64.7	214	2	US-09-466-635-4	Sequence 4, Appl1	348	32	62.7	285	2	US-08-149-476-470	Sequence 470, App
276	33	64.7	214	2	US-09-248-796A-21352	Sequence 21352, A	349	32	62.7	285	2	US-09-354-151-2	Sequence 5975, Ap
277	33	64.7	307	2	US-08-812-586-2	Sequence 2, Appl1	350	32	62.7	350	2	US-09-328-352-5975	Sequence 2, Appl1
278	33	64.7	307	2	US-09-535-832A-2	Sequence 2, Appl1	351	32	62.7	397	1	US-08-098-141-2	Sequence 7, Appl1
279	33	64.7	359	2	US-09-646-028-16	Sequence 16, Appl	352	32	62.7	424	2	US-09-173-581-7	Sequence 7, Appl1
280	33	64.7	361	2	US-09-646-028-13	Sequence 13, Appl	353	32	62.7	424	2	US-09-420-915-7	Sequence 7, Appl1
281	33	64.7	374	2	US-08-812-586-15	Sequence 15, Appl	354	32	62.7	495	2	US-09-275-252A-5	Sequence 5, Appl1
282	33	64.7	374	2	US-09-535-832A-16	Sequence 16, Appl	355	32	62.7	498	2	US-09-354-151-2	Sequence 2, Appl1
283	33	64.7	374	2	US-09-646-028-15	Sequence 15, Appl	356	32	62.7	555	1	US-08-588-258B-24	Sequence 24, Appl1
284	33	64.7	943	2	US-09-802-540-10641	Sequence 10641, A	357	32	62.7	555	2	US-08-460-505-25	Sequence 24, Appl1
285	33	62.7	11	1	US-08-137-117D-117	Sequence 117, App	358	32	62.7	555	4	PCT-US96-08295-24	Sequence 24, Appl1
286	32	62.7	11	1	US-08-480-434-76	Sequence 76, Appl	359	32	62.7	567	2	US-09-902-540-15245	Sequence 15245, A
287	32	62.7	11	1	US-08-436-717-117	Sequence 117, Appl	360	32	62.7	637	1	US-08-235-838-16	Sequence 16, Appl
288	32	62.7	11	1	US-08-053-451B-76	Sequence 76, Appl	361	32	62.7	637	1	US-08-465-473B-16	Sequence 16, Appl
289	32	62.7	11	2	US-08-649-100-11	Sequence 11, Appl	362	32	62.7	661	2	US-09-564-805-240	Sequence 240, App
290	32	62.7	11	2	US-08-649-100-27	Sequence 27, Appl	363	32	62.7	869	2	US-09-543-681A-4814	Sequence 4814, Ap
291	32	62.7	11	2	US-09-424-712-31	Sequence 31, Appl	364	32	62.7	869	2	US-09-489-037A-7727	Sequence 7727, Ap
292	32	62.7	11	2	US-09-192-854-153	Sequence 153, App	365	32	62.7	889	2	US-09-540-236-2916	Sequence 2916, Ap
293	32	62.7	11	2	US-09-511-939-268	Sequence 268, App	366	32	62.7	889	2	US-09-252-991A-18702	Sequence 18702, A
294	32	62.7	31	2	US-08-525-539A-5	Sequence 5, Appl1	367	32	62.7	919	2	US-09-328-352-8164	Sequence 8164, Ap
295	32	62.7	99	2	US-08-899-896-6	Sequence 6, Appl1	368	32	62.7	919	2	US-08-985-916-16	Sequence 16, Appl
296	32	62.7	99	2	US-09-899-896-10	Sequence 10, Appl	369	31	60.8	11	1	US-07-942-245-494	Sequence 494, Appl
297	32	62.7	106	1	US-08-276-852-83	Sequence 83, Appl	370	31	60.8	11	2	US-08-407-620A-4	Sequence 4, Appl1
298	32	62.7	106	1	US-08-276-852-85	Sequence 85, Appl	371	31	60.8	11	2	US-09-948-004-29	Sequence 29, Appl1
299	32	62.7	106	1	US-08-899-575-83	Sequence 85, Appl	372	31	60.8	11	2	US-09-798-058-8	Sequence 8, Appl1
300	32	62.7	106	1	US-08-899-575-85	Sequence 85, Appl	373	31	60.8	49	1	US-08-476-3349A-87	Sequence 87, Appl1
301	32	62.7	106	1	US-08-899-575-83	Sequence 85, Appl	374	31	60.8	49	1	US-08-476-3349A-87	Sequence 87, Appl1
302	32	62.7	106	1	US-08-899-575-85	Sequence 85, Appl	375	31	60.8	88	2	US-09-905-243-31	Sequence 31, Appl1
303	32	62.7	106	4	PCT-US95-08743-83	Sequence 83, Appl	376	31	60.8	92	2	US-09-948-004-12	Sequence 12, Appl1
304	32	62.7	106	4	PCT-US95-08743-85	Sequence 85, Appl	377	31	60.8	92	2	US-08-881-037-68	Sequence 68, Appl1
305	32	62.7	107	1	US-08-300-386A-66	Sequence 66, Appl	378	31	60.8	99	2	US-08-881-037-32	Sequence 32, Appl1
306	32	62.7	107	1	US-08-488-113B-149	Sequence 149, App	379	31	60.8	99	2	US-08-881-037-33	Sequence 33, Appl1
307	32	62.7	107	1	US-08-477-484B-149	Sequence 149, App	380	31	60.8	99	2	US-08-881-037-34	Sequence 34, Appl1
308	32	62.7	107	1	US-08-107-669D-13	Sequence 13, Appl	381	31	60.8	99	2	US-08-881-037-35	Sequence 35, Appl1
309	32	62.7	107	1	US-08-472-788A-13	Sequence 13, Appl	382	31	60.8	100	2	US-09-899-896-2	Sequence 2, Appl1
310	32	62.7	107	1	US-08-480-434-74	Sequence 74, Appl	383	31	60.8	101	2	US-10-092-246-18	Sequence 18, Appl1
311	32	62.7	107	1	US-08-477-531B-13	Sequence 13, Appl	384	31	60.8	101	2	US-10-096-266A-18	Sequence 18, Appl1
312	32	62.7	107	1	US-08-646-360-149	Sequence 149, App	385	31	60.8	102	2	US-09-270-767-33230	Sequence 33230, A
313	32	62.7	107	1	US-08-082-842A-13	Sequence 13, Appl	386	31	60.8	102	2	US-09-276-852-101	Sequence 48447, A
314	32	62.7	107	1	US-08-053-451B-74	Sequence 74, Appl	387	31	60.8	106	1	US-08-276-852-101	Sequence 101, App
315	32	62.7	107	1	US-08-053-451B-176	Sequence 176, App	388	31	60.8	106	1	US-08-899-575-101	Sequence 101, App
316	32	62.7	107	2	US-08-483-749A-28	Sequence 28, Appl	389	31	60.8	106	1	US-08-202-047-26	Sequence 26, Appl
317	32	62.7	107	2	US-08-931-645-66	Sequence 66, Appl	390	31	60.8	106	1	US-08-899-575-101	Sequence 101, App
318	32	62.7	107	2	US-08-839-765-149	Sequence 149, App	391	31	60.8	106	2	US-08-964-690-26	Sequence 26, Appl
319	32	62.7	107	2	US-09-136-389-149	Sequence 149, App	392	31	60.8	106	2	US-09-240-274-171	Sequence 171, App

393	31	60.8	106	2	US-10-092-246-15	Sequence 15, Appl	466	30	58.8	17	1	US-08-318-970B-12	Sequence 12, Appl
394	31	60.8	106	2	US-10-096-246A-15	Sequence 15, Appl	467	30	58.8	27	1	US-08-682-621-1	Sequence 1, Appl
395	31	60.8	106	2	US-09-848-798-171	Sequence 171, App	468	30	58.8	51	1	US-08-472-788A-73	Sequence 73, Appl
396	31	60.8	106	4	PCT-US95-08743-101	Sequence 101, App	469	30	58.8	51	1	US-08-472-788A-74	Sequence 74, Appl
397	31	60.8	107	2	US-08-881-037-69	Sequence 69, Appl	470	30	58.8	51	1	US-08-082-842A-73	Sequence 73, Appl
398	31	60.8	107	2	US-08-881-037-70	Sequence 70, Appl	471	30	58.8	51	1	US-08-082-842A-74	Sequence 74, Appl
399	31	60.8	107	2	US-08-881-037-71	Sequence 71, Appl	472	30	58.8	55	2	US-09-935-937A-9	Sequence 9, Appl
400	31	60.8	107	2	US-08-881-037-72	Sequence 72, Appl	473	30	58.8	55	2	US-09-300-985-9	Sequence 9, Appl
401	31	60.8	107	2	US-08-397-411-1	Sequence 1, Appl	474	30	58.8	84	2	US-09-471-276-816	Sequence 816, App
402	31	60.8	107	2	US-08-397-411-2	Sequence 2, Appl	475	30	58.8	88	2	US-09-905-243-35	Sequence 35, Appl
403	31	60.8	107	2	US-09-240-274-36	Sequence 36, Appl	476	30	58.8	95	2	US-10-194-975-60	Sequence 60, Appl
404	31	60.8	107	2	US-09-240-274-112	Sequence 172, App	477	30	58.8	95	2	US-10-194-975-65	Sequence 65, Appl
405	31	60.8	107	2	US-09-240-274-174	Sequence 174, App	478	30	58.8	95	2	US-10-194-975-66	Sequence 66, Appl
406	31	60.8	107	2	US-09-948-004-10	Sequence 10, Appl	479	30	58.8	95	2	US-10-194-975-68	Sequence 68, Appl
407	31	60.8	107	2	US-09-848-798-36	Sequence 36, Appl	480	30	58.8	95	2	US-10-194-975-70	Sequence 70, Appl
408	31	60.8	107	2	US-09-848-798-112	Sequence 172, App	481	30	58.8	104	2	US-09-328-352-6307	Sequence 6307, App
409	31	60.8	107	2	US-09-848-798-114	Sequence 172, App	482	30	58.8	107	1	US-08-425-316-125	Sequence 125, App
410	31	60.8	108	1	US-08-378-939-16	Sequence 16, Appl	483	30	58.8	107	1	US-08-276-882-103	Sequence 103, App
411	31	60.8	108	1	US-08-378-939-18	Sequence 18, Appl	484	30	58.8	107	1	US-08-300-386A-67	Sequence 67, Appl
412	31	60.8	108	1	US-08-378-939-24	Sequence 24, Appl	485	30	58.8	107	1	US-08-488-113B-125	Sequence 125, App
413	31	60.8	108	1	US-08-602-725-29	Sequence 29, Appl	486	30	58.8	107	1	US-08-477-484B-125	Sequence 27, Appl
414	31	60.8	108	2	US-08-407-620A-8	Sequence 8, Appl	487	30	58.8	107	1	US-08-107-669D-27	Sequence 27, Appl
415	31	60.8	108	2	US-08-407-620A-10	Sequence 10, Appl	488	30	58.8	107	1	US-08-107-669D-65	Sequence 65, Appl
416	31	60.8	108	2	US-10-268-883-12	Sequence 12, Appl	489	30	58.8	107	1	US-08-472-788A-27	Sequence 27, Appl
417	31	60.8	109	1	US-07-942-245-1	Sequence 1, Appl	490	30	58.8	107	1	US-08-472-788A-87	Sequence 87, Appl
418	31	60.8	109	1	US-08-300-386A-68	Sequence 68, Appl	491	30	58.8	107	1	US-08-899-575-103	Sequence 103, App
419	31	60.8	109	1	US-08-300-386A-69	Sequence 68, Appl	492	30	58.8	107	1	US-08-899-575-103	Sequence 103, App
420	31	60.8	109	2	US-08-931-645-68	Sequence 68, Appl	493	30	58.8	107	1	US-08-477-531B-27	Sequence 27, Appl
421	31	60.8	109	2	US-08-931-645-69	Sequence 68, Appl	494	30	58.8	107	1	US-08-477-531B-65	Sequence 65, Appl
422	31	60.8	109	2	US-09-798-058-4	Sequence 4, Appl	495	30	58.8	107	1	US-08-646-360-125	Sequence 125, App
423	31	60.8	109	4	PCT-US95-11235-69	Sequence 68, Appl	496	30	58.8	107	1	US-08-082-842A-27	Sequence 27, Appl
424	31	60.8	109	4	PCT-US95-11235-69	Sequence 69, Appl	497	30	58.8	107	2	US-08-599-226-1	Sequence 87, Appl
425	31	60.8	130	2	US-10-268-883-11	Sequence 11, Appl	498	30	58.8	107	2	US-08-599-226-9	Sequence 9, Appl
426	31	60.8	139	2	US-09-472-087-22	Sequence 22, Appl	499	30	58.8	107	2	US-08-839-765-67	Sequence 67, App
427	31	60.8	139	2	US-09-472-087-96	Sequence 96, Appl	500	30	58.8	107	2	US-08-839-765-125	Sequence 125, App
428	31	60.8	200	2	US-09-018-635-47	Sequence 47, App	501	30	58.8	107	2	US-09-136-389-125	Sequence 125, App
429	31	60.8	200	2	US-09-198-452A-571	Sequence 571, App	502	30	58.8	107	2	US-09-125-098-1	Sequence 1, Appl
430	31	60.8	200	2	US-09-912-962-47	Sequence 47, Appl	503	30	58.8	107	2	US-09-125-098-9	Sequence 9, Appl
431	31	60.8	214	2	US-08-397-411-5	Sequence 5, Appl	504	30	58.8	107	2	US-09-610-838-125	Sequence 125, App
432	31	60.8	214	2	US-09-472-087-71	Sequence 71, Appl	505	30	58.8	107	2	US-09-540-018-1	Sequence 1, Appl
433	31	60.8	214	2	US-09-438-185A-534	Sequence 534, App	506	30	58.8	107	2	US-09-540-018-9	Sequence 9, Appl
434	31	60.8	241	2	US-09-107-532A-4941	Sequence 4941, App	507	30	58.8	107	2	US-09-711-485-135	Sequence 135, App
435	31	60.8	243	3	US-07-958-140-2	Sequence 2, Appl	508	30	58.8	107	2	US-10-330-613A-30	Sequence 30, Appl
436	31	60.8	243	4	PCT-US93-09166-2	Sequence 2, Appl	509	30	58.8	107	4	PCT-US95-08743-103	Sequence 103, App
437	31	60.8	244	2	US-09-248-796A-19447	Sequence 19447, A	510	30	58.8	107	4	PCT-US95-11235-67	Sequence 67, Appl
438	31	60.8	407	2	US-09-710-279-1056	Sequence 1056, App	511	30	58.8	108	1	US-08-652-816A-3	Sequence 3, Appl
439	31	60.8	407	2	US-09-134-001C-3399	Sequence 3399, App	512	30	58.8	108	1	US-08-652-816A-4	Sequence 4, Appl
440	31	60.8	446	2	US-09-018-635-31	Sequence 31, Appl	513	30	58.8	108	1	US-08-652-816A-5	Sequence 5, Appl
441	31	60.8	446	2	US-09-912-962-31	Sequence 31, Appl	514	30	58.8	108	2	US-09-240-274-161	Sequence 161, App
442	31	60.8	495	2	US-09-018-635-29	Sequence 29, Appl	515	30	58.8	108	2	US-09-240-274-177	Sequence 177, App
443	31	60.8	495	2	US-09-912-962-29	Sequence 29, Appl	516	30	58.8	108	2	US-09-848-798-161	Sequence 161, App
444	31	60.8	495	2	US-09-948-004-18	Sequence 18, App	517	30	58.8	108	2	US-09-848-798-177	Sequence 177, App
445	31	60.8	687	2	US-09-107-433-3382	Sequence 3382, App	518	30	58.8	108	2	US-09-848-798-117	Sequence 8, Appl
446	31	60.8	690	2	US-09-134-001C-4938	Sequence 4938, App	519	30	58.8	108	2	US-09-920-262A-8	Sequence 8, Appl
447	31	60.8	691	2	US-08-946-475-2	Sequence 2, Appl	520	30	58.8	116	2	US-09-328-352-6755	Sequence 6755, App
448	31	60.8	691	2	US-09-340-479-2	Sequence 2, Appl	521	30	58.8	116	1	US-08-053-131-185	Sequence 185, App
449	31	60.8	705	2	US-09-153-277-2	Sequence 2, Appl	522	30	58.8	117	2	US-08-096-762-185	Sequence 48, Appl
450	31	60.8	791	2	US-09-583-110-4537	Sequence 4537, App	523	30	58.8	117	2	US-09-042-353-48	Sequence 48, Appl
451	31	60.8	711	2	US-08-946-475-9	Sequence 9, Appl	524	30	58.8	117	2	US-08-758-417A-113	Sequence 313, App
452	31	60.8	711	2	US-09-340-479-9	Sequence 9, Appl	525	30	58.8	126	1	US-08-765-783A-73	Sequence 73, Appl
453	31	60.8	856	2	US-09-902-540-11879	Sequence 11879, A	526	30	58.8	126	1	US-08-765-783A-77	Sequence 77, Appl
454	30	58.8	1120	2	US-09-792-024-95	Sequence 95, Appl	527	30	58.8	126	2	US-08-921-100-73	Sequence 73, Appl
455	30.5	60.8	106	2	US-08-844-215-14	Sequence 14, Appl	528	30	58.8	126	2	US-08-921-100-77	Sequence 77, Appl
456	30.5	59.8	278	2	US-09-134-001C-3651	Sequence 3651, App	529	30	58.8	126	2	US-08-880-142-73	Sequence 73, Appl
457	30	58.8	11	1	US-08-765-783A-81	Sequence 81, Appl	530	30	58.8	126	2	US-08-880-142-77	Sequence 77, Appl
458	30	58.8	11	2	US-08-599-226-7	Sequence 7, Appl	531	30	58.8	126	2	US-08-902-201-73	Sequence 73, Appl
459	30	58.8	11	2	US-09-416-557-81	Sequence 81, Appl	532	30	58.8	126	2	US-08-902-201-77	Sequence 77, Appl
460	30	58.8	11	2	US-09-125-098-7	Sequence 7, Appl	533	30	58.8	126	2	US-09-416-557-73	Sequence 73, Appl
461	30	58.8	11	2	US-09-540-018-7	Sequence 7, Appl	534	30	58.8	126	1	US-08-765-783A-27	Sequence 27, Appl
462	30	58.8	11	2	US-09-424-712-33	Sequence 33, Appl	535	30	58.8	127	2	US-08-921-100-27	Sequence 27, Appl
463	30	58.8	11	2	US-09-192-854-149	Sequence 149, App	536	30	58.8	127	2	US-08-880-142-27	Sequence 27, Appl
464	30	58.8	11	2	US-09-511-939-262	Sequence 262, App	537	30	58.8	127	2	US-08-880-142-27	Sequence 27, Appl
465	30	58.8	11	2	US-09-920-262A-4	Sequence 4, Appl	538	30	58.8	127	2	US-08-284-516C-37	Sequence 37, Appl

539	30	58.8	127	2	US-08-284-516C-41	Sequence 41, Appl	612	30	58.8	336	2	US-09-270-767-40561	Sequence 40561, A
540	30	58.8	127	2	US-08-284-516C-47	Sequence 47, Appl	613	30	58.8	336	2	US-09-270-767-55777	Sequence 55777, A
541	30	58.8	127	2	US-08-284-516C-65	Sequence 65, Appl	614	30	58.8	357	2	US-09-724-623-93	Sequence 93, Appl
542	30	58.8	127	2	US-08-902-201-27	Sequence 27, Appl	615	30	58.8	358	2	US-09-198-452A-188	Sequence 188, App
543	30	58.8	127	2	US-09-416-557-27	Sequence 27, Appl	616	30	58.8	358	2	US-09-438-185A-172	Sequence 172, App
544	30	58.8	127	2	US-09-537-911A-37	Sequence 37, Appl	617	30	58.8	366	2	US-09-328-352-6309	Sequence 6309, A
545	30	58.8	127	2	US-09-537-911A-41	Sequence 41, Appl	618	30	58.8	378	2	US-09-270-767-59898	Sequence 59898, A
546	30	58.8	127	2	US-09-537-911A-47	Sequence 47, Appl	619	30	58.8	384	2	US-09-634-238-263	Sequence 263, App
547	30	58.8	127	2	US-09-537-911A-65	Sequence 65, Appl	620	30	58.8	392	2	US-09-710-279-1008	Sequence 1008, Ap
548	30	58.8	127	2	US-08-259-372A-14	Sequence 14, Appl	621	30	58.8	398	2	US-09-134-001C-4724	Sequence 4724, Ap
549	30	58.8	128	1	US-08-468-671-14	Sequence 14, Appl	622	30	58.8	398	2	US-09-134-001C-5523	Sequence 5523, Ap
550	30	58.8	128	1	US-08-470-139-8	Sequence 8, Appl	623	30	58.8	419	2	US-09-543-681A-4221	Sequence 4221, Ap
551	30	58.8	128	1	US-08-470-139-8	Sequence 8, Appl	624	30	58.8	444	2	US-09-489-039A-10106	Sequence 10106, A
552	30	58.8	128	2	US-09-347-061-8	Sequence 26, Appl	625	30	58.8	484	2	US-09-902-540-13606	Sequence 13606, A
553	30	58.8	128	2	US-09-347-061-8	Sequence 26, Appl	626	30	58.8	504	2	US-10-104-047-3467	Sequence 3467, Ap
554	30	58.8	128	2	US-09-537-911A-68	Sequence 68, Appl	627	30	58.8	532	2	US-09-252-991A-25769	Sequence 25769, A
555	30	58.8	128	2	US-09-855-271-8	Sequence 8, Appl	628	30	58.8	549	2	US-09-252-991A-26721	Sequence 26721, A
556	30	58.8	128	2	US-09-855-271-8	Sequence 8, Appl	629	30	58.8	550	2	US-09-533-447-14	Sequence 14, Appl
557	30	58.8	129	2	US-08-943-136-2	Sequence 26, Appl	630	30	58.8	551	2	US-09-248-766A-14711	Sequence 14711, A
558	30	58.8	129	2	US-08-973-518-2	Sequence 2, Appl	631	30	58.8	610	2	US-09-533-427-3	Sequence 3, Appl
559	30	58.8	129	2	US-08-973-518-2	Sequence 2, Appl	632	30	58.8	638	2	US-09-107-532A-3919	Sequence 3919, Ap
560	30	58.8	129	2	US-09-270-767-37099	Sequence 37099, A	633	30	58.8	705	2	US-09-270-767-4461	Sequence 4461, A
561	30	58.8	129	2	US-09-270-767-52316	Sequence 52316, A	634	30	58.8	795	2	US-09-134-000C-5968	Sequence 5968, A
562	30	58.8	140	2	US-09-270-767-34254	Sequence 34254, A	635	30	58.8	895	2	US-09-489-039A-7893	Sequence 7893, Ap
563	30	58.8	140	2	US-09-318-786-25	Sequence 49471, A	636	30	58.8	1404	1	US-08-400-159-2	Sequence 2, Appl
564	30	58.8	152	2	US-09-472-087-18	Sequence 18, Appl	637	30	58.8	1404	2	US-08-611-729A-2	Sequence 2, Appl
565	30	58.8	152	2	US-09-472-087-18	Sequence 18, Appl	638	30	58.8	1404	2	US-09-195-524-2	Sequence 2, Appl
566	30	58.8	171	2	US-09-583-110-4903	Sequence 4903, Ap	639	30	58.8	1956	2	US-08-843-417-2	Sequence 2, Appl
567	30	58.8	172	2	US-09-107-433-4439	Sequence 4439, Ap	640	30	58.8	1956	2	US-09-527-013-2	Sequence 2, Appl
568	30	58.8	183	2	US-09-252-991A-28670	Sequence 28670, A	641	30	58.8	1957	2	US-08-669-656A-8	Sequence 8, Appl
569	30	58.8	225	2	US-09-543-681A-6750	Sequence 6750, A	642	30	58.8	2132	2	US-08-669-656A-8	Sequence 8, Appl
570	30	58.8	233	2	US-08-812-586-45	Sequence 45, Appl	643	30	57.8	29.5	2	US-09-134-000C-6675	Sequence 6675, A
571	30	58.8	233	2	US-09-535-832A-42	Sequence 42, Appl	644	29	56.9	11	1	US-07-942-245-495	Sequence 495, App
572	30	58.8	233	2	US-09-303-518D-740	Sequence 740, App	645	29	56.9	11	1	US-07-942-245-522	Sequence 522, App
573	30	58.8	233	2	US-09-303-518D-742	Sequence 742, App	646	29	56.9	11	1	US-09-024-253-16	Sequence 16, Appl
574	30	58.8	233	2	US-09-303-518D-744	Sequence 744, App	647	29	56.9	11	1	US-09-649-063-16	Sequence 16, Appl
575	30	58.8	233	2	US-09-303-518D-746	Sequence 746, App	648	29	56.9	11	2	US-09-802-083-10	Sequence 10, Appl
576	30	58.8	233	2	US-09-303-518D-748	Sequence 748, App	649	29	56.9	26	1	US-07-932-455A-8	Sequence 8, Appl
577	30	58.8	234	1	US-07-690-192-2	Sequence 2, Appl	650	29	56.9	26	1	US-08-766-725A-8	Sequence 2, Appl
578	30	58.8	234	2	US-09-770-916-4	Sequence 4, Appl	651	29	56.9	27	1	US-07-932-455A-2	Sequence 2, Appl
579	30	58.8	240	1	US-08-488-113B-147	Sequence 147, App	652	29	56.9	27	1	US-07-932-455A-12	Sequence 12, Appl
580	30	58.8	240	1	US-08-488-113B-148	Sequence 148, App	653	29	56.9	27	1	US-08-766-725A-7	Sequence 7, Appl
581	30	58.8	240	1	US-08-477-484B-147	Sequence 147, App	654	29	56.9	27	1	US-08-766-725A-12	Sequence 12, Appl
582	30	58.8	240	1	US-08-477-484B-148	Sequence 148, App	655	29	56.9	30	2	US-08-525-539A-9	Sequence 9, Appl
583	30	58.8	240	1	US-08-464-360-147	Sequence 147, App	656	29	56.9	38	1	US-07-932-455A-10	Sequence 10, Appl
584	30	58.8	240	1	US-08-646-360-148	Sequence 148, App	657	29	56.9	38	1	US-08-766-725A-10	Sequence 10, Appl
585	30	58.8	240	1	US-08-839-765-147	Sequence 147, App	658	29	56.9	44	2	US-09-929-788-4	Sequence 4, Appl
586	30	58.8	240	2	US-08-839-765-148	Sequence 148, App	659	29	56.9	62	2	US-09-134-001C-5647	Sequence 5647, Ap
587	30	58.8	240	2	US-09-136-389-147	Sequence 147, App	660	29	56.9	64	2	US-09-248-796A-25172	Sequence 25172, A
588	30	58.8	240	2	US-09-136-389-148	Sequence 148, App	661	29	56.9	85	2	US-09-134-001C-3985	Sequence 3985, Ap
589	30	58.8	240	2	US-09-610-838-148	Sequence 148, App	662	29	56.9	92	2	US-09-248-796A-25172	Sequence 25172, A
590	30	58.8	240	2	US-09-610-838-148	Sequence 148, App	663	29	56.9	94	2	US-09-248-796A-25149	Sequence 25149, A
591	30	58.8	240	2	US-09-711-485-147	Sequence 147, App	664	29	56.9	100	2	US-09-899-896-8	Sequence 8, Appl
592	30	58.8	240	2	US-09-711-485-148	Sequence 148, App	665	29	56.9	105	2	US-08-851-362D-36	Sequence 36, Appl
593	30	58.8	244	2	US-09-328-352-6861	Sequence 6861, Ap	666	29	56.9	106	1	US-08-561-521-7	Sequence 5, Appl
594	30	58.8	254	2	US-09-419-788-29	Sequence 29, Appl	667	29	56.9	106	1	US-08-561-521-7	Sequence 5, Appl
595	30	58.8	284	2	US-08-564-164A-2	Sequence 2, Appl	668	29	56.9	106	4	PCR-US95-01219-5	Sequence 7, Appl
596	30	58.8	287	2	US-09-318-786-37	Sequence 37, Appl	669	29	56.9	106	4	PCR-US95-01219-5	Sequence 7, Appl
597	30	58.8	317	2	US-08-996-139-13	Sequence 13, Appl	670	29	56.9	107	1	US-07-634-278-2	Sequence 2, Appl
598	30	58.8	317	2	US-08-995-659-13	Sequence 13, Appl	671	29	56.9	107	1	US-07-634-278-17	Sequence 17, Appl
599	30	58.8	317	2	US-09-215-649A-13	Sequence 13, Appl	672	29	56.9	107	1	US-07-634-278-70	Sequence 70, Appl
600	30	58.8	317	2	US-09-052-521C-4	Sequence 4, Appl	673	29	56.9	107	1	US-08-477-728-2	Sequence 2, Appl
601	30	58.8	317	2	US-09-577-780-13	Sequence 13, Appl	674	29	56.9	107	1	US-08-477-728-17	Sequence 17, Appl
602	30	58.8	317	2	US-09-577-800-13	Sequence 13, Appl	675	29	56.9	107	1	US-08-477-728-70	Sequence 70, Appl
603	30	58.8	317	2	US-09-466-496-13	Sequence 13, Appl	676	29	56.9	107	1	US-08-477-728-102	Sequence 102, App
604	30	58.8	317	2	US-09-871-856-13	Sequence 13, Appl	677	29	56.9	107	1	US-08-474-040-17	Sequence 17, Appl
605	30	58.8	317	2	US-09-871-856-13	Sequence 13, Appl	678	29	56.9	107	1	US-08-474-040-17	Sequence 17, Appl
606	30	58.8	317	2	US-09-396-937-2	Sequence 2, Appl	679	29	56.9	107	1	US-08-474-040-70	Sequence 70, Appl
607	30	58.8	317	2	US-09-877-650-13	Sequence 13, Appl	680	29	56.9	107	1	US-08-474-040-102	Sequence 102, App
608	30	58.8	317	2	US-09-865-363-13	Sequence 13, Appl	681	29	56.9	107	1	US-08-487-200-2	Sequence 2, Appl
609	30	58.8	317	2	US-09-688-459-13	Sequence 13, Appl	682	29	56.9	107	1	US-08-487-200-17	Sequence 17, Appl
610	30	58.8	317	2	US-09-957-944-6	Sequence 6, Appl	683	29	56.9	107	1	US-08-487-200-17	Sequence 17, Appl
611	30	58.8	329	2	US-09-489-039A-8390	Sequence 8390, Ap	684	29	56.9	107	1	US-08-487-200-17	Sequence 70, Appl

665	29	56.9	107	1	US-08-487-200-102	Sequence 102, App	758	29	56.9	214	2	US-09-097-111A-2	Sequence 2, Appli
666	29	56.9	107	1	US-08-488-113B-162	Sequence 162, App	759	29	56.9	214	2	US-09-249-230-1	Sequence 1, Appli
667	29	56.9	107	1	US-08-477-484B-162	Sequence 162, App	760	29	56.9	214	2	US-09-460-587-2	Sequence 2, Appli
668	29	56.9	107	1	US-08-107-669D-48	Sequence 48, Appl	761	29	56.9	214	2	US-08-146-206C-24	Sequence 24, Appl
669	29	56.9	107	1	US-08-472-798A-48	Sequence 48, Appl	762	29	56.9	214	2	US-09-705-686-24	Sequence 24, Appl
670	29	56.9	107	1	US-08-458-516-8	Sequence 8, Appli	763	29	56.9	214	2	US-09-940-166A-2	Sequence 2, Appli
671	29	56.9	107	1	US-08-458-516-8	Sequence 8, Appli	764	29	56.9	214	2	US-09-705-352A-24	Sequence 24, Appl
672	29	56.9	107	1	US-08-477-513B-48	Sequence 48, Appl	765	29	56.9	214	2	US-09-705-388-24	Sequence 24, Appl
673	29	56.9	107	1	US-08-646-360-162	Sequence 162, App	766	29	56.9	214	4	PCT-US93-07832-34	Sequence 34, Appl
674	29	56.9	107	1	US-08-082-842A-48	Sequence 48, Appl	767	29	56.9	214	4	PCT-US93-07832-40	Sequence 40, Appl
675	29	56.9	107	1	US-08-888-365-24	Sequence 24, Appl	768	29	56.9	214	4	PCT-US93-07832-40	Sequence 40, Appl
676	29	56.9	107	1	US-08-933-983-75	Sequence 75, Appl	769	29	56.9	215	2	US-09-247-373B-40	Sequence 40, Appl
677	29	56.9	107	2	US-08-933-983-75	Sequence 76, Appl	770	29	56.9	220	2	US-08-896-933-20	Sequence 20, Appl
678	29	56.9	107	2	US-08-933-983-76	Sequence 77, Appl	771	29	56.9	220	2	US-09-314-255-20	Sequence 20, Appl
679	29	56.9	107	2	US-08-839-765-162	Sequence 162, App	772	29	56.9	220	2	US-09-708-008B-20	Sequence 20, Appl
700	29	56.9	107	2	US-09-136-389-162	Sequence 162, App	773	29	56.9	229	2	US-09-270-767-61637	Sequence 61637, A
701	29	56.9	107	2	US-08-484-537-2	Sequence 2, Appli	774	29	56.9	233	1	US-07-934-373C-25	Sequence 25, Appl
702	29	56.9	107	2	US-08-484-537-17	Sequence 17, Appli	775	29	56.9	233	1	US-08-792-824-6	Sequence 6, Appli
703	29	56.9	107	2	US-08-484-537-70	Sequence 70, Appl	776	29	56.9	233	2	US-08-437-642B-25	Sequence 25, Appl
704	29	56.9	107	2	US-08-484-537-102	Sequence 102, App	777	29	56.9	233	2	US-08-146-206C-25	Sequence 25, Appl
705	29	56.9	107	2	US-09-240-274-34	Sequence 34, Appl	778	29	56.9	233	2	US-09-705-686-25	Sequence 25, Appl
706	29	56.9	107	2	US-09-240-274-179	Sequence 179, App	779	29	56.9	233	2	US-09-705-392A-25	Sequence 25, Appl
707	29	56.9	107	2	US-09-450-520A-12	Sequence 12, Appl	780	29	56.9	233	2	US-09-705-392A-25	Sequence 25, Appl
708	29	56.9	107	2	US-09-610-838-162	Sequence 162, App	781	29	56.9	233	4	PCT-US93-07832-25	Sequence 25, Appl
709	29	56.9	107	2	US-09-711-485-162	Sequence 162, App	782	29	56.9	236	1	US-08-792-824-3	Sequence 3, Appli
710	29	56.9	107	2	US-09-848-798-34	Sequence 34, Appl	783	29	56.9	236	1	US-08-792-824-9	Sequence 9, Appli
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837	29	56.9	512	1	US-09-360-197-6	Sequence 6, Appl	910	28	54.9	110	2	US-10-092-246-15	Sequence 16, Appl
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980 28 54.9 391 2 US-09-107-532A-4513
981 28 54.9 396 2 US-09-248-796A-20944
982 28 54.9 403 2 US-10-104-047-2454
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ALIGNMENTS

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Sequence 14387, A
Sequence 5109, Ap

RESULT 1
US-08-974-899-13
; Sequence 13, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-974-899-13
Query Match 100.0%; Score 51; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0024;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKTISKYLA 11
Db 1 RASKTISKYLA 11

RESULT 2
US-09-795-798-13
; Sequence 13, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-795-798-13

Query Match 100.0%; Score 51; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
Db 1 RASKTISKYLA 11

RESULT 3
US-08-974-899-1
; Sequence 1, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-1

Query Match 100.0%; Score 51; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYIA 11
|||||
DB 24 RASKTISKYIA 34

RESULT 4
US-08-974-899-2
Sequence 2, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-795-798-1

Query Match 100.0%; Score 51; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYIA 11
|||||
DB 24 RASKTISKYIA 34

RESULT 5
US-09-795-798-1
Sequence 1, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-795-798-1

Query Match 100.0%; Score 51; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYIA 11
|||||
DB 24 RASKTISKYIA 34

RESULT 6
US-09-795-798-2
Sequence 2, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.

SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-2

Query Match 100.0%; Score 51; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYIA 11
|||||
DB 24 RASKTISKYIA 34

RESULT 5
US-09-795-798-1
Sequence 1, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-795-798-1

Query Match 100.0%; Score 51; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYIA 11
|||||
DB 24 RASKTISKYIA 34

RESULT 6
US-09-795-798-2
Sequence 2, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.

Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-795-798-2
Query Match 100.0%; Score 51; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKTISKYLA 11
|||
Db 24 RASKTISKYLA 34
RESULT 7
US-09-027-449-47
Sequence 47, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-47
Query Match 100.0%; Score 51; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKTISKYLA 11
|||
Db 24 RASKTISKYLA 34
RESULT 8
US-08-804-444A-47
Sequence 47, Application US/0880444A
Patent No. 6117980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-804-444A-47
Query Match 100.0%; Score 51; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKITSKYLA 11
|||||
Db 24 RASKITSKYLA 34

RESULT 9

US-09-026-985-47
; Sequence 47, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-47
Query Match 100.0%; Score 51; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKITSKYLA 11
|||||
Db 24 RASKITSKYLA 34
RESULT 10
US-09-121-952A-47
; Sequence 47, Application US/09121952A
; Patent No. 645835
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hseil, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shaikh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-47
Query Match 100.0%; Score 51; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASKITSKYLA 11
|||||
Db 24 RASKITSKYLA 34

RESULT 11
US-09-234-340A-47
; Sequence 47, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hseil, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shaikh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952

FILING DATE: 24-JUL-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-5530
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-47

Query Match 100.0%; Score 51; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RASKTISKYLA 11
|||
Db 24 RASKTISKYLA 34

RESULT 12

US-09-355-014-47
Sequence 47, Application US/09355014
Patent No. 6870033

GENERAL INFORMATION:

APPLICANT: Genentech, Inc., Hsui, Vanessa
Leong, Steven R.
Koumenis, Iphigenia
Presta, Leonard G.
Shahrokh, Zahra
Zapata, Gerardo A.

TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
Antibody Fragment-Polymer Conjugates and
Humantized Anti-IL-8 Monoclonal Antibodies

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/355,014

FILING DATE: 21-JUL-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P1085R3PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/952-9881

TELEFAX: 650/952-5530

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-355-014-47

Query Match 100.0%; Score 51; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RASKTISKYLA 11
|||
Db 24 RASKTISKYLA 34

RESULT 13

US-08-182-067-4
Sequence 4, Application US/08182067
Patent No. 5985279

GENERAL INFORMATION:

APPLICANT: WALDMANN, HERMAN

APPLICANT: SIMS, MARTIN

APPLICANT: CROWE, SCOTT

TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSER: Rothwell, Figg Ernet & Kurz

STREET: Suite 701-E, 555 Thirteenth St., N.W

CITY: Washington

STATE: D. C.

COUNTRY: U.S.A.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/182,067

FILING DATE: 23-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB92/01289

FILING DATE: 15-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9115364.3

FILING DATE: 16-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: ERNST, BARBARA G.

REGISTRATION NUMBER: 30,377

REFERENCE/DOCKET NUMBER: 1786-118A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)783-6031

TELEFAX: (202)783-6040

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-182-067-4

Query Match 76.5%; Score 39; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.43;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RASKTISKYLA 11
|||
Db 1 RASKTISKYLA 11

RESULT 14

US-08-465-313-4
Sequence 4, Application US/08465313
Patent No. 5987867

GENERAL INFORMATION:

APPLICANT: WALDMANN, HERMAN

APPLICANT: SIMS, MARTIN J.

APPLICANT: CROME, J. SCOTT
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO MILITIA DRIVE
CITY: LEXINGTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,313
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,067
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01289
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA: GB 9115364.3
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, DAVID E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LYNN91-01A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-313-4

Query Match 76.5%; Score 39; DB 1; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.43;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKXYLA 11
:|||||
1 KASKSISNYLA 11

Db 1 KASKSISNYLA 11

RESULT 15
US-09-809-739-2
Sequence 2, Application US/09809739
Patent No. 6663863
GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
TITLE OF INVENTION: Restenosis
FILE REFERENCE: 185,1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 11
TYPE: PRT
ORGANISM: Unknown
FEATURE:

NAME/KEY: SITE
LOCATION: (1)....(11)
OTHER INFORMATION: CD1 of YFC51.1 light chain
OTHER INFORMATION: Rat
US-09-809-739-2

Query Match 76.5%; Score 39; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.43;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKXYLA 11
:|||||
1 KASKSISNYLA 11

Db 1 KASKSISNYLA 11

RESULT 16
US-09-378-967-4
Sequence 4, Application US/09378967
Patent No. 6689869
GENERAL INFORMATION:
APPLICANT: WALDMANN, HERMAN
APPLICANT: SIMS, MARTIN J.
APPLICANT: CROME, J. SCOTT
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO MILITIA DRIVE
CITY: LEXINGTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02421
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,967
FILING DATE: 23-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,313
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,067
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01289
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9115364.3
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: WENDLER, HELEN E.
REGISTRATION NUMBER: 37,964
REFERENCE/DOCKET NUMBER: LYNN91-01A3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-378-967-4

Query Match 76.5%; Score 39; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.43;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKXYLA 11

Db 1 KASKISNYIA 11

```

RESULT 17
US-09-905-243-32
; Sequence 32, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; TITLE OF INVENTION: Immunogenicity
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Pan troglodytes
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (50)...(66)
; OTHER INFORMATION: CDRII
US-09-905-243-32

```

Query Match 76.5%; Score 39; DB 2; Length 88;
 Best Local Similarity 63.6%; Pred. No. 3.8;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 |||:::||||
 Db 24 RASQSVNYIA 34

```

RESULT 18
US-08-635-109-6
; Sequence 6, Application US/08635109
; Patent No. 6538114
; GENERAL INFORMATION:
; APPLICANT: Persson, Mats A. A.
; APPLICANT: Allander, Tobias E.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,109
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McCracken, Thomas P
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 2300-6146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-3400

```

```

; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-635-109-6

```

Query Match 76.5%; Score 39; DB 2; Length 105;
 Best Local Similarity 63.6%; Pred. No. 4.5;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 |||:::||||
 Db 23 RASQSVNYIA 33

```

RESULT 19
US-08-844-215-9
; Sequence 9, Application US/08844215
; Patent No. 6747136
; GENERAL INFORMATION:
; APPLICANT: PERSSON, MATS AXEL
; APPLICANT: ALLANDER, TOBIAS ERIK
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,215
; FILING DATE: 17-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/635,109
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 80146.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-844-215-9

```

Query Match 76.5%; Score 39; DB 2; Length 105;
 Best Local Similarity 63.6%; Pred. No. 4.5;
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
 |||:::||||
 Db 23 RASQSVNYIA 33

RESULT 20
US-08-039-198B-12
Sequence 12 Application US/08039198B
Patent No. 5858725
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PREPARATION OF CHIMERIC ANTIBODIES
TITLE OF INVENTION: RECOMBINANT FOR STRATEGY
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/039,198B
FILING DATE: 29-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01744
FILING DATE: 08-OCT-91
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1430-86
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-039-198B-12

Query Match 76.5%; Score 39; DB 1; Length 125;
Best Local Similarity 72.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
:|||||
Db 44 KASKSISNYLA 54

RESULT 21
US-08-182-067-2
Sequence 2 Application US/08182067
Patent No. 5955279
GENERAL INFORMATION:
APPLICANT: WALDMANN, HERMAN
APPLICANT: SIMS, MARTIN
APPLICANT: CROME, SCOTT
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rotwell, Figg Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,067
FILING DATE: 23-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01289
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9115364.3
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1786-118A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-182-067-2

Query Match 76.5%; Score 39; DB 1; Length 125;
Best Local Similarity 72.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
:|||||
Db 44 KASKSISNYLA 54

RESULT 22
US-08-465-313-2
Sequence 2 Application US/08465313
Patent No. 5997867
GENERAL INFORMATION:
APPLICANT: WALDMANN, HERMAN
APPLICANT: SIMS, MARTIN J.
APPLICANT: CROME, J. SCOTT
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P. C.
STREET: TWO MILITIA DRIVE
CITY: LEXINGTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,313
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,067
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01289
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9115364.3
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, DAVID E.

```

;
;   REGISTRATION NUMBER: 22,592
;   REFERENCE/DOCKET NUMBER: LYNX91-01A2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 861-6240
;   TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 125 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
US-08-465-313-2

Query Match          76.5%; Score 39; DB 1; Length 125;
Best Local Similarity 72.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASKTISKYLA 11
       :|||:|||
Db      44 KASKSISNYLA 54

RESULT 23
US-09-809-739-1
; Sequence 1, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(125)
; OTHER INFORMATION: yfcs1.1 light chain variable region with signal
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: Rat
;
US-09-809-739-1

Query Match          76.5%; Score 39; DB 2; Length 125;
Best Local Similarity 72.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASKTISKYLA 11
       :|||:|||
Db      44 KASKSISNYLA 54

RESULT 24
US-09-378-967-2
; Sequence 2, Application US/09378967
; Patent No. 6689869
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN J.
; APPLICANT: CROME, J. SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
```

```

;
;   STREET: TWO MILITIA DRIVE
;   CITY: LEXINGTON
;   STATE: MASSACHUSETTS
;   COUNTRY: USA
;   ZIP: 02421
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/378,967
;   FILING DATE: 23-AUG-1999
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/465,313
;   FILING DATE: 05-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/182,067
;   FILING DATE: 23-MAR-1994
;   APPLICATION NUMBER: PCT/G892/01289
;   FILING DATE: 15-JUL-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: GB 9115364.3
;   FILING DATE: 16-JUL-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: WENDLER, HELEN E.
;   REGISTRATION NUMBER: 37,964
;   REFERENCE/DOCKET NUMBER: LYNX91-01A3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781) 861-6240
;   TELEFAX: (781) 861-9540
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 125 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
US-09-378-967-2

Query Match          76.5%; Score 39; DB 2; Length 125;
Best Local Similarity 72.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASKTISKYLA 11
       :|||:|||
Db      44 KASKSISNYLA 54

RESULT 25
US-09-809-739-10
; Sequence 10, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain variable region with signal
; OTHER INFORMATION: sequence
```


NAME/KEY: SIGNAL
LOCATION: (1)....(19)
US-09-809-739-10

Query Match
Best Local Similarity 76.5%; Score 39; DB 2; Length 127;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
:|||||
DB 43 KASKSISNYLA 53

RESULT 26
US-09-848-832-4
Sequence 4, Application US/09848832
Patent No. 6890532
GENERAL INFORMATION:
APPLICANT: Hooper, Douglas
APPLICANT: Dietzschold, Bernhard
TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
FILE REFERENCE: H0001.NP0002
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/204,518
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 234
TYPE: PRF
ORGANISM: Homo sapien
US-09-848-832-4

Query Match
Best Local Similarity 72.7%; Score 39; DB 2; Length 234;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
:|||||
DB 44 RASQTASRYLA 54

RESULT 27
US-08-276-852-106
Sequence 106, Application US/08276852
Patent No. 5652138
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-852-106

Query Match
Best Local Similarity 74.5%; Score 38; DB 1; Length 104;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
:|||||
DB 19 RASQTISSYL 28

RESULT 28
US-08-899-575-106
Sequence 106, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-106

Query Match 74.5%; Score 38; DB 1; Length 104;
Best Local Similarity 80.0%; Pred. No. 6.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYL 10
|||:||||
Db 19 RASQTSSYL 28

RESULT 29
US-08-899-575-106

; Sequence 106, Application US/08899575

; Patent No. 5804440

; GENERAL INFORMATION:

; APPLICANT: Burton, Dennis R

; APPLICANT: Barbas, Carlos F

; APPLICANT: Lerner, Richard A

; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 170

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute, Office of

; ADDRESSEE: Patent Counsel

; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,

; STREET: Mail Drop TPC8

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/899,575

; FILING DATE: 24-JUL-1997

; CLASSIFICATION:

; APPLICATION DATA:

; APPLICATION NUMBER: US 08/276,852

; FILING DATE: 18-JUL-1994

; APPLICATION NUMBER: US 08/178,302

; FILING DATE: 30-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/954,148

; FILING DATE: 30-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitting, Thomas

; REGISTRATION NUMBER: 34,163

; REFERENCE/DOCKET NUMBER: SC1452P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-554-2937

; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 106:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 104 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-899-575-106

Query Match 74.5%; Score 38; DB 1; Length 104;

Best Local Similarity 80.0%; Pred. No. 6.9;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYL 10
|||:||||
Db 19 RASQTSSYL 28

RESULT 30
PCT-US95-08743-106

; Sequence 106, Application PC/TUS9508743

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

; NUMBER OF SEQUENCES: 170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08743

; FILING DATE: 11-JUL-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/276,852

; FILING DATE: 18-JUL-1994

; INFORMATION FOR SEQ ID NO: 106:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 104 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US95-08743-106

Query Match 74.5%; Score 38; DB 4; Length 104;
Best Local Similarity 80.0%; Pred. No. 6.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYL 10
|||:||||
Db 19 RASQTSSYL 28

RESULT 31
US-07-934-373C-18

; Sequence 18, Application US/07934373C

; Patent No. 5821337

; GENERAL INFORMATION:

; APPLICANT: Paul J. Carter

; APPLICANT: Leonard G. Presta

; TITLE OF INVENTION: Immunoglobulin Variants

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/934,373C

; FILING DATE: 21-Aug-1992

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/05126

; FILING DATE: 15-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/715272

; FILING DATE: 14-JUN-1991

Query Match 74.5%; Score 38; DB 4; Length 104;

Best Local Similarity 80.0%; Pred. No. 6.9;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-18

Query Match 74.5%; Score 38; DB 1; Length 107;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||::|||
24 RASQSIISNYLA 34

Db 24 RASQSIISNYLA 34

RESULT 32
US-08-437-642B-18
Sequence 18, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-18

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||::|||
24 RASQSIISNYLA 34

Db 24 RASQSIISNYLA 34

RESULT 33
US-08-146-206C-18
Sequence 18, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,206C
FILING DATE: 17-No. 6407213-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-146-206C-18

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||::|||
24 RASQSIISNYLA 34

Db 24 RASQSIISNYLA 34

RESULT 34
US-09-648-067A-14
Sequence 14, Application US/09648067A
Patent No. 6627196
GENERAL INFORMATION:
APPLICANT: Baughman, Sharon A.
APPLICANT: Shak Steven
TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
FILE REFERENCE: P1775R1
CURRENT APPLICATION NUMBER: US/09/648,067A
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 60/151,018

PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/213,822
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 14
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:|||||
DB 24 RASQISINYLA 34

RESULT 35
US-09-705-686-18
Sequence 18, Application US/09705686
Patent No. 6639055
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
PRESTA, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-NO. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:|||||
DB 24 RASQISINYLA 34

RESULT 36
US-09-705-392A-18
Sequence 18, Application US/09705392A
Patent No. 671971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
PRESTA, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-NO. 671971-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:|||||
DB 24 RASQISINYLA 34

RESULT 37
US-09-705-398-18
Sequence 18, Application US/09705398
Patent No. 6800738
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
PRESTA, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398A
FILING DATE: 02-NO. 6800738-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-NOV-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||::|||
DB 24 RASQSIISNYLA 34

RESULT 38
US-09-602-812A-5
Sequence 5, Application US/09602812A
Patent No. 6949245
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Presta, Leonard G.
APPLICANT: Sliwowski, Mark X.
TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
FILE REFERENCE: P1467R2
CURRENT APPLICATION NUMBER: US/09/602,812A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141,316
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 5
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: light chain consensus sequence
US-09-602-812A-5

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||::|||
DB 24 RASQSIISNYLA 34

RESULT 39
PCT-US93-07832-18
Sequence 18, Application PC/TUS9307832

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-18

Query Match 74.5%; Score 38; DB 4; Length 107;
Best Local Similarity 72.7%; Pred. No. 7.1;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||::|||
DB 24 RASQSIISNYLA 34

RESULT 40
US-08-974-899-3
Sequence 3, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-974-899-3

Query Match          74.5%; Score 38; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 7.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 41
US-09-795-798-3
; Sequence 3, Application US/09795798
; Patent No. 6703018
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
;
US-09-795-798-3
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Query Match          74.5%; Score 38; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 7.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 42
US-08-908-469-12
; Sequence 12, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/908,469
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,504
; FILING DATE: 07-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Cui, Steven X.
; REGISTRATION NUMBER: 44,637
; REFERENCE/DOCKET NUMBER: P1093P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
;
US-08-908-469-12

Query Match          74.5%; Score 38; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 7.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 43
US-09-157-370-3
; Sequence 3, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEINBE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
```

```
FILE REFERENCE: P8341-8072
CURRENT APPLICATION NUMBER: US/09/157,370A
CURRENT FILING DATE: 1998-09-21
EARLIER APPLICATION NUMBER: 08/765,179
EARLIER FILING DATE: 1997-01-14
EARLIER APPLICATION NUMBER: PCT/EP95/02626
EARLIER FILING DATE: 1995-07-06
EARLIER APPLICATION NUMBER: DE/P44 25 115.7
EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 3
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-157-370-3

Query Match
Best Local Similarity 72.5%; Score 37; DB 2; Length 109;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
   |||::|||
Db 24 RASQSVSYLA 34

RESULT 44
US-10-194-975-86
Sequence 86, Application US/10194975
Patent No. 6881557
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501331.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentln version 3.1
SEQ ID NO 86
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-86

Query Match
Best Local Similarity 72.5%; Score 37; DB 2; Length 95;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
   |||::|||
Db 24 RASQSVSYLA 34

RESULT 45
US-09-899-896-4
Sequence 4, Application US/09899896
Patent No. 6569431
GENERAL INFORMATION:
APPLICANT: von Balingen, Hans-Christian
APPLICANT: Genain, Claude P.
APPLICANT: Hauser, Stephen L.
TITLE OF INVENTION: Recombinant Antibody Fragments as Autoantibody
FILE REFERENCE: SF01-025-2
CURRENT APPLICATION NUMBER: US/09/899,896
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/691,654
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 4
```

```
LENGTH: 100
TYPE: PRT
ORGANISM: human
US-09-899-896-4

Query Match
Best Local Similarity 72.5%; Score 37; DB 2; Length 100;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
   |||::|||
Db 24 RASQSVSYLA 34

RESULT 46
US-08-107-669D-14
Sequence 14, Application US/08107669D
Patent No. 5766886
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbalia
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-669D-14

Query Match
Best Local Similarity 72.5%; Score 37; DB 1; Length 107;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
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Db 24 RASQSVSYLA 34

RESULT 47
US-08-472-788A-14
Sequence 14, Application US/08472788A
Patent No. 5770196
GENERAL INFORMATION:
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APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESSES:
ADDRESS: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-14

Query Match 72.5%; Score 37; DB 1; Length 107;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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|||::|
24 RASQSVSYLA 34

Db

RESULT 48
US-08-477-531B-14
Sequence 14, Application US/08477531B
Patent No. 582123
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2540
TELEFAX: 202/371-2600
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-531B-14

Query Match 72.5%; Score 37; DB 1; Length 107;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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24 RASQSVSYLA 34

Db

RESULT 49
US-08-082-842A-14
Sequence 14, Application US/08082842A
Patent No. 3869619
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,842A
FILING DATE: 23-JUN-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842A-14

Query Match 72.5%; Score 37; DB 1; Length 107;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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DB 24 RASQSVSYLA 34

RESULT 50

US-09-438-954-1
Sequence 1, Application US/09438954
Patent No. 6458934
GENERAL INFORMATION:
APPLICANT: HONG, Hyo Jeong
APPLICANT: PARK, Sung Sup
APPLICANT: KANG, Young Jun
APPLICANT: KANG, Chang-YuIl
APPLICANT: YOON, Sung Kwan
TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
FILE REFERENCE: 1303-124P
CURRENT APPLICATION NUMBER: US/09/438,954
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Variable
OTHER INFORMATION: region of light chain of humanized antibody
OTHER INFORMATION: H4B4-1
US-09-438-954-1

Query Match 72.5%; Score 37; DB 2; Length 107;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
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DB 24 RASQTISDYL 33

Search completed: January 17, 2006, 12:07:42
Job time : 23 secs

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:50:44 ; Search time 53.5 Seconds

(without alignments)
85.909 Million cell updates/sec

Title: US-10-665-658-13

Perfect score: 51

Sequence: 1 RASKRISKXIA 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 1000 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	51	100.0	11 4	US-10-727-737-53 Sequence 53, Appl
3	51	100.0	108 3	US-09-795-798-1 Sequence 1, Appl
4	51	100.0	108 3	US-09-795-798-2 Sequence 2, Appl
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6	51	100.0	108 4	US-10-727-737-2 Sequence 5, Appl
7	51	100.0	108 5	US-09-726-558-47 Sequence 47, Appl
8	51	100.0	109 3	US-09-726-558-47 Sequence 47, Appl
9	51	100.0	214 4	US-10-423-299-3 Sequence 3, Appl
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13	39	76.5	11 3	US-09-378-967-4 Sequence 4, Appl
14	39	76.5	11 5	US-10-783-311-248 Sequence 248, App
15	39	76.5	11 5	US-10-484-790A-2 Sequence 4, Appl
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18	39	76.5	88 6	US-11-099-331-32 Sequence 9, Appl
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58	38	74.5	111 5	US-10-916-840-100
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Sequence 10, Appl
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117	37	72.5	107	5	US-10-916-840-157	Sequence 157, App	190	37	72.5	236	5	US-10-961-567A-6	Sequence 6, Appl
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123	37	72.5	107	6	US-11-102-403-3	Sequence 3, Appl	196	36	70.6	11	4	US-10-279-633-49	Sequence 49, Appl
124	37	72.5	107	6	US-11-102-403-17	Sequence 17, Appl	197	36	70.6	11	5	US-10-783-311-152	Sequence 152, App
125	37	72.5	107	6	US-11-133-775-14	Sequence 14, Appl	198	36	70.6	102	5	US-10-989-462-55	Sequence 55, Appl
126	37	72.5	108	3	US-09-920-267C-8	Sequence 8, Appl	199	36	70.6	102	5	US-10-916-840-26	Sequence 26, Appl
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140	37	72.5	109	4	US-10-480-843-1	Sequence 1, Appl	213	36	70.6	253	3	US-09-811-737-18	Sequence 18, Appl
141	37	72.5	111	5	US-10-916-840-66	Sequence 66, Appl	214	36	70.6	253	3	US-09-811-737-15	Sequence 15, Appl
142	37	72.5	116	5	US-10-783-311-230	Sequence 230, App	215	36	70.6	256	3	US-09-880-748-1027	Sequence 1027, Ap
143	37	72.5	119	4	US-10-714-353-16	Sequence 16, Appl	216	36	70.6	256	4	US-10-293-418-1027	Sequence 32, Appl
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145	37	72.5	126	4	US-10-693-629-30	Sequence 30, Appl	218	36	70.6	260	3	US-09-811-737-16	Sequence 16, Appl
146	37	72.5	127	4	US-10-687-799-4	Sequence 4, Appl	219	36	70.6	260	3	US-09-811-737-17	Sequence 17, Appl
147	37	72.5	127	4	US-10-687-799-8	Sequence 8, Appl	220	36	70.6	262	3	US-09-811-737-19	Sequence 19, Appl
148	37	72.5	127	4	US-10-687-799-12	Sequence 12, Appl	221	35	68.6	11	3	US-09-192-834-105	Sequence 105, App
149	37	72.5	127	4	US-10-687-799-57	Sequence 57, Appl	222	35	68.6	11	3	US-09-828-708-37	Sequence 37, Appl
150	37	72.5	128	4	US-10-656-766-12	Sequence 12, Appl	223	35	68.6	11	3	US-09-968-561A-184	Sequence 184, App
151	37	72.5	128	4	US-10-478-056-31	Sequence 31, Appl	224	35	68.6	11	3	US-09-968-561A-184	Sequence 184, App
152	37	72.5	129	4	US-10-693-629-34	Sequence 34, Appl	225	35	68.6	11	3	US-09-968-561A-184	Sequence 184, App
153	37	72.5	130	5	US-10-394-471B-16	Sequence 16, Appl	226	35	68.6	11	4	US-10-320-231A-57	Sequence 57, Appl
154	37	72.5	130	5	US-10-683-451-29	Sequence 29, Appl	227	35	68.6	11	4	US-10-783-311-128	Sequence 128, App
155	37	72.5	139	4	US-10-153-382-25	Sequence 25, Appl	228	35	68.6	11	5	US-10-725-962-107	Sequence 107, Appl
156	37	72.5	139	4	US-10-687-799-55	Sequence 55, Appl	229	35	68.6	11	5	US-10-630-009-37	Sequence 37, Appl
157	37	72.5	139	5	US-10-612-497-16	Sequence 16, Appl	230	35	68.6	11	5	US-10-867-506-57	Sequence 57, Appl
158	37	72.5	139	5	US-10-612-497-90	Sequence 90, Appl	231	35	68.6	11	5	US-10-893-576-62	Sequence 62, Appl
159	37	72.5	139	5	US-10-776-649-16	Sequence 16, Appl	232	35	68.6	11	6	US-11-115-689-184	Sequence 184, App
160	37	72.5	139	5	US-10-776-649-90	Sequence 90, Appl	233	35	68.6	74	4	US-10-425-115-287288	Sequence 287288, Sequence 218753,
161	37	72.5	139	6	US-11-085-368-25	Sequence 25, Appl	234	35	68.6	74	4	US-10-425-115-218753	Sequence 21, Appl
162	37	72.5	139	6	US-11-085-368-51	Sequence 51, Appl	235	35	68.6	88	3	US-09-905-243-29	Sequence 29, Appl
163	37	72.5	142	4	US-10-153-382-26	Sequence 26, Appl	236	35	68.6	88	3	US-09-905-243-36	Sequence 36, Appl
164	37	72.5	142	5	US-10-612-497-91	Sequence 91, Appl	237	35	68.6	88	6	US-11-099-331-29	Sequence 29, Appl
165	37	72.5	142	5	US-10-776-649-91	Sequence 91, Appl	238	35	68.6	88	6	US-11-099-331-36	Sequence 36, Appl
166	37	72.5	142	6	US-11-085-368-26	Sequence 26, Appl	239	35	68.6	95	4	US-10-194-975-58	Sequence 58, Appl
167	37	72.5	146	5	US-10-153-382-28	Sequence 28, Appl	240	35	68.6	95	4	US-10-194-975-61	Sequence 61, Appl
168	37	72.5	146	5	US-10-612-497-21	Sequence 21, Appl	241	35	68.6	95	4	US-10-194-975-67	Sequence 67, Appl
169	37	72.5	146	5	US-10-612-497-93	Sequence 93, Appl	242	35	68.6	95	4	US-10-194-975-69	Sequence 69, Appl
170	37	72.5	146	5	US-10-776-649-21	Sequence 21, Appl	243	35	68.6	95	4	US-10-041-860-9	Sequence 9, Appl
171	37	72.5	146	5	US-10-776-649-93	Sequence 93, Appl	244	35	68.6	95	4	US-10-041-860-333	Sequence 333, App
172	37	72.5	146	6	US-11-085-368-28	Sequence 28, Appl	245	35	68.6	95	4	US-10-041-860-335	Sequence 335, App
173	37	72.5	146	6	US-11-085-368-71	Sequence 71, Appl	246	35	68.6	95	4	US-10-041-860-345	Sequence 345, App

247	35	68.6	95	4	US-10-308-817-5	Sequence 5, Appl1	320	35	68.6	134	6	US-11-085-368-75	Sequence 75, Appl
248	35	68.6	95	4	US-10-308-817-8	Sequence 8, Appl1	321	35	68.6	136	6	US-10-473-287-49	Sequence 49, Appl
249	35	68.6	95	4	US-10-308-817-14	Sequence 14, Appl	322	35	68.6	136	6	US-11-031-485-12	Sequence 12, Appl
250	35	68.6	95	4	US-10-308-817-16	Sequence 16, Appl	323	35	68.6	241	3	US-09-880-748-1932	Sequence 1932, Ap
251	35	68.6	95	4	US-10-453-698-5	Sequence 5, Appl1	324	35	68.6	241	3	US-09-880-748-2054	Sequence 2054, Ap
252	35	68.6	95	4	US-10-453-698-8	Sequence 8, Appl1	325	35	68.6	241	4	US-10-293-418-1932	Sequence 1932, Ap
253	35	68.6	95	4	US-10-453-698-14	Sequence 14, Appl	326	35	68.6	244	4	US-10-293-418-2054	Sequence 2054, Ap
254	35	68.6	95	4	US-10-453-698-16	Sequence 16, Appl	327	35	68.6	244	6	US-11-090-847-69	Sequence 69, Appl
255	35	68.6	95	4	US-10-379-392-61	Sequence 61, Appl	328	35	68.6	249	3	US-09-880-748-1919	Sequence 919, App
256	35	68.6	95	4	US-10-379-392-63	Sequence 63, Appl	329	35	68.6	249	4	US-09-880-748-1635	Sequence 1635, Ap
257	35	68.6	95	4	US-10-379-392-68	Sequence 68, Appl	330	35	68.6	249	4	US-10-293-418-919	Sequence 919, App
258	35	68.6	95	4	US-10-379-392-72	Sequence 72, Appl	331	35	68.6	249	4	US-10-293-418-1635	Sequence 1635, Ap
259	35	68.6	95	5	US-10-986-089A-42	Sequence 42, Appl	332	34	66.7	11	3	US-09-192-854-6	Sequence 6, Appl1
260	35	68.6	96	4	US-10-041-860-329	Sequence 329, App	333	34	66.7	11	3	US-09-968-561A-10	Sequence 10, Appl
261	35	68.6	96	4	US-10-041-860-327	Sequence 327, App	334	34	66.7	11	3	US-09-968-561A-16	Sequence 16, Appl
262	35	68.6	102	4	US-10-502-307-8	Sequence 35, Appl	335	34	66.7	11	3	US-09-968-561A-22	Sequence 22, Appl
263	35	68.6	102	5	US-10-502-307-8	Sequence 8, Appl1	336	34	66.7	11	3	US-09-968-561A-28	Sequence 28, Appl
264	35	68.6	102	5	US-10-916-840-46	Sequence 46, Appl	337	34	66.7	11	3	US-09-968-561A-34	Sequence 34, Appl
265	35	68.6	104	3	US-09-828-708-2	Sequence 2, Appl1	338	34	66.7	11	3	US-09-968-561A-40	Sequence 40, Appl
266	35	68.6	104	5	US-10-630-009-2	Sequence 2, Appl1	339	34	66.7	11	3	US-09-968-561A-46	Sequence 46, Appl
267	35	68.6	107	4	US-10-041-860-32	Sequence 32, Appl	340	34	66.7	11	3	US-09-968-561A-52	Sequence 52, Appl
268	35	68.6	107	4	US-10-041-860-34	Sequence 34, Appl	341	34	66.7	11	3	US-09-968-561A-100	Sequence 100, App
269	35	68.6	107	4	US-10-041-860-223	Sequence 223, App	342	34	66.7	11	3	US-09-968-561A-106	Sequence 106, App
270	35	68.6	107	4	US-10-041-860-224	Sequence 224, App	343	34	66.7	11	3	US-09-968-561A-112	Sequence 112, App
271	35	68.6	107	4	US-10-041-860-257	Sequence 257, App	344	34	66.7	11	3	US-09-968-561A-118	Sequence 118, App
272	35	68.6	107	4	US-10-041-860-258	Sequence 258, App	345	34	66.7	11	3	US-09-968-561A-124	Sequence 124, App
273	35	68.6	107	4	US-10-041-860-334	Sequence 334, App	346	34	66.7	11	3	US-09-968-561A-136	Sequence 136, App
274	35	68.6	107	4	US-10-016-986-82	Sequence 82, Appl	347	34	66.7	11	3	US-09-968-561A-154	Sequence 154, App
275	35	68.6	107	4	US-10-016-986-84	Sequence 84, Appl	348	34	66.7	11	3	US-09-968-561A-160	Sequence 160, App
276	35	68.6	107	4	US-10-309-762-86	Sequence 86, Appl	349	34	66.7	11	3	US-09-968-561A-166	Sequence 166, App
277	35	68.6	107	4	US-10-665-383-44	Sequence 44, Appl	350	34	66.7	11	3	US-09-968-561A-172	Sequence 172, App
278	35	68.6	107	5	US-10-665-383-48	Sequence 48, Appl	351	34	66.7	11	3	US-09-968-561A-178	Sequence 178, App
279	35	68.6	107	5	US-10-461-885-264	Sequence 14, Appl	352	34	66.7	11	3	US-09-968-561A-202	Sequence 202, App
280	35	68.6	107	5	US-10-727-155-264	Sequence 264, App	353	34	66.7	11	3	US-09-968-561A-208	Sequence 208, App
281	35	68.6	107	5	US-10-727-155-306	Sequence 306, App	354	34	66.7	11	3	US-09-968-561A-225	Sequence 225, App
282	35	68.6	107	5	US-10-893-576-178	Sequence 178, App	355	34	66.7	11	3	US-09-968-561A-232	Sequence 232, App
283	35	68.6	107	6	US-11-003-819-10	Sequence 10, Appl	356	34	66.7	11	3	US-09-968-561A-244	Sequence 244, App
284	35	68.6	107	6	US-11-021-715-71	Sequence 71, Appl	357	34	66.7	11	3	US-09-968-561A-250	Sequence 250, App
285	35	68.6	108	4	US-10-125-687-8	Sequence 8, Appl1	358	34	66.7	11	3	US-09-968-561A-256	Sequence 256, App
286	35	68.6	108	4	US-10-041-860-328	Sequence 328, App	359	34	66.7	11	3	US-09-968-561A-280	Sequence 280, App
287	35	68.6	108	4	US-10-016-986-109	Sequence 109, App	360	34	66.7	11	3	US-09-968-561A-292	Sequence 292, App
288	35	68.6	108	5	US-10-783-311-126	Sequence 126, App	361	34	66.7	11	3	US-09-968-744A-304	Sequence 304, App
289	35	68.6	108	5	US-10-725-962-36	Sequence 36, Appl	362	34	66.7	11	3	US-09-968-744A-340	Sequence 340, Appl
290	35	68.6	108	5	US-10-725-962-38	Sequence 38, Appl	363	34	66.7	11	3	US-09-968-744A-346	Sequence 346, Appl
291	35	68.6	108	5	US-10-725-962-39	Sequence 39, Appl	364	34	66.7	11	3	US-09-968-744A-34	Sequence 40, Appl
292	35	68.6	108	5	US-10-725-962-40	Sequence 40, Appl	365	34	66.7	11	3	US-09-968-744A-28	Sequence 28, Appl
293	35	68.6	108	5	US-10-625-307A-39	Sequence 39, Appl	366	34	66.7	11	3	US-09-968-744A-34	Sequence 40, Appl
294	35	68.6	108	5	US-10-625-307A-67	Sequence 67, Appl	367	34	66.7	11	3	US-09-968-744A-46	Sequence 46, Appl
295	35	68.6	108	5	US-10-996-191-8	Sequence 8, Appl1	368	34	66.7	11	3	US-09-968-744A-52	Sequence 52, Appl
296	35	68.6	109	4	US-10-320-231A-26	Sequence 26, Appl	369	34	66.7	11	3	US-09-968-744A-64	Sequence 64, Appl
297	35	68.6	109	5	US-10-835-641-3	Sequence 3, Appl1	370	34	66.7	11	3	US-09-968-744A-64	Sequence 100, App
298	35	68.6	109	5	US-10-867-506-26	Sequence 26, Appl	371	34	66.7	11	3	US-09-968-744A-100	Sequence 106, App
299	35	68.6	109	5	US-10-734-661A-91	Sequence 91, Appl	372	34	66.7	11	3	US-09-968-744A-106	Sequence 112, App
300	35	68.6	109	5	US-10-505-313-225	Sequence 225, App	373	34	66.7	11	3	US-09-968-744A-112	Sequence 118, App
301	35	68.6	110	4	US-10-251-215-41	Sequence 41, Appl	374	34	66.7	11	3	US-09-968-744A-118	Sequence 124, App
302	35	68.6	110	4	US-10-251-215-43	Sequence 43, Appl	375	34	66.7	11	3	US-09-968-744A-124	Sequence 136, App
303	35	68.6	113	4	US-10-364-743-44	Sequence 44, Appl	376	34	66.7	11	3	US-09-968-744A-136	Sequence 154, App
304	35	68.6	113	4	US-10-364-743-45	Sequence 45, Appl	377	34	66.7	11	3	US-09-968-744A-150	Sequence 160, App
305	35	68.6	113	4	US-10-364-743-46	Sequence 46, Appl	378	34	66.7	11	3	US-09-968-744A-154	Sequence 166, App
306	35	68.6	113	5	US-10-452-593-44	Sequence 44, Appl	379	34	66.7	11	3	US-09-968-744A-166	Sequence 172, App
307	35	68.6	113	5	US-10-452-593-45	Sequence 45, Appl	380	34	66.7	11	3	US-09-968-744A-172	Sequence 178, App
308	35	68.6	113	5	US-10-452-593-46	Sequence 46, Appl	381	34	66.7	11	3	US-09-968-744A-178	Sequence 202, App
309	35	68.6	125	5	US-10-473-887-48	Sequence 48, Appl	382	34	66.7	11	3	US-09-968-744A-202	Sequence 208, App
310	35	68.6	127	4	US-10-385-894-17	Sequence 17, Appl	383	34	66.7	11	3	US-09-968-744A-208	Sequence 226, App
311	35	68.6	127	4	US-10-695-667-17	Sequence 17, Appl	384	34	66.7	11	3	US-09-968-744A-226	Sequence 232, App
312	35	68.6	127	5	US-10-976-352-17	Sequence 17, Appl	385	34	66.7	11	3	US-09-968-744A-232	Sequence 244, App
313	35	68.6	129	5	US-10-893-576-28	Sequence 28, Appl	386	34	66.7	11	3	US-09-968-744A-244	Sequence 250, App
314	35	68.6	134	4	US-10-153-382-32	Sequence 32, Appl	387	34	66.7	11	3	US-09-968-744A-250	Sequence 256, App
315	35	68.6	134	5	US-10-612-497-23	Sequence 23, Appl	388	34	66.7	11	3	US-09-968-744A-256	Sequence 280, App
316	35	68.6	134	5	US-10-612-497-23	Sequence 23, Appl	389	34	66.7	11	3	US-09-968-744A-280	Sequence 292, App
317	35	68.6	134	5	US-10-776-649-23	Sequence 23, Appl	390	34	66.7	11	3	US-09-968-744A-280	Sequence 304, App
318	35	68.6	134	5	US-10-776-649-97	Sequence 97, Appl	391	34	66.7	11	3	US-09-968-744A-280	Sequence 304, App
319	35	68.6	134	6	US-11-085-368-32	Sequence 32, Appl	392	34	66.7	11	3	US-09-968-744A-304	Sequence 304, App

393	34	66.7	11	3	US-09-968-561A-10	Sequence 10, App1	466	34	66.7	11	6	US-11-115-682-250	Sequence 250, App
394	34	66.7	11	3	US-09-968-561A-16	Sequence 16, App1	467	34	66.7	11	6	US-11-115-682-256	Sequence 256, App
395	34	66.7	11	3	US-09-968-561A-22	Sequence 22, App1	468	34	66.7	11	6	US-11-115-682-280	Sequence 280, App
396	34	66.7	11	3	US-09-968-561A-28	Sequence 28, App1	469	34	66.7	11	6	US-11-115-682-292	Sequence 292, App
397	34	66.7	11	3	US-09-968-561A-34	Sequence 34, App1	470	34	66.7	11	6	US-11-115-682-304	Sequence 304, App
398	34	66.7	11	3	US-09-968-561A-40	Sequence 40, App1	471	34	66.7	61	4	US-10-379-151-18	Sequence 18, App1
399	34	66.7	11	3	US-09-968-561A-46	Sequence 46, App1	472	34	66.7	61	4	US-10-736-188-18	Sequence 18, App1
400	34	66.7	11	3	US-09-968-561A-52	Sequence 52, App1	473	34	66.7	73	4	US-10-078-958-13	Sequence 13, App1
401	34	66.7	11	3	US-09-968-561A-58	Sequence 58, App1	474	34	66.7	76	6	US-09-187-693-37	Sequence 37, App1
402	34	66.7	11	3	US-09-968-561A-64	Sequence 64, App1	475	34	66.7	76	6	US-11-021-795-37	Sequence 37, App1
403	34	66.7	11	3	US-09-968-561A-100	Sequence 100, App	476	34	66.7	81	4	US-10-425-115-339429	Sequence 339429, App
404	34	66.7	11	3	US-09-968-561A-106	Sequence 106, App	477	34	66.7	88	4	US-10-066-985-9	Sequence 9, App1
405	34	66.7	11	3	US-09-968-561A-112	Sequence 112, App	478	34	66.7	88	4	US-10-424-599-166302	Sequence 166302, App
406	34	66.7	11	3	US-09-968-561A-118	Sequence 118, App	479	34	66.7	88	5	US-10-887-698-1	Sequence 9, App1
407	34	66.7	11	3	US-09-968-561A-124	Sequence 124, App	480	34	66.7	88	5	US-10-194-975-54	Sequence 54, App1
408	34	66.7	11	3	US-09-968-561A-136	Sequence 136, App	481	34	66.7	95	4	US-10-194-975-55	Sequence 55, App1
409	34	66.7	11	3	US-09-968-561A-154	Sequence 154, App	482	34	66.7	95	4	US-10-194-975-87	Sequence 87, App1
410	34	66.7	11	3	US-09-968-561A-160	Sequence 160, App	483	34	66.7	95	4	US-10-125-687-22	Sequence 22, App1
411	34	66.7	11	3	US-09-968-561A-166	Sequence 166, App	484	34	66.7	95	4	US-10-153-362-39	Sequence 39, App1
412	34	66.7	11	3	US-09-968-561A-172	Sequence 172, App	485	34	66.7	95	4	US-10-308-817-1	Sequence 1, App1
413	34	66.7	11	3	US-09-968-561A-178	Sequence 178, App	486	34	66.7	95	4	US-10-308-817-2	Sequence 2, App1
414	34	66.7	11	3	US-09-968-561A-202	Sequence 202, App	487	34	66.7	95	4	US-10-308-817-34	Sequence 34, App1
415	34	66.7	11	3	US-09-968-561A-208	Sequence 208, App	488	34	66.7	95	4	US-10-309-762-65	Sequence 65, App1
416	34	66.7	11	3	US-09-968-561A-226	Sequence 226, App	489	34	66.7	95	4	US-10-453-698-1	Sequence 1, App1
417	34	66.7	11	3	US-09-968-561A-232	Sequence 232, App	490	34	66.7	95	4	US-10-453-698-2	Sequence 2, App1
418	34	66.7	11	3	US-09-968-561A-244	Sequence 244, App	491	34	66.7	95	4	US-10-453-698-1	Sequence 1, App1
419	34	66.7	11	3	US-09-968-561A-250	Sequence 250, App	492	34	66.7	95	4	US-10-453-698-2	Sequence 2, App1
420	34	66.7	11	3	US-09-968-561A-256	Sequence 256, App	493	34	66.7	95	4	US-10-379-392-78	Sequence 78, App1
421	34	66.7	11	3	US-09-968-561A-280	Sequence 280, App	494	34	66.7	95	4	US-10-379-392-94	Sequence 94, App1
422	34	66.7	11	3	US-09-968-561A-292	Sequence 292, App	495	34	66.7	95	5	US-10-612-427-94	Sequence 94, App1
423	34	66.7	11	3	US-09-968-561A-304	Sequence 304, App	496	34	66.7	95	5	US-10-776-649-94	Sequence 94, App1
424	34	66.7	11	4	US-10-161-145-6	Sequence 6, App1	497	34	66.7	95	5	US-10-776-649-94	Sequence 94, App1
425	34	66.7	11	4	US-10-203-754A-48	Sequence 48, App1	498	34	66.7	95	5	US-10-869-355-19	Sequence 19, App1
426	34	66.7	11	4	US-10-279-633-61	Sequence 61, App1	499	34	66.7	95	6	US-10-996-161-22	Sequence 22, App1
427	34	66.7	11	4	US-10-279-633-46	Sequence 46, App1	500	34	66.7	96	4	US-11-085-368-29	Sequence 29, App1
428	34	66.7	11	4	US-10-279-633-51	Sequence 51, App1	501	34	66.7	96	4	US-10-078-551-42	Sequence 42, App1
429	34	66.7	11	4	US-10-279-633-60	Sequence 60, App1	502	34	66.7	96	4	US-10-775-444A-42	Sequence 42, App1
430	34	66.7	11	4	US-10-279-633-61	Sequence 61, App1	503	34	66.7	102	4	US-10-078-958-14	Sequence 14, App1
431	34	66.7	11	4	US-10-632-706-245	Sequence 245, App	504	34	66.7	102	4	US-10-803-653-173	Sequence 173, App
432	34	66.7	11	5	US-10-396-578-89	Sequence 89, App1	505	34	66.7	102	5	US-10-803-653-173	Sequence 173, App
433	34	66.7	11	5	US-10-783-311-160	Sequence 160, App	506	34	66.7	103	3	US-10-916-840-42	Sequence 42, App1
434	34	66.7	11	5	US-10-783-311-200	Sequence 200, App	507	34	66.7	103	3	US-09-848-798-42	Sequence 42, App1
435	34	66.7	11	5	US-10-894-672-4	Sequence 4, App1	508	34	66.7	106	4	US-10-309-762-155	Sequence 155, App
436	34	66.7	11	5	US-10-891-658-132	Sequence 132, App	509	34	66.7	106	6	US-11-021-711-50	Sequence 50, App1
437	34	66.7	11	5	US-10-891-658-132	Sequence 132, App	510	34	66.7	106	6	US-11-021-711-50	Sequence 50, App1
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439	34	66.7	11	6	US-11-074-803-89	Sequence 89, App1	512	34	66.7	107	3	US-09-848-798-33	Sequence 33, App1
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442	34	66.7	11	6	US-11-115-682-16	Sequence 16, App1	515	34	66.7	107	3	US-09-848-798-39	Sequence 39, App1
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445	34	66.7	11	6	US-11-115-682-34	Sequence 34, App1	518	34	66.7	107	3	US-09-848-798-158	Sequence 158, App
446	34	66.7	11	6	US-11-115-682-40	Sequence 40, App1	519	34	66.7	107	3	US-09-848-798-168	Sequence 168, App
447	34	66.7	11	6	US-11-115-682-46	Sequence 46, App1	520	34	66.7	107	3	US-09-848-798-173	Sequence 173, App
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452	34	66.7	11	6	US-11-115-682-112	Sequence 112, App	525	34	66.7	107	4	US-10-268-883-6	Sequence 6, App1
453	34	66.7	11	6	US-11-115-682-118	Sequence 118, App	526	34	66.7	107	4	US-10-325-694-148	Sequence 148, App
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457	34	66.7	11	6	US-11-115-682-160	Sequence 160, App	530	34	66.7	107	4	US-10-309-762-67	Sequence 67, App1
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459	34	66.7	11	6	US-11-115-682-172	Sequence 172, App	532	34	66.7	107	4	US-10-309-762-88	Sequence 88, App1
460	34	66.7	11	6	US-11-115-682-178	Sequence 178, App	533	34	66.7	107	4	US-10-309-762-89	Sequence 89, App1
461	34	66.7	11	6	US-11-115-682-202	Sequence 202, App	534	34	66.7	107	4	US-10-363-349-4	Sequence 4, App1
462	34	66.7	11	6	US-11-115-682-208	Sequence 208, App	535	34	66.7	107	4	US-10-460-595-9	Sequence 9, App1
463	34	66.7	11	6	US-11-115-682-226	Sequence 226, App	536	34	66.7	107	4	US-10-251-095B-141	Sequence 141, App
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465	34	66.7	11	6	US-11-115-682-244	Sequence 244, App	538	34	66.7	107	4	US-10-737-252-141	Sequence 141, App

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540	34	66.7	107	5	US-10-927-155-308	Sequence 108, App	613	34	66.7	236	6	US-11-031-488-58	Sequence 58, App1
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542	34	66.7	107	5	US-10-891-658-89	Sequence 89, App1	615	34	66.7	240	3	US-09-968-561A-2	Sequence 2, App1
543	34	66.7	107	5	US-10-937-596-27	Sequence 27, App1	616	34	66.7	240	3	US-09-968-744A-2	Sequence 2, App1
544	34	66.7	107	5	US-10-977-369-8	Sequence 8, App1	617	34	66.7	240	3	US-09-968-561A-2	Sequence 2, App1
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548	34	66.7	107	5	US-10-977-369-46	Sequence 46, App1	621	34	66.7	260	4	US-10-293-418-1174	Sequence 1174, Ap
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552	34	66.7	107	5	US-10-977-369-53	Sequence 53, App1	625	34	66.7	315	4	US-10-406-830-10	Sequence 10, App1
553	34	66.7	107	5	US-10-977-369-56	Sequence 56, App1	626	34	66.7	329	5	US-10-774-3358A-2538	Sequence 2538, Ap
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565	34	66.7	108	4	US-10-016-986-102	Sequence 167, App	638	33	64.7	11	4	US-10-632-706-241	Sequence 241, App
566	34	66.7	108	4	US-10-409-814A-4	Sequence 102, App	639	33	64.7	11	5	US-10-396-578-17	Sequence 17, App1
567	34	66.7	108	4	US-10-744-774-15	Sequence 4, App1	640	33	64.7	11	5	US-10-783-311-280	Sequence 280, App
568	34	66.7	108	5	US-10-744-774-16	Sequence 15, App1	641	33	64.7	11	5	US-10-783-311-332	Sequence 312, App
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570	34	66.7	108	5	US-10-726-332-22	Sequence 22, App1	643	33	64.7	11	6	US-10-916-840-152	Sequence 17, App1
571	34	66.7	108	5	US-10-726-332-209	Sequence 28, App1	644	33	64.7	56	4	US-10-724-972A-5615	Sequence 5615, Ap
572	34	66.7	108	5	US-10-726-332-214	Sequence 209, App	645	33	64.7	95	3	US-09-158-120A-19	Sequence 19, App1
573	34	66.7	108	5	US-10-805-177-64	Sequence 214, App	646	33	64.7	95	3	US-09-158-120A-13	Sequence 33, App1
574	34	66.7	108	5	US-10-477-830-90	Sequence 64, App1	647	33	64.7	95	4	US-10-194-975-72	Sequence 72, App1
575	34	66.7	108	6	US-11-009-731-92	Sequence 90, App1	648	33	64.7	95	4	US-10-308-817-19	Sequence 19, App1
576	34	66.7	109	6	US-11-031-485-126	Sequence 92, App1	649	33	64.7	95	4	US-10-453-698-19	Sequence 19, App1
577	34	66.7	109	4	US-10-330-613-10	Sequence 126, App	650	33	64.7	103	3	US-10-379-392-59	Sequence 59, App1
578	34	66.7	109	4	US-10-330-530-10	Sequence 10, App1	651	33	64.7	106	4	US-09-791-153A-70	Sequence 70, App1
579	34	66.7	109	4	US-10-408-901-8	Sequence 10, App1	652	33	64.7	106	4	US-10-466-242-44	Sequence 44, App1
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581	34	66.7	110	4	US-10-251-0858-276	Sequence 10, App1	654	33	64.7	107	3	US-09-982-464-1	Sequence 1, App1
582	34	66.7	110	4	US-10-251-0858-277	Sequence 276, App	655	33	64.7	107	4	US-10-011-931-4	Sequence 4, App1
583	34	66.7	110	4	US-10-251-0858-278	Sequence 277, App	656	33	64.7	107	4	US-10-233-996-3	Sequence 3, App1
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587	34	66.7	111	4	US-10-203-754A-56	Sequence 56, App1	660	33	64.7	107	5	US-10-697-399-1	Sequence 1, App1
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589	34	66.7	111	5	US-10-726-332-216	Sequence 216, App	662	33	64.7	108	3	US-09-848-798-41	Sequence 41, App1
590	34	66.7	111	5	US-10-726-332-220	Sequence 220, App	663	33	64.7	108	4	US-10-371-942-8	Sequence 8, App1
591	34	66.7	111	5	US-10-726-332-221	Sequence 221, App	664	33	64.7	108	4	US-10-371-942-20	Sequence 20, App1
592	34	66.7	113	4	US-10-364-743-55	Sequence 55, App1	665	33	64.7	108	4	US-10-371-942-20	Sequence 20, App1
593	34	66.7	113	5	US-10-452-593-55	Sequence 55, App1	666	33	64.7	109	5	US-10-744-774-17	Sequence 17, App1
594	34	66.7	113	5	US-10-916-758-78	Sequence 78, App1	667	33	64.7	109	4	US-10-371-942-76	Sequence 76, App1
595	34	66.7	114	4	US-10-452-593-54	Sequence 54, App1	668	33	64.7	109	4	US-10-371-942-76	Sequence 76, App1
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597	34	66.7	116	5	US-10-783-311-158	Sequence 158, App	670	33	64.7	112	5	US-10-916-758-66	Sequence 66, App1
598	34	66.7	116	5	US-10-783-311-198	Sequence 198, App	671	33	64.7	113	3	US-10-114-716A-48	Sequence 48, App1
599	34	66.7	116	5	US-10-916-758-38	Sequence 38, App1	672	33	64.7	113	5	US-10-930-548-48	Sequence 48, App1
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601	34	66.7	127	4	US-10-309-762-101	Sequence 101, App	674	33	64.7	116	5	US-10-783-311-278	Sequence 278, App
602	34	66.7	127	4	US-10-395-894-25	Sequence 25, App1	675	33	64.7	116	5	US-10-783-311-310	Sequence 310, App
603	34	66.7	127	5	US-10-695-667-25	Sequence 25, App1	676	33	64.7	128	5	US-10-473-287-35	Sequence 35, App1
604	34	66.7	127	5	US-10-976-352-25	Sequence 25, App1	677	33	64.7	128	5	US-10-473-287-50	Sequence 50, App1
605	34	66.7	137	6	US-10-390-986-24	Sequence 24, App1	678	33	64.7	129	4	US-10-478-056-13	Sequence 13, App1
606	34	66.7	157	6	US-11-131-648-27	Sequence 27, App1	679	33	64.7	130	4	US-10-443-466A-25	Sequence 25, App1
607	34	66.7	157	6	US-11-131-648-63	Sequence 63, App1	680	33	64.7	131	4	US-10-207-655-244	Sequence 244, App
608	34	66.7	214	5	US-10-916-758-20	Sequence 20, App1	681	33	64.7	131	5	US-10-627-556-33	Sequence 33, App1
609	34	66.7	215	4	US-10-408-901-32	Sequence 32, App1	682	33	64.7	133	5	US-10-627-556-33	Sequence 33, App1
610	34	66.7	224	3	US-09-453-234-36	Sequence 36, App1	683	33	64.7	133	6	US-10-174-693-277	Sequence 277, App
611	34	66.7	224	3	US-09-453-234-48	Sequence 48, App1	684	33	64.7	133	6	US-11-097-143-16461	Sequence 16461, A

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687	33	64.7	153	4	US-10-424-599-229875	Sequence 229875, A	760	32	62.7	107	3	US-09-892-613C-10	Sequence 8, Appl
688	33	64.7	189	3	US-09-895-913A-14	Sequence 14, Appl	761	32	62.7	107	3	US-09-851-614-2	Sequence 2, Appl
689	33	64.7	212	5	US-10-513-725-8	Sequence 47, Appl	762	32	62.7	107	4	US-10-035-637-2	Sequence 21, Appl
690	33	64.7	215	3	US-09-791-153A-47	Sequence 47, Appl	763	32	62.7	107	4	US-10-127-890-149	Sequence 149, App
691	33	64.7	221	4	US-10-282-122A-67808	Sequence 67808, A	764	32	62.7	107	4	US-10-340-189-13	Sequence 13, Appl
692	33	64.7	223	4	US-10-693-629-62	Sequence 62, Appl	765	32	62.7	107	4	US-10-325-696-13	Sequence 13, Appl
693	33	64.7	236	4	US-10-719-642-62	Sequence 62, Appl	766	32	62.7	107	4	US-10-251-085B-145	Sequence 145, App
694	33	64.7	236	4	US-11-031-485-20	Sequence 20, Appl	767	32	62.7	107	4	US-10-723-434-21	Sequence 21, Appl
695	33	64.7	243	4	US-10-097-558-2	Sequence 2, Appl	768	32	62.7	107	4	US-10-723-434-26	Sequence 26, Appl
696	33	64.7	243	4	US-10-097-558-3	Sequence 3, Appl	769	32	62.7	107	4	US-10-723-434-31	Sequence 31, Appl
697	33	64.7	243	5	US-10-505-658-2	Sequence 2, Appl	770	32	62.7	107	4	US-10-723-434-35	Sequence 35, Appl
698	33	64.7	243	5	US-10-505-658-3	Sequence 3, Appl	771	32	62.7	107	4	US-10-737-252-145	Sequence 145, App
699	33	64.7	245	5	US-11-017-030-65	Sequence 65, Appl	772	32	62.7	107	4	US-10-741-657A-16	Sequence 16, Appl
700	33	64.7	261	6	US-10-424-559-280021	Sequence 280021, A	773	32	62.7	107	5	US-10-769-147-8	Sequence 8, Appl
701	33	64.7	267	4	US-10-207-655-248	Sequence 248, App	774	32	62.7	107	5	US-10-473-977-69	Sequence 69, Appl
702	33	64.7	267	4	US-10-425-115-303734	Sequence 303734, A	775	32	62.7	107	5	US-10-482-759-10	Sequence 10, Appl
703	33	64.7	267	5	US-10-627-556-36	Sequence 36, Appl	776	32	62.7	107	5	US-10-717-243-149	Sequence 149, App
704	33	64.7	276	4	US-10-320-797-3078	Sequence 3078, Ap	777	32	62.7	107	5	US-10-949-135-10	Sequence 10, Appl
705	33	64.7	293	4	US-10-425-115-303735	Sequence 303735, A	778	32	62.7	107	5	US-10-490-535-4	Sequence 4, Appl
706	33	64.7	313	4	US-10-291-265-427	Sequence 427, App	779	32	62.7	107	5	US-10-837-904-115	Sequence 115, Appl
707	33	64.7	319	4	US-10-335-394-16	Sequence 16, Appl	780	32	62.7	107	5	US-10-938-992-17	Sequence 17, Appl
708	33	64.7	361	4	US-10-335-394-13	Sequence 13, Appl	781	32	62.7	107	5	US-10-903-131-8	Sequence 8, Appl
709	33	64.7	363	4	US-10-291-265-335	Sequence 335, App	782	32	62.7	107	6	US-11-133-775-13	Sequence 13, Appl
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711	33	64.7	374	4	US-10-425-114-63625	Sequence 63625, A	784	32	62.7	108	4	US-10-140-555-4	Sequence 67, Appl
712	33	64.7	391	4	US-10-369-493-22382	Sequence 22382, A	785	32	62.7	109	3	US-09-905-243-67	Sequence 67, Appl
713	33	64.7	393	4	US-10-425-114-56946	Sequence 56946, A	786	32	62.7	109	6	US-11-009-321-67	Sequence 57, Appl
714	33	64.7	404	4	US-10-369-493-15297	Sequence 15297, A	787	32	62.7	111	4	US-10-763-74A-57	Sequence 57, Appl
715	33	64.7	493	4	US-10-207-655-266	Sequence 266, App	788	32	62.7	116	5	US-10-783-311-326	Sequence 326, App
716	33	64.7	552	4	US-10-627-556-50	Sequence 50, Appl	789	32	62.7	126	5	US-10-837-904-64	Sequence 64, Appl
717	33	64.7	552	5	US-10-425-115-303736	Sequence 303736, A	790	32	62.7	126	5	US-10-837-904-68	Sequence 68, Appl
718	33	64.7	564	4	US-09-815-242-11517	Sequence 11517, A	791	32	62.7	127	4	US-10-084-139-2	Sequence 2, Appl
719	33	64.7	656	3	US-10-282-122A-58751	Sequence 58751, A	792	32	62.7	127	4	US-10-084-139-6	Sequence 6, Appl
720	33	64.7	656	4	US-10-335-977-7466	Sequence 7466, Ap	793	32	62.7	127	4	US-10-395-894-21	Sequence 21, Appl
721	33	64.7	656	4	US-11-097-143-13011	Sequence 13011, A	794	32	62.7	127	4	US-10-695-667-21	Sequence 21, Appl
722	33	64.7	697	6	US-10-207-655-350	Sequence 350, App	795	32	62.7	127	5	US-10-837-904-39	Sequence 39, Appl
723	33	64.7	768	4	US-10-627-556-115	Sequence 115, App	796	32	62.7	127	5	US-10-837-904-47	Sequence 47, Appl
724	33	64.7	1007	4	US-10-437-963-177533	Sequence 177533, A	797	32	62.7	127	5	US-10-976-352-21	Sequence 21, Appl
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726	33	64.7	1045	4	US-10-425-115-213295	Sequence 213295, A	799	32	62.7	130	5	US-10-683-431-35	Sequence 35, Appl
727	33	64.7	1360	4	US-09-968-744A-268	Sequence 268, App	800	32	62.7	131	2	US-08-779-784-21	Sequence 21, Appl
728	33	64.7	1360	4	US-10-192-854-153	Sequence 153, App	801	32	62.7	131	4	US-10-010-729-64	Sequence 64, Appl
729	32	62.7	11	3	US-09-974-449-46	Sequence 46, Appl	802	32	62.7	134	4	US-10-437-963-152265	Sequence 152265, A
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731	32	62.7	11	3	US-10-203-754A-51	Sequence 51, Appl	804	32	62.7	166	5	US-10-275-555A-12	Sequence 12, Appl
732	32	62.7	11	3	US-09-977-797A-18	Sequence 18, Appl	805	32	62.7	201	4	US-09-974-449-36	Sequence 36, Appl
733	32	62.7	11	3	US-09-968-744A-268	Sequence 268, App	806	32	62.7	211	3	US-10-660-148-9	Sequence 9, Appl
734	32	62.7	11	3	US-10-769-144-16	Sequence 16, Appl	807	32	62.7	233	4	US-10-769-144-6	Sequence 6, Appl
735	32	62.7	11	3	US-10-473-977-18	Sequence 18, App	808	32	62.7	233	5	US-10-903-191-6	Sequence 80, Appl
736	32	62.7	11	4	US-10-783-311-338	Sequence 328, App	809	32	62.7	233	5	US-10-935-280-80	Sequence 80, Appl
737	32	62.7	11	4	US-10-725-962-102	Sequence 102, App	810	32	62.7	239	5	US-09-880-748-1577	Sequence 1577, App
738	32	62.7	11	4	US-10-949-135-12	Sequence 12, Appl	811	32	62.7	241	3	US-10-293-418-1577	Sequence 1577, App
739	32	62.7	11	5	US-10-903-191-16	Sequence 16, Appl	812	32	62.7	242	4	US-09-880-748-1915	Sequence 1915, App
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840	32	62.7	495	5	US-10-697-340-328	Sequence 328, App	913	31	60.8	62	4	US-10-379-151-19	Sequence 19, App1
841	32	62.7	498	5	US-10-723-860-1227	Sequence 1227, Ap	914	31	60.8	72	4	US-10-736-188-19	Sequence 19, App1
842	32	62.7	498	6	US-11-050-926-328	Sequence 328, App	915	31	60.8	79	4	US-10-425-115-223534	Sequence 223534,
843	32	62.7	534	4	US-10-282-122A-55599	Sequence 55599, A	916	31	60.8	83	4	US-10-408-768A-1468	Sequence 1468, Ap
844	32	62.7	534	4	US-10-437-963-1197953	Sequence 1197953,	917	31	60.8	88	3	US-09-905-243-31	Sequence 31, App1
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847	32	62.7	554	4	US-10-352-843-8	Sequence 8, App1	920	31	60.8	92	5	US-10-672-932-12	Sequence 12, App1
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851	32	62.7	602	4	US-10-282-122A-49703	Sequence 49703, A	924	31	60.8	103	4	US-10-379-392-99	Sequence 99, App1
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853	32	62.7	641	4	US-10-369-493-2165	Sequence 2165, Ap	926	31	60.8	106	3	US-09-848-798-171	Sequence 171, App
854	32	62.7	661	3	US-09-988-626-240	Sequence 240, App	927	31	60.8	106	4	US-10-096-246-15	Sequence 15, App1
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871	32	62.7	868	4	US-10-282-122A-58502	Sequence 58502, A	944	31	60.8	107	4	US-10-723-433-43	Sequence 43, App1
872	32	62.7	868	4	US-10-282-122A-58502	Sequence 58502, A	945	31	60.8	107	5	US-10-482-630-95	Sequence 95, App1
873	32	62.7	868	4	US-10-282-122A-67041	Sequence 67041, A	946	31	60.8	107	5	US-10-482-630-97	Sequence 97, App1
874	32	62.7	869	4	US-10-282-122A-67602	Sequence 67602, A	947	31	60.8	107	5	US-10-822-300-8	Sequence 8, App1
875	32	62.7	869	4	US-10-282-122A-69531	Sequence 69531, A	948	31	60.8	107	5	US-10-822-300-8	Sequence 8, App1
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898	31	60.8	11	4	US-10-279-633-54	Sequence 54, App1	971	31	60.8	107	5	US-10-672-932-10	Sequence 10, App1
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902	31	60.8	11	5	US-10-482-630-118	Sequence 118, App	975	31	60.8	107	6	US-11-029-574-14	Sequence 14, App1
903	31	60.8	11	5	US-10-482-630-121	Sequence 121, App	976	31	60.8	107	6	US-11-029-574-15	Sequence 15, App1
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982 31 60.8 109 3 US-09-798-058-4 Sequence 4, Appl
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988 31 60.8 116 5 US-10-783-311-174 Sequence 11, App
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ALIGNMENTS

RESULT 1
US-09-795-798-13
Sequence 13, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-795-798-13
Query Match 100.0%; Score 51; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
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Db 1 RASKTISKYLA 11

RESULT 2
US-10-727-737-53
Sequence 53, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.

TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-727-737-53

Query Match 100.0%; Score 51; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||||
Db 1 RASKTISKYLA 11

RESULT 3
US-09-795-798-1
Sequence 1, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.

TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-795-798-1

Query Match 100.0%; Score 51; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||
Db 24 RASKTISKYLA 34

RESULT 4
US-09-795-798-2
Sequence 2, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-795-798-2

Query Match 100.0%; Score 51; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||
Db 24 RASKTISKYLA 34

RESULT 5
US-10-727-737-1
Sequence 1, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-727-737-1

Query Match 100.0%; Score 51; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||
Db 24 RASKTISKYLA 34


```
RESULT 9
US-10-423-299-3
; Sequence 3, Application US/104232299
; Publication No. US20030229212A1
; GENERAL INFORMATION:
; APPLICANT: FAHRNER, ROBERT
; APPLICANT: FOLLMAN, DEBORAH
; APPLICANT: LEBRETON, BENEDICTE
; APPLICANT: VAN REIS, ROBERT
; TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
; FILE REFERENCE: 39766-0121A
; CURRENT FILING DATE: US/10/423,299
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/375,953
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-423-299-3

Query Match          100.0%; Score 51; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASKTISKXYLA 11
        |||||
Db      24 RASKTISKXYLA 34

RESULT 10
US-10-010-729-23
; Sequence 23, Application US/100107729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-23

Query Match          92.2%; Score 47; DB 4; Length 101;
Best Local Similarity 90.9%; Pred. No. 0.43;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASKTISKXYLA 11
```

```
Db      24 RASKSISKXYLA 34

RESULT 11
US-10-010-729-43
; Sequence 43, Application US/100107729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-43

Query Match          92.2%; Score 47; DB 4; Length 108;
Best Local Similarity 90.9%; Pred. No. 0.46;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASKTISKXYLA 11
        |||||
Db      24 RASKSISKXYLA 34

RESULT 12
US-09-809-739-2
; Sequence 2, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)-(11)
; OTHER INFORMATION: CDR1 of YFC51.1 light chain
; OTHER INFORMATION: Rat
US-09-809-739-2
```

Query Match 76.5%; Score 39; DB 3; Length 11;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
:||||:||||
Db 1 KASKSISNYLA 11

RESULT 13
US-09-378-967-4
; Sequence 4, Application US/09378967
; Publication No. US20030185818A1
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN J.
; APPLICANT: CROME, J. SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,967
; FILING DATE: 23-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,313
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,067
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01289
; FILING DATE: 15-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9115364.3
; FILING DATE: 16-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WENDLER, HELEN E.
; REGISTRATION NUMBER: 37,964
; REFERENCE/DOCKET NUMBER: LYNX91-01A3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-378-967-4

Query Match 76.5%; Score 39; DB 3; Length 11;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
:||||:||||
Db 1 KASKSISNYLA 11

RESULT 14

US-10-783-311-248
; Sequence 248, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 248
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-248

Query Match 76.5%; Score 39; DB 5; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.4;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
:||||:||||
Db 1 RASQSVSRXYLA 11

RESULT 15
US-10-484-790A-4
; Sequence 4, Application US/10484790A
; Publication No. US20050070694A1
; GENERAL INFORMATION:
; APPLICANT: Gellanova, et al., Valentina
; TITLE OF INVENTION: Antagonistic Anti-RTNFR313b Human Antibodies
; FILE REFERENCE: X-15239
; CURRENT APPLICATION NUMBER: US/10/484,790A
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-484-790A-4

Query Match 76.5%; Score 39; DB 5; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.4;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
:||||:||||
Db 1 RASQSVSRXYLA 11

RESULT 16
US-10-662-061-2
; Sequence 2, Application US/10662061
; Publication No. US20050214299A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia E.
; APPLICANT: Horvath, Christopher J.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855, 1069-003
; CURRENT APPLICATION NUMBER: US/10/662,061
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US/09/809,739
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267

PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 11
TYPE: PRP
ORGANISM: Unknown
FEATURE:
NAME/KEY: SITE
LOCATION: (1)...(11)
OTHER INFORMATION: CDRI of YFC51.1 light chain
FEATURE:
OTHER INFORMATION: Rat
US-10-662-061-2

Query Match 76.5%; Score 39; DB 5; Length 11;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
Db 1 RASKSISNYLA 11

RESULT 17
US-09-905-243-32

Sequence 32, Application US/09905243
Patent No. US2002006209A1
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 88
TYPE: PRP
ORGANISM: Pan troglodytes
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (24)...(34)
OTHER INFORMATION: CDRI
NAME/KEY: DOMAIN
LOCATION: (50)...(66)
OTHER INFORMATION: CDRII
US-09-905-243-32

Query Match 76.5%; Score 39; DB 3; Length 88;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
Db 24 RASQSVSRYLA 34

RESULT 18
US-11-099-331-32

Sequence 32, Application US/11099331
Publication No. US20050208625A1
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/11/099,331
CURRENT FILING DATE: 2005-04-05
PRIOR APPLICATION NUMBER: US/09/905,243

PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 88
TYPE: PRP
ORGANISM: Pan troglodytes
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (24)...(34)
OTHER INFORMATION: CDRI
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (50)...(66)
OTHER INFORMATION: CDRII
US-11-099-331-32

Query Match 76.5%; Score 39; DB 6; Length 88;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
Db 24 RASQSVSRYLA 34

RESULT 19
US-08-844-215-9

Sequence 9, Application US/08844215
Publication No. US20020016445A1
GENERAL INFORMATION:
APPLICANT: PERSSON, MATS AXEL
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
HEPATITIS C VIRUS (HCV) E2 ANTIGEN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,215
FILING DATE: 17-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/635,109
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 80146,002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-844-215-9

Query Match 76.5%; Score 39; DB 2; Length 105;
Best Local Similarity 63.6%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:|:|
Db 23 RASQSVNRYLA 33

RESULT 20

US-10-484-790A-2
; Sequence 2, Application US/10484790A
; Publication No. US20050070694A1
; GENERAL INFORMATION:
; APPLICANT: Gelfanova, et al.; Valentina
; TITLE OF INVENTION: Antagonistic Anti-htnfsf1b Human Antibodies
; FILE REFERENCE: X-15239
; CURRENT APPLICATION NUMBER: US/10/484,790A
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-484-790A-2

Query Match 76.5%; Score 39; DB 5; Length 109;
Best Local Similarity 63.6%; Pred. No. 15;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:|:|
Db 24 RASQSVNRYLA 34

RESULT 21

US-10-783-311-246
; Sequence 246, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-246

Query Match 76.5%; Score 39; DB 5; Length 115;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:|:|
Db 25 RASQSVNRYLA 35

RESULT 22

US-09-809-739-1
; Sequence 1, Application US/09809739
; Patent No. US2020106369A1
; GENERAL INFORMATION:

; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis

; FILE REFERENCE: 1955.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Unknown

; NAME/KEY: SITE
; LOCATION: (1)...(125)
; OTHER INFORMATION: YFC51.1 light chain variable region with signal
; OTHER INFORMATION: sequence
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: Rat
US-09-809-739-1

Query Match 76.5%; Score 39; DB 3; Length 125;
Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:|:|
Db 44 RASKSISNYLA 54

RESULT 23

US-09-378-967-2
; Sequence 2, Application US/09378967
; Publication No. US20030185818A1
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, HERMAN
; APPLICANT: SIMS, MARTIN J.
; APPLICANT: CROME, J. SCOTT
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST CD18
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILITIA DRIVE
; CITY: LEXINGTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,967
; FILING DATE: 23-AUG-1999
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,313
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,067
; FILING DATE: 23-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01289
; FILING DATE: 15-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 915364.3
; FILING DATE: 16-JUL-1991
; ATTORNEY/AGENT INFORMATION:

NAME: WENDLER, HELEN E.
REGISTRATION NUMBER: 37,964
REFERENCE/DOCKET NUMBER: LYNX91-01A3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-9540
TELEFAX: (781) 861-6240
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-378-967-2

Query Match 76.5%; Score 39; DB 3; Length 125;
Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
:|||||
Db 44 KASKSISNYLA 54

RESULT 24
US-10-662-061-1
Sequence 1, Application US/10662061
Publication No. US20050214299A1
GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
FILE REFERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: US/10/662,061
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US/09/809,739
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 125
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: SITE
LOCATION: (1)...(125)
OTHER INFORMATION: YFCS1.1 light chain variable region with signal
OTHER INFORMATION: sequence
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(20)
OTHER INFORMATION: Rat
US-10-662-061-1

Query Match 76.5%; Score 39; DB 5; Length 125;
Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
:|||||
Db 44 KASKSISNYLA 54

RESULT 25
US-09-809-739-10
Sequence 10, Application US/09809739
Patent No. US20020106369A1
GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
TITLE OF INVENTION: Method of Inhibiting Stenosis and

TITLE OF INVENTION: Restenosis
FILE REFERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 127
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized light chain variable region with signal
OTHER INFORMATION: sequence
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-09-809-739-10

Query Match 76.5%; Score 39; DB 3; Length 127;
Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
:|||||
Db 43 KASKSISNYLA 53

RESULT 26
US-10-662-061-10
Sequence 10, Application US/10662061
Publication No. US20050214299A1
GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
FILE REFERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: US/10/662,061
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US/09/809,739
PRIOR FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 127
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized light chain variable region with signal
OTHER INFORMATION: sequence
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-10-662-061-10

Query Match 76.5%; Score 39; DB 5; Length 127;
Best Local Similarity 72.7%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
:|||||
Db 43 KASKSISNYLA 53

RESULT 27
US-10-484-790A-19
Sequence 19, Application US/10484790A
Publication No. US20050070694A1
GENERAL INFORMATION:
APPLICANT: Gelfanova, et al., Valentina

```

; TITLE OF INVENTION: Antagonistic Anti-HTNFS13b Human Antibodies
; FILE REFERENCE: X-15239
; CURRENT APPLICATION NUMBER: US/10/484,790A
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-484-790A-19
```

```

Query Match          76.5%; Score 39; DB 5; Length 214;
Best Local Similarity 63.6%; Pred. No. 31;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 RASKTISKYLA 11
      |||:|:|
Db      24 RASQSVSRYLE 34
```

```

RESULT 28
US-10-404-724-68
; Sequence 68, Application US/10404724
; Publication No. US20030203447A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; FILE REFERENCE: 13698US01
; CURRENT APPLICATION NUMBER: US/10/404,724
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-724-68
```

```

Query Match          76.5%; Score 39; DB 4; Length 233;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 RASKTISKYLA 11
      |||:|:|
Db      43 KASKSISNYLA 53
```

```

RESULT 29
US-09-848-832-4
; Sequence 4, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
; APPLICANT: Hooper, Douglas
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
; FILE REFERENCE: H0001.NP0002
; CURRENT APPLICATION NUMBER: US/09/848,832
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-848-832-4
```

```

Query Match          76.5%; Score 39; DB 3; Length 234;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 RASKTISKYLA 11
      |||:|:|
Db      44 RASQTASRYLA 54
```

```

RESULT 30
US-10-225-108A-4
; Sequence 4, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225,108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-4
```

```

Query Match          76.5%; Score 39; DB 4; Length 234;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 RASKTISKYLA 11
      |||:|:|
Db      44 RASQTASRYLA 54
```

```

RESULT 31
US-10-461-148-2
; Sequence 2, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 8321-110C11-185685
; CURRENT APPLICATION NUMBER: US/10/461,148
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 10/225,108
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Human
US-10-461-148-2
```

```

Query Match          76.5%; Score 39; DB 4; Length 234;
```

Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:||||
Db 44 RASQTSISYLA 54

RESULT 32

US-10-279-633-50
; Sequence 50, Application US/10279633
; Publication No. US20040005709A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Somers, Veerle
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; FILE REFERENCE: 10280-027001
; CURRENT APPLICATION NUMBER: US/10/279,633
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-633-50

Query Match 74.5%; Score 38; DB 4; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
|||:||||
Db 1 RASQTIKRYL 10

RESULT 33

US-10-279-633-52
; Sequence 52, Application US/10279633
; Publication No. US20040005709A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Somers, Veerle
; TITLE OF INVENTION: HYBRIDIZATION CONTROL OF SEQUENCE
; FILE REFERENCE: 10280-027001
; CURRENT APPLICATION NUMBER: US/10/279,633
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 60/343,954
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-633-52

Query Match 74.5%; Score 38; DB 4; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.1;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
|||:||||
Db 1 RASQTSISYLA 10

RESULT 34

US-10-016-986-106
; Sequence 106, Application US/10016986

Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-106

Query Match 74.5%; Score 38; DB 4; Length 104;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
|||:||||
Db 19 RASQTSISYLA 28

RESULT 35

US-10-268-501-5
; Sequence 51, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain consensus sequence
US-10-268-501-5

Query Match 74.5%; Score 38; DB 4; Length 107;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:||||
Db 24 RASQTSISYLA 34

```
RESULT 36
US-10-608-626-5
; Sequence 5, Application US/10608626
; Publication No. US2004001367A1
; GENERAL INFORMATION:
; APPLICANT: Kelsey, Stephen M.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P2
; CURRENT APPLICATION NUMBER: US/10/608,626
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 10/268,501
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain consensus sequence
US-10-608-626-5

Query Match          74.5%; Score 38; DB 4; Length 107;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 37
US-10-600-152-14
; Sequence 14, Application US/10600152
; Publication No. US20040037824A1
; GENERAL INFORMATION:
; APPLICANT: Baugman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/10/600,152
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: 09/648,067
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-10-600-152-14

Query Match          74.5%; Score 38; DB 4; Length 107;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 38
US-10-619-754-5
; Sequence 5, Application US/10619754

Publication No. US20040106161A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Koll, Hans
; APPLICANT: Bossemater, Birgit
; APPLICANT: Muller, Hans-Joachim
; APPLICANT: Sliwowski, Mark
; APPLICANT: Kelsey, Stephen
; TITLE OF INVENTION: Methods For Identifying Tumors That Are
; Responsive To Treatment With Anti-ErbB2 Antibodies
; FILE REFERENCE: 39766-0114A
; CURRENT APPLICATION NUMBER: US/10/619,754
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 60/396,290
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US 60/480,043
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-619-754-5

Query Match          74.5%; Score 38; DB 4; Length 107;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 39
US-10-723-434-16
; Sequence 16, Application US/10723434
; Publication No. US2004013357A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Pingyu
; APPLICANT: Luo, Peizhi
; APPLICANT: Wang, Kevin C.
; APPLICANT: Hsieh, Mark
; APPLICANT: Li, Yan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 26050-709,501
; CURRENT APPLICATION NUMBER: US/10/723,434
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/153,176
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/443,134
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL
US-10-723-434-16

Query Match          74.5%; Score 38; DB 4; Length 107;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34
```

RESULT 40
US-10-835-641-18
; Sequence 18, Application US/10835641
; Publication No. US20040236078A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Prestia, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/835,641
; FILING DATE: 30-Apr-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-Nov-2000
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-Nov-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-Jun-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-10-835-641-18
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
; US-10-835-641-18
; Query Match 74.5%; Score 38; DB 5; Length 107;
; Best Local Similarity 72.7%; Pred. No. 23;
; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; QY 1 RASKTISKYLA 11
; |||:|||||
; Db 24 RASQSIISNYLA 34
; |||:|||||
; RESULT 41
US-10-473-977-72
; Sequence 72, Application US/10473977
; Publication No. US2004025323A1
; GENERAL INFORMATION:
; APPLICANT: MATEO DE ACOSTA DEL RIO, Cristina M. et al
; TITLE OF INVENTION: GANGLIOSIDE-ASSOCIATED RECOMBINANT ANTIBODIES AND THE USE THEREOF
; FILE REFERENCE: 4565-0107P
; CURRENT APPLICATION NUMBER: US/10/473,977
; FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: PCT/US02/00003
; PRIOR FILING DATE: 2002-04-06
; PRIOR APPLICATION NUMBER: CU 84/2001
; PRIOR FILING DATE: 2001-04-06

; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(107)
US-10-473-977-72
; Query Match 74.5%; Score 38; DB 5; Length 107;
; Best Local Similarity 80.0%; Pred. No. 23;
; Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
; QY 1 RASKTISKYL 10
; |||:|||||
; Db 24 RASZTISYLA 33
; |||:|||||
; RESULT 42
US-10-719-310-5
; Sequence 5, Application US/10719310
; Publication No. US2004025865A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; APPLICANT: Sliwkowski, Mark X.
; TITLE OF INVENTION: THERAPY OF NON-MALIGNANT DISEASES OR DISORDERS WITH
; FILE REFERENCE: P1979R1
; CURRENT APPLICATION NUMBER: US/10/719,310
; FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/428,027
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-719-310-5
; Query Match 74.5%; Score 38; DB 5; Length 107;
; Best Local Similarity 72.7%; Pred. No. 23;
; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; QY 1 RASKTISKYLA 11
; |||:|||||
; Db 24 RASQSIISNYLA 34
; |||:|||||
; RESULT 43
US-10-916-840-158
; Sequence 158, Application US/10916840
; Publication No. US20050136053A1
; GENERAL INFORMATION:
; APPLICANT: Hufton, Simon E.
; APPLICANT: Hoet, Rene
; APPLICANT: Pieters, Henk
; APPLICANT: Kent, Rachel Baribault
; APPLICANT: Rookey, Kristen
; TITLE OF INVENTION: TIR1-BINDING LIGANDS
; FILE REFERENCE: 10280-083001
; CURRENT APPLICATION NUMBER: US/10/916,840
; FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 107
; TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated oligonucleotide
US-10-916-840-158

Query Match 74.5%; Score 38; DB 5; Length 107;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
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DB 24 RASQSISSYLA 34

RESULT 44
US-11-044-749-5
Sequence 5, Application US/11044749
Publication No. US20050208043A1
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Presta, Leonard G.
APPLICANT: Sliwowski, Mark X.
TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
FILE REFERENCE: P1467R2
CURRENT APPLICATION NUMBER: US/11/044,749
CURRENT FILING DATE: 2005-01-27
PRIOR APPLICATION NUMBER: US/09/602,812
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141,316
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 5
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: light chain consensus sequence
US-11-044-749-5

Query Match 74.5%; Score 38; DB 6; Length 107;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||::|||
DB 24 RASQSISSYLA 34

RESULT 45
US-11-154-465-5
Sequence 5, Application US/11154465
Publication No. US20050238640A1
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Presta, Leonard G.
APPLICANT: Sliwowski, Mark X.
TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
FILE REFERENCE: P1467R2
CURRENT APPLICATION NUMBER: US/11/154,465
CURRENT FILING DATE: 2005-06-16
PRIOR APPLICATION NUMBER: US/09/602,812
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141,316
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 5
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: light chain consensus sequence

US-11-154-465-5

Query Match 74.5%; Score 38; DB 6; Length 107;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||::|||
DB 24 RASQSISSYLA 34

RESULT 46
US-09-056-160B-12
Sequence 12, Application US/09056160B
Patent No. US20020032315A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
APPLICANT: Wells, James A.
APPLICANT: Presta, Leonard G.
APPLICANT: Loman, Henry B.
APPLICANT: Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,160B
FILING DATE: 06-Apr-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/054,856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1093R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/225-1896
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-160B-12

Query Match 74.5%; Score 38; DB 3; Length 108;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||::|||
DB 24 RASQSISSYLA 34

RESULT 47
US-09-795-798-3
Sequence 3, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies

US-10-727-737-3

Query Match 74.5%; Score 38; DB 4; Length 108;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
|||:|
Db 24 RASQISNYLA 34

RESULT 50

US-10-861-049-38
; Sequence 38, Application US/10861049
; Publication NO. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 38
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-049-38

Query Match 74.5%; Score 38; DB 5; Length 108;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
|||:|
Db 24 RASQISNYLA 34

Search completed: January 17, 2006, 12:13:08
Job time : 55.5 secs

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:59:34 ; Search time 3.6667 Seconds
(without alignments)
28.363 Million cell updates/sec

Title: US-10-665-658-13
Perfect score: 51
Sequence: 1 RASKRISKYLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA New:*
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep:*
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4: /cgn2_6/prodata/2/pubppaa/PCRT_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	11	6	US-10-665-658-13
2	51	100.0	11	6	US-10-665-658-59
3	51	100.0	107	7	US-11-107-028-49
4	51	100.0	107	7	US-11-107-028-51
5	51	100.0	108	6	US-10-665-658-1
6	51	100.0	108	6	US-10-665-658-2
7	40	78.4	108	6	US-10-771-257-32
8	40	78.4	108	7	US-11-127-677-32
9	38	74.5	108	6	US-10-665-658-3
10	38	74.5	108	7	US-11-120-338-3
11	38	74.5	108	7	US-11-106-820-3
12	38	74.5	109	7	US-11-096-046-5
13	37	72.5	11	7	US-11-093-274-10
14	37	72.5	11	7	US-11-093-274-11
15	37	72.5	11	7	US-11-093-274-12
16	37	72.5	11	7	US-11-051-453-19
17	37	72.5	94	7	US-11-093-274-33
18	37	72.5	95	7	US-11-054-669-86
19	37	72.5	95	7	US-11-084-554-138
20	37	72.5	95	7	US-11-061-848-52
21	37	72.5	95	7	US-11-061-848-65
22	37	72.5	95	7	US-11-061-848-66
23	37	72.5	107	7	US-11-040-159-17
24	37	72.5	107	7	US-11-093-274-24
25	37	72.5	108	7	US-11-093-274-22

26	37	72.5	108	7	US-11-093-274-23	Sequence 23, Appl
27	37	72.5	108	7	US-11-051-453-5	Sequence 51, Appl
28	37	72.5	128	6	US-10-721-763-31	Sequence 31, Appl
29	37	72.5	128	7	US-11-051-453-50	Sequence 50, Appl
30	37	72.5	139	7	US-11-128-900-16	Sequence 16, Appl
31	37	72.5	139	7	US-11-128-900-91	Sequence 91, Appl
32	37	72.5	142	7	US-11-128-900-91	Sequence 91, Appl
33	37	72.5	146	7	US-11-128-900-21	Sequence 21, Appl
34	37	72.5	146	7	US-11-128-900-93	Sequence 93, Appl
35	37	72.5	234	7	US-11-128-900-17	Sequence 17, Appl
36	37	72.5	234	7	US-11-128-900-69	Sequence 69, Appl
37	37	72.5	251	7	US-11-054-515-1049	Sequence 1049, Ap
38	36	70.6	107	7	US-11-064-174-44	Sequence 44, Appl
39	36	70.6	107	7	US-11-064-174-169	Sequence 169, App
40	36	70.6	108	7	US-11-127-932-12	Sequence 12, Appl
41	36	70.6	108	7	US-11-127-932-13	Sequence 13, Appl
42	36	70.6	108	7	US-11-064-174-181	Sequence 181, App
43	36	70.6	108	7	US-11-127-903-12	Sequence 12, Appl
44	36	70.6	108	7	US-11-127-903-13	Sequence 13, Appl
45	36	70.6	109	7	US-11-127-932-16	Sequence 16, Appl
46	36	70.6	109	7	US-11-127-932-17	Sequence 17, Appl
47	36	70.6	109	7	US-11-127-932-20	Sequence 20, Appl
48	36	70.6	109	7	US-11-127-903-16	Sequence 16, Appl
49	36	70.6	109	7	US-11-127-903-17	Sequence 17, Appl
50	36	70.6	109	7	US-11-127-903-20	Sequence 20, Appl
51	36	70.6	109	7	US-11-054-515-1027	Sequence 1027, Ap
52	35	68.6	11	7	US-11-096-046-7	Sequence 7, Appl
53	35	68.6	95	7	US-11-054-669-58	Sequence 58, Appl
54	35	68.6	95	7	US-11-054-669-61	Sequence 61, Appl
55	35	68.6	95	7	US-11-054-669-67	Sequence 67, Appl
56	35	68.6	95	7	US-11-054-669-69	Sequence 69, Appl
57	35	68.6	95	7	US-11-084-554-111	Sequence 111, App
58	35	68.6	95	7	US-11-084-554-121	Sequence 121, App
59	35	68.6	95	7	US-11-084-554-139	Sequence 139, App
60	35	68.6	95	7	US-11-084-554-140	Sequence 140, App
61	35	68.6	95	7	US-11-061-848-35	Sequence 35, Appl
62	35	68.6	95	7	US-11-061-848-44	Sequence 44, Appl
63	35	68.6	95	7	US-11-061-848-46	Sequence 46, Appl
64	35	68.6	95	7	US-11-061-848-57	Sequence 57, Appl
65	35	68.6	95	7	US-11-061-848-70	Sequence 70, Appl
66	35	68.6	95	7	US-11-061-848-73	Sequence 73, Appl
67	35	68.6	102	6	US-10-771-257-108	Sequence 108, App
68	35	68.6	103	6	US-10-771-257-102	Sequence 102, App
69	35	68.6	103	6	US-10-771-257-114	Sequence 114, App
70	35	68.6	109	6	US-10-771-257-29	Sequence 29, Appl
71	35	68.6	109	6	US-10-834-397-28	Sequence 28, Appl
72	35	68.6	109	6	US-10-834-397-43	Sequence 43, Appl
73	35	68.6	109	7	US-11-127-677-23	Sequence 23, Appl
74	35	68.6	134	7	US-11-128-900-23	Sequence 23, Appl
75	35	68.6	134	7	US-11-128-900-97	Sequence 97, Appl
76	35	68.6	241	7	US-11-054-515-1932	Sequence 1932, Ap
77	35	68.6	241	7	US-11-054-515-2054	Sequence 2054, Ap
78	35	68.6	249	7	US-11-054-515-919	Sequence 919, App
79	35	68.6	249	7	US-11-054-515-1655	Sequence 1655, Ap
80	34	66.7	95	7	US-11-054-669-54	Sequence 54, Appl
81	34	66.7	95	7	US-11-054-669-55	Sequence 55, Appl
82	34	66.7	95	7	US-11-054-669-87	Sequence 87, Appl
83	34	66.7	95	7	US-11-084-554-131	Sequence 131, App
84	34	66.7	95	7	US-11-084-554-143	Sequence 143, App
85	34	66.7	95	7	US-11-084-554-146	Sequence 146, App
86	34	66.7	95	7	US-11-061-848-36	Sequence 36, Appl
87	34	66.7	95	7	US-11-061-848-37	Sequence 37, Appl
88	34	66.7	95	7	US-11-061-848-63	Sequence 63, Appl
89	34	66.7	95	7	US-11-128-900-94	Sequence 94, Appl
90	34	66.7	96	7	US-11-144-248-42	Sequence 42, Appl
91	34	66.7	96	7	US-11-144-222-42	Sequence 42, Appl
92	34	66.7	103	7	US-11-064-174-52	Sequence 52, Appl
93	34	66.7	105	7	US-11-155-775-42	Sequence 52, Appl
94	34	66.7	107	6	US-10-925-366A-234	Sequence 234, App
95	34	66.7	107	7	US-11-064-174-33	Sequence 33, Appl
96	34	66.7	107	7	US-11-064-174-37	Sequence 37, Appl
97	34	66.7	107	7	US-11-064-174-38	Sequence 38, Appl
98	34	66.7	107	7	US-11-064-174-39	Sequence 39, Appl

99	34	66.7	107	7	US-11-064-174-40	Sequence 40, Appl	172	31	60.8	103	6	US-10-771-257-106	Sequence 106, App
100	34	66.7	107	7	US-11-064-174-156	Sequence 156, App	173	31	60.8	106	7	US-11-064-174-171	Sequence 171, App
101	34	66.7	107	7	US-11-064-174-158	Sequence 158, App	174	31	60.8	107	6	US-10-507-662-40	Sequence 40, Appl
102	34	66.7	107	7	US-11-064-174-168	Sequence 168, App	175	31	60.8	107	6	US-10-507-662-41	Sequence 41, Appl
103	34	66.7	107	7	US-11-064-174-173	Sequence 173, App	176	31	60.8	107	7	US-11-108-135-46	Sequence 46, Appl
104	34	66.7	107	7	US-11-064-174-175	Sequence 175, App	177	31	60.8	107	7	US-11-102-621-8	Sequence 8, Appl
105	34	66.7	107	7	US-11-064-174-176	Sequence 176, App	178	31	60.8	107	7	US-11-064-174-36	Sequence 36, Appl
106	34	66.7	108	6	US-10-925-366A-3	Sequence 3, Appl	179	31	60.8	107	7	US-11-064-174-172	Sequence 172, App
107	34	66.7	108	6	US-10-925-366A-6	Sequence 6, Appl	180	31	60.8	107	7	US-11-064-174-174	Sequence 174, App
108	34	66.7	108	6	US-10-925-366A-232	Sequence 232, App	181	31	60.8	139	7	US-11-128-900-22	Sequence 22, Appl
109	34	66.7	108	6	US-10-771-257-28	Sequence 28, Appl	182	31	60.8	139	7	US-11-128-900-96	Sequence 96, Appl
110	34	66.7	108	6	US-10-771-257-36	Sequence 36, Appl	183	31	60.8	214	7	US-11-128-900-71	Sequence 71, Appl
111	34	66.7	108	6	US-10-771-257-63	Sequence 63, Appl	184	31	60.8	400	6	US-10-793-626-1056	Sequence 106, App
112	34	66.7	108	6	US-10-834-397-14	Sequence 14, Appl	185	30	58.8	11	6	US-10-850-635-60	Sequence 60, Appl
113	34	66.7	108	7	US-11-127-677-28	Sequence 28, Appl	186	30	58.8	11	6	US-10-850-635-72	Sequence 72, Appl
114	34	66.7	108	7	US-11-127-677-36	Sequence 36, Appl	187	30	58.8	11	7	US-11-051-453-16	Sequence 16, Appl
115	34	66.7	108	7	US-11-127-677-61	Sequence 61, Appl	188	30	58.8	11	7	US-11-051-453-22	Sequence 22, Appl
116	34	66.7	108	7	US-11-127-932-19	Sequence 19, Appl	189	30	58.8	57	7	US-11-000-463-770	Sequence 770, App
117	34	66.7	108	7	US-11-064-174-32	Sequence 32, Appl	190	30	58.8	72	7	US-11-000-463-298	Sequence 298, App
118	34	66.7	108	7	US-11-064-174-43	Sequence 43, Appl	191	30	58.8	95	7	US-11-054-669-60	Sequence 60, Appl
119	34	66.7	108	7	US-11-064-174-163	Sequence 163, App	192	30	58.8	95	7	US-11-054-669-65	Sequence 65, Appl
120	34	66.7	108	7	US-11-064-174-167	Sequence 167, App	193	30	58.8	95	7	US-11-054-669-66	Sequence 66, Appl
121	34	66.7	108	7	US-11-127-903-19	Sequence 19, Appl	194	30	58.8	95	7	US-11-054-669-68	Sequence 68, Appl
122	34	66.7	109	7	US-11-127-932-14	Sequence 14, Appl	195	30	58.8	95	7	US-11-054-669-70	Sequence 70, Appl
123	34	66.7	109	7	US-11-127-932-18	Sequence 18, Appl	196	30	58.8	95	7	US-11-084-554-125	Sequence 125, App
124	34	66.7	109	7	US-11-127-903-14	Sequence 14, Appl	197	30	58.8	95	7	US-11-084-554-126	Sequence 126, App
125	34	66.7	109	7	US-11-127-903-18	Sequence 18, Appl	198	30	58.8	95	7	US-11-084-554-129	Sequence 129, App
126	34	66.7	236	7	US-11-086-289-8	Sequence 8, Appl	199	30	58.8	95	7	US-11-084-554-133	Sequence 133, App
127	34	66.7	240	6	US-10-925-366A-219	Sequence 219, App	200	30	58.8	95	7	US-11-084-554-134	Sequence 134, App
128	34	66.7	250	7	US-11-054-515-1174	Sequence 1174, App	201	30	58.8	95	7	US-11-084-554-137	Sequence 137, App
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131	33	64.7	95	7	US-11-084-554-124	Sequence 124, Appl	204	30	58.8	95	7	US-11-061-848-43	Sequence 43, Appl
132	33	64.7	103	6	US-10-771-257-99	Sequence 99, Appl	205	30	58.8	95	7	US-11-061-848-45	Sequence 45, Appl
133	33	64.7	103	6	US-10-771-257-110	Sequence 110, App	206	30	58.8	95	7	US-11-061-848-47	Sequence 47, Appl
134	33	64.7	103	6	US-10-771-257-111	Sequence 111, App	207	30	58.8	95	7	US-11-061-848-56	Sequence 56, Appl
135	33	64.7	103	6	US-10-771-257-113	Sequence 113, App	208	30	58.8	95	7	US-11-061-848-58	Sequence 58, Appl
136	33	64.7	105	6	US-10-771-257-103	Sequence 103, App	209	30	58.8	95	7	US-11-061-848-59	Sequence 59, Appl
137	33	64.7	107	7	US-11-064-174-162	Sequence 162, App	210	30	58.8	95	7	US-11-061-848-64	Sequence 64, Appl
138	33	64.7	108	6	US-10-925-366A-233	Sequence 233, App	211	30	58.8	95	7	US-11-061-848-71	Sequence 71, Appl
139	33	64.7	108	6	US-10-771-257-35	Sequence 35, Appl	212	30	58.8	95	7	US-11-061-848-72	Sequence 72, Appl
140	33	64.7	108	6	US-10-771-257-78	Sequence 78, Appl	213	30	58.8	102	6	US-10-771-257-104	Sequence 104, App
141	33	64.7	108	7	US-11-127-677-35	Sequence 35, Appl	214	30	58.8	103	6	US-10-771-257-98	Sequence 98, Appl
142	33	64.7	108	7	US-11-127-677-76	Sequence 76, Appl	215	30	58.8	107	6	US-10-771-257-100	Sequence 100, App
143	33	64.7	108	7	US-11-064-174-41	Sequence 41, Appl	216	30	58.8	107	6	US-10-850-635-14	Sequence 14, Appl
144	33	64.7	109	6	US-10-771-257-71	Sequence 71, Appl	217	30	58.8	105	7	US-10-850-635-18	Sequence 18, Appl
145	33	64.7	109	7	US-11-040-159-7	Sequence 7, Appl	218	30	58.8	105	7	US-11-084-554-12	Sequence 12, Appl
146	33	64.7	109	7	US-11-040-159-9	Sequence 9, Appl	219	30	58.8	105	7	US-11-155-775-12	Sequence 12, Appl
147	33	64.7	109	7	US-11-040-159-11	Sequence 11, Appl	220	30	58.8	105	7	US-11-155-775-60	Sequence 60, Appl
148	33	64.7	109	7	US-11-040-159-13	Sequence 13, Appl	221	30	58.8	107	6	US-10-850-635-14	Sequence 14, Appl
149	33	64.7	109	7	US-11-127-677-69	Sequence 69, Appl	222	30	58.8	107	6	US-10-850-635-18	Sequence 18, Appl
150	33	64.7	129	6	US-10-721-763-19	Sequence 19, Appl	223	30	58.8	107	7	US-11-084-554-1	Sequence 1, Appl
151	33	64.7	129	6	US-10-721-763-23	Sequence 23, Appl	224	30	58.8	107	7	US-11-051-453-4	Sequence 4, Appl
152	33	64.7	313	7	US-11-000-463-427	Sequence 427, App	225	30	58.8	107	7	US-11-051-453-6	Sequence 6, Appl
153	33	64.7	367	7	US-11-000-463-335	Sequence 335, App	226	30	58.8	107	7	US-11-051-453-30	Sequence 30, Appl
154	33	64.7	367	7	US-11-000-463-899	Sequence 899, App	227	30	58.8	107	7	US-11-051-453-31	Sequence 31, Appl
155	32	62.7	106	7	US-11-149-943-54	Sequence 54, Appl	228	30	58.8	107	7	US-11-051-453-32	Sequence 32, Appl
156	32	62.7	108	6	US-10-771-257-4	Sequence 4, Appl	229	30	58.8	107	7	US-11-051-453-33	Sequence 33, Appl
157	32	62.7	108	7	US-11-127-677-4	Sequence 4, Appl	230	30	58.8	107	7	US-11-051-453-34	Sequence 34, Appl
158	32	62.7	108	7	US-11-127-932-11	Sequence 11, Appl	231	30	58.8	108	6	US-10-925-366A-176	Sequence 176, App
159	32	62.7	108	7	US-11-064-174-31	Sequence 31, Appl	232	30	58.8	108	6	US-10-925-366A-288	Sequence 288, App
160	32	62.7	108	7	US-11-127-903-11	Sequence 11, Appl	233	30	58.8	108	6	US-10-771-257-33	Sequence 33, Appl
161	32	62.7	127	7	US-11-089-872-5	Sequence 5, Appl	234	30	58.8	108	6	US-10-771-257-39	Sequence 39, Appl
162	32	62.7	241	7	US-11-054-515-157	Sequence 157, App	235	30	58.8	108	6	US-10-771-257-40	Sequence 40, Appl
163	32	62.7	242	7	US-11-054-515-1915	Sequence 1915, App	236	30	58.8	108	7	US-11-127-677-33	Sequence 33, Appl
164	32	62.7	247	7	US-11-054-515-3240	Sequence 3240, App	237	30	58.8	108	7	US-11-127-677-39	Sequence 39, Appl
165	32	62.7	248	7	US-11-054-515-1360	Sequence 1360, App	238	30	58.8	108	7	US-11-127-677-40	Sequence 40, Appl
166	32	62.7	248	7	US-11-054-515-1446	Sequence 1446, App	239	30	58.8	108	7	US-11-064-174-161	Sequence 161, App
167	32	62.7	251	7	US-11-054-515-1921	Sequence 1921, App	240	30	58.8	108	7	US-11-064-174-177	Sequence 177, App
168	32	62.7	495	6	US-10-613-744-5	Sequence 5, Appl	241	30	58.8	114	6	US-10-925-366A-12	Sequence 12, Appl
169	32	62.7	919	6	US-10-858-730-206	Sequence 206, Appl	242	30	58.8	129	7	US-11-116-144-149	Sequence 149, App
170	31	60.8	11	6	US-10-665-658-60	Sequence 60, Appl	243	30	58.8	129	7	US-11-116-144-149	Sequence 149, App
171	31	60.8	11	7	US-11-108-135-38	Sequence 38, Appl	244	30	58.8	129	7	US-11-051-453-43	Sequence 43, Appl

245	30	58.8	129	7	US-11-051-453-45	Sequence 45, Appl	318	29	56.9	316	7	US-11-032-797-4	Sequence 4, Appl
246	30	58.8	129	7	US-11-051-453-46	Sequence 46, Appl	319	29	56.9	354	6	US-10-467-657-5634	Sequence 5634, Ap
247	30	58.8	129	7	US-11-051-453-47	Sequence 47, Appl	320	29	56.9	373	6	US-10-793-626-372	Sequence 372, Appl
248	30	58.8	129	7	US-11-051-453-48	Sequence 48, Appl	321	29	56.9	391	6	US-10-979-821-12	Sequence 12, Appl
249	30	58.8	129	7	US-11-051-453-52	Sequence 52, Appl	322	29	56.9	391	6	US-11-114-922-12	Sequence 12, Appl
250	30	58.8	152	7	US-11-128-900-18	Sequence 18, Appl	323	28.5	55.9	272	6	US-10-793-626-520	Sequence 520, App
251	30	58.8	152	7	US-11-128-900-95	Sequence 95, Appl	324	28	54.9	11	7	US-11-009-939-28	Sequence 28, Appl
252	30	58.8	233	6	US-10-467-657-7054	Sequence 7054, Ap	325	28	54.9	11	7	US-11-009-939-28	Sequence 28, Appl
253	30	58.8	237	7	US-11-054-515-1906	Sequence 1906, Ap	326	28	54.9	95	7	US-11-054-669-56	Sequence 56, Appl
254	30	58.8	237	7	US-11-054-515-2003	Sequence 2003, Ap	327	28	54.9	95	7	US-11-054-669-57	Sequence 57, Appl
255	30	58.8	237	7	US-11-054-515-2005	Sequence 2005, Ap	328	28	54.9	95	7	US-11-054-669-84	Sequence 85, Appl
256	30	58.8	237	7	US-11-054-515-2017	Sequence 2017, Ap	329	28	54.9	95	7	US-11-054-669-85	Sequence 127, App
257	30	58.8	237	7	US-11-054-515-2019	Sequence 2019, Ap	330	28	54.9	95	7	US-11-084-554-130	Sequence 130, App
258	30	58.8	237	7	US-11-054-515-2020	Sequence 2020, Ap	331	28	54.9	95	7	US-11-084-554-145	Sequence 145, App
259	30	58.8	237	7	US-11-054-515-2027	Sequence 2027, Ap	332	28	54.9	95	7	US-11-084-554-148	Sequence 148, App
260	30	58.8	237	7	US-11-054-515-2028	Sequence 2028, Ap	333	28	54.9	95	7	US-11-061-848-33	Sequence 33, Appl
261	30	58.8	237	7	US-11-054-515-2040	Sequence 2040, Ap	334	28	54.9	95	7	US-11-061-848-50	Sequence 50, Appl
262	30	58.8	237	7	US-11-054-515-2043	Sequence 2043, Ap	335	28	54.9	95	7	US-11-061-848-51	Sequence 51, Appl
263	30	58.8	237	7	US-11-054-515-2104	Sequence 2104, Ap	336	28	54.9	95	7	US-11-061-848-62	Sequence 62, Appl
264	30	58.8	237	7	US-11-054-515-2110	Sequence 2110, Ap	337	28	54.9	95	7	US-11-061-848-67	Sequence 67, Appl
265	30	58.8	237	7	US-11-054-515-2111	Sequence 2111, Ap	338	28	54.9	107	7	US-11-112-240-8	Sequence 8, Appl
266	30	58.8	237	7	US-11-054-515-2114	Sequence 2114, Ap	339	28	54.9	107	7	US-11-112-304A-8	Sequence 237, App
267	30	58.8	237	7	US-11-054-515-2115	Sequence 2115, Ap	340	28	54.9	108	6	US-10-925-366A-237	Sequence 38, Appl
268	30	58.8	238	7	US-11-054-515-2115	Sequence 2053, Ap	341	28	54.9	108	6	US-10-771-257-38	Sequence 38, Appl
269	30	58.8	242	7	US-11-054-515-1580	Sequence 1580, Ap	342	28	54.9	108	6	US-10-771-257-80	Sequence 80, Appl
270	30	58.8	244	7	US-11-054-515-82	Sequence 82, Appl	343	28	54.9	108	6	US-11-009-939-27	Sequence 27, Appl
271	30	58.8	244	7	US-11-054-515-164	Sequence 164, App	344	28	54.9	108	7	US-11-127-677-38	Sequence 38, Appl
272	30	58.8	244	7	US-11-054-515-261	Sequence 261, App	345	28	54.9	108	7	US-11-127-677-78	Sequence 78, Appl
273	30	58.8	244	7	US-11-054-515-280	Sequence 280, App	346	28	54.9	108	7	US-11-127-677-78	Sequence 38, Appl
274	30	58.8	244	7	US-11-054-515-1881	Sequence 1881, Ap	347	28	54.9	184	6	US-10-467-657-356	Sequence 3356, Ap
275	30	58.8	245	7	US-11-054-515-1291	Sequence 1291, Ap	348	28	54.9	184	6	US-10-467-657-360	Sequence 3860, Ap
276	30	58.8	246	7	US-11-054-515-2075	Sequence 2075, Ap	349	28	54.9	206	7	US-11-217-562-10	Sequence 10, Appl
277	30	58.8	248	7	US-11-054-515-1004	Sequence 1004, Ap	350	28	54.9	246	7	US-11-054-515-1268	Sequence 1268, Ap
278	30	58.8	248	7	US-11-054-515-1385	Sequence 1385, Ap	351	28	54.9	250	7	US-11-054-515-1952	Sequence 1952, Ap
279	30	58.8	248	7	US-11-054-515-1717	Sequence 1717, Ap	352	28	54.9	251	7	US-11-054-515-1238	Sequence 1238, Ap
280	30	58.8	248	7	US-11-054-515-1719	Sequence 1719, Ap	353	28	54.9	256	7	US-11-179-977-15	Sequence 15, Appl
281	30	58.8	248	7	US-11-054-515-1733	Sequence 1733, Ap	354	28	54.9	285	6	US-10-467-657-9158	Sequence 9158, Ap
282	30	58.8	248	7	US-11-054-515-1737	Sequence 1737, Ap	355	28	54.9	313	7	US-11-010-792-20	Sequence 20, Appl
283	30	58.8	248	7	US-11-054-515-1876	Sequence 1876, Ap	356	28	54.9	353	6	US-10-131-826A-296	Sequence 296, Appl
284	30	58.8	248	7	US-11-054-515-1879	Sequence 1879, Ap	357	28	54.9	456	7	US-11-112-882-17	Sequence 17, Appl
285	30	58.8	249	7	US-11-054-515-1321	Sequence 1321, Ap	358	28	54.9	525	7	US-11-112-882-27	Sequence 27, Appl
286	30	58.8	250	7	US-11-054-515-1410	Sequence 1410, Ap	359	28	54.9	585	6	US-10-793-626-2124	Sequence 2124, Ap
287	30	58.8	250	7	US-11-054-515-1410	Sequence 1410, Ap	360	28	54.9	602	6	US-10-793-626-2362	Sequence 2362, Ap
288	30	58.8	550	7	US-10-793-626-1008	Sequence 1008, Ap	361	28	54.9	795	6	US-10-821-234-1675	Sequence 1675, Ap
289	30	58.8	610	7	US-11-184-380-14	Sequence 14, Appl	362	28	54.9	853	6	US-10-821-234-1110	Sequence 1110, Ap
290	30	58.8	1294	7	US-11-184-380-3	Sequence 3, Appl	363	28	54.9	961	6	US-10-831-997-4	Sequence 4, Appl
291	30	56.9	11	6	US-11-052-554A-340	Sequence 340, App	364	28	54.9	2335	6	US-10-821-234-1610	Sequence 1610, Ap
292	29	56.9	11	7	US-10-999-866-55	Sequence 55, Appl	365	27.5	53.9	108	7	US-11-064-174-178	Sequence 178, App
293	29	56.9	11	7	US-11-009-939-38	Sequence 38, Appl	366	27.5	53.9	254	7	US-11-064-174-1905	Sequence 905, App
294	29	56.9	92	7	US-11-062-186-49	Sequence 49, Appl	367	27	52.9	11	6	US-11-054-515-905	Sequence 6, Appl
295	29	56.9	92	7	US-11-144-248-18	Sequence 18, Appl	368	27	52.9	49	6	US-10-473-037-6	Sequence 307, App
296	29	56.9	92	7	US-11-144-248-18	Sequence 18, Appl	369	27	52.9	90	6	US-10-925-366A-307	Sequence 307, App
297	29	56.9	105	7	US-11-096-074-55	Sequence 55, Appl	370	27	52.9	70	6	US-10-986-501-143	Sequence 143, App
298	29	56.9	105	7	US-11-095-822-55	Sequence 55, Appl	371	27	52.9	96	6	US-11-173-071-23	Sequence 23, Appl
299	29	56.9	106	7	US-11-095-822-55	Sequence 55, Appl	372	27	52.9	96	6	US-10-467-657-8364	Sequence 8364, Ap
300	29	56.9	106	7	US-11-096-074-51	Sequence 51, Appl	373	27	52.9	96	7	US-11-084-554-144	Sequence 144, App
301	29	56.9	106	7	US-11-155-775-8	Sequence 8, Appl	374	27	52.9	104	7	US-11-084-554-147	Sequence 147, App
302	29	56.9	106	7	US-11-107-028-8	Sequence 8, Appl	375	27	52.9	107	6	US-11-155-775-28	Sequence 28, Appl
303	29	56.9	106	7	US-11-107-028-9	Sequence 9, Appl	376	27	52.9	107	6	US-10-771-257-65	Sequence 65, Appl
304	29	56.9	107	6	US-11-095-822-51	Sequence 51, Appl	377	27	52.9	107	7	US-11-096-074-54	Sequence 54, Appl
305	29	56.9	107	6	US-10-999-866-43	Sequence 43, Appl	378	27	52.9	107	7	US-11-087-677-63	Sequence 63, Appl
306	29	56.9	107	6	US-11-064-174-34	Sequence 34, Appl	379	27	52.9	107	7	US-11-127-677-63	Sequence 63, Appl
307	29	56.9	108	7	US-11-064-174-179	Sequence 179, App	380	27	52.9	108	6	US-11-064-174-160	Sequence 160, App
308	29	56.9	108	7	US-11-054-669-94	Sequence 94, Appl	381	27	52.9	108	6	US-11-095-822-54	Sequence 54, Appl
309	29	56.9	108	7	US-11-054-669-111	Sequence 111, App	382	27	52.9	108	6	US-10-473-037-10	Sequence 10, Appl
310	29	56.9	108	7	US-11-009-939-37	Sequence 37, Appl	383	27	52.9	108	6	US-10-473-037-50	Sequence 50, Appl
311	29	56.9	150	7	US-10-467-657-910	Sequence 910, App	384	27	52.9	108	6	US-10-925-366A-149	Sequence 149, App
312	29	56.9	150	7	US-11-128-900-24	Sequence 24, Appl	385	27	52.9	108	6	US-10-925-366A-170	Sequence 170, App
313	29	56.9	214	7	US-11-128-900-98	Sequence 98, Appl	386	27	52.9	108	6	US-10-925-366A-183	Sequence 183, App
314	29	56.9	214	7	US-11-025-712-11	Sequence 11, Appl	387	27	52.9	108	6	US-10-771-257-77	Sequence 77, Appl
315	29	56.9	214	7	US-11-173-564-1	Sequence 1, Appl	388	27	52.9	108	7	US-11-127-677-75	Sequence 75, Appl
316	29	56.9	253	7	US-11-054-669-109	Sequence 109, App	389	27	52.9	110	6	US-11-221-900-7	Sequence 7, Appl
317	29	56.9	257	7	US-11-054-515-936	Sequence 936, App	390	27	52.9	110	6	US-10-648-816-1	Sequence 1, Appl
					Sequence 10, Appl							US-10-648-816-2	Sequence 2, Appl

391	27	52.9	110	6	US-10-648-816-3	Sequence 3, Appli	464	26	51.0	108	6	US-10-925-366A-297	Sequence 297, App
392	27	52.9	110	6	US-10-648-816-4	Sequence 4, Appli	465	26	51.0	108	6	US-10-925-366A-332	Sequence 332, App
393	27	52.9	110	6	US-10-648-816-5	Sequence 5, Appli	466	26	51.0	108	7	US-11-061-848-2	Sequence 2, Appli
394	27	52.9	110	6	US-10-648-816-6	Sequence 6, Appli	467	26	51.0	108	7	US-11-061-848-10	Sequence 10, Appli
395	27	52.9	110	6	US-10-648-816-7	Sequence 7, Appli	468	26	51.0	108	7	US-11-061-848-11	Sequence 11, Appli
396	27	52.9	110	6	US-10-648-816-8	Sequence 8, Appli	469	26	51.0	108	7	US-11-061-848-12	Sequence 12, Appli
397	27	52.9	126	6	US-10-467-657-4260	Sequence 4260, Ap	470	26	51.0	108	7	US-11-061-848-13	Sequence 13, Appli
398	27	52.9	128	6	US-10-473-037-2	Sequence 2, Appli	471	26	51.0	108	7	US-11-061-848-14	Sequence 14, Appli
399	27	52.9	247	7	US-11-084-717-21	Sequence 21, Appli	472	26	51.0	108	7	US-11-061-848-15	Sequence 15, Appli
400	27	52.9	247	7	US-11-084-717-23	Sequence 23, Appli	473	26	51.0	129	7	US-11-116-144-145	Sequence 145, App
401	27	52.9	247	7	US-11-084-717-25	Sequence 25, Appli	474	26	51.0	129	7	US-11-116-144-150	Sequence 150, App
402	27	52.9	247	7	US-11-179-244-21	Sequence 21, Appli	475	26	51.0	129	7	US-11-116-144-151	Sequence 151, App
403	27	52.9	247	7	US-11-179-244-23	Sequence 23, Appli	476	26	51.0	132	6	US-10-467-657-4284	Sequence 4284, Ap
404	27	52.9	247	7	US-11-179-244-25	Sequence 25, Appli	477	26	51.0	133	7	US-11-010-748A-2	Sequence 2, Appli
405	27	52.9	367	7	US-11-012-762-36	Sequence 36, Appli	478	26	51.0	133	7	US-11-010-748A-3	Sequence 3, Appli
406	27	52.9	491	6	US-10-763-712A-4	Sequence 4, Appli	479	26	51.0	133	7	US-11-010-748A-4	Sequence 4, Appli
407	27	52.9	506	6	US-10-467-657-2434	Sequence 2434, Ap	480	26	51.0	154	7	US-11-137-142-2	Sequence 2, Appli
408	27	52.9	519	6	US-10-821-234-1373	Sequence 1373, Ap	481	26	51.0	189	6	US-10-995-561-806	Sequence 806, App
409	27	52.9	790	6	US-10-763-712A-75	Sequence 75, Appli	482	26	51.0	189	7	US-11-036-797-11	Sequence 31, Appli
410	27	52.9	804	7	US-11-070-080-18	Sequence 18, Appli	483	26	51.0	200	7	US-11-073-605-3	Sequence 3, Appli
411	27	52.9	805	7	US-11-108-539-2	Sequence 2, Appli	484	26	51.0	213	7	US-11-158-505-14	Sequence 34, Appli
412	27	52.9	848	7	US-11-108-539-4	Sequence 4, Appli	485	26	51.0	216	6	US-10-995-561-522	Sequence 522, App
413	27	52.9	929	7	US-11-063-343-37	Sequence 37, Appli	486	26	51.0	236	7	US-11-086-289-4	Sequence 4, Appli
414	26.5	52.0	12	6	US-10-850-635-30	Sequence 30, Appli	487	26	51.0	236	7	US-11-086-289-20	Sequence 20, Appli
415	26.5	52.0	12	6	US-10-850-635-36	Sequence 36, Appli	488	26	51.0	237	7	US-11-054-515-2118	Sequence 2118, Ap
416	26.5	52.0	12	7	US-11-051-453-68	Sequence 38, Appli	489	26	51.0	239	6	US-10-821-234-1259	Sequence 1259, Ap
417	26.5	52.0	96	7	US-11-144-248-38	Sequence 38, Appli	490	26	51.0	258	7	US-11-000-463-871	Sequence 871, App
418	26.5	52.0	96	7	US-11-054-669-82	Sequence 82, Appli	491	26	51.0	270	6	US-10-495-597-11	Sequence 12, Appli
419	26.5	52.0	96	7	US-11-084-554-114	Sequence 114, App	492	26	51.0	270	6	US-10-495-597-12	Sequence 12, Appli
420	26.5	52.0	96	7	US-11-144-222-38	Sequence 38, Appli	493	26	51.0	283	7	US-11-052-554A-226	Sequence 226, App
421	26.5	52.0	96	7	US-11-051-453-82	Sequence 82, Appli	494	26	51.0	284	6	US-10-131-826A-118	Sequence 118, App
422	26.5	52.0	96	7	US-11-128-900-87	Sequence 87, Appli	495	26	51.0	297	7	US-11-195-968-3	Sequence 3, Appli
423	26.5	52.0	101	6	US-11-127-677-2	Sequence 2, Appli	496	26	51.0	308	6	US-10-793-6266-1072	Sequence 1072, Ap
424	26.5	52.0	101	7	US-11-127-677-2	Sequence 2, Appli	497	26	51.0	308	6	US-10-793-6266-2706	Sequence 2706, Ap
425	26.5	52.0	108	6	US-10-850-635-4	Sequence 4, Appli	498	26	51.0	311	6	US-10-793-6266-1080	Sequence 3080, Ap
426	26.5	52.0	108	6	US-10-850-635-6	Sequence 6, Appli	499	26	51.0	312	6	US-10-467-657-4414	Sequence 4414, Ap
427	26.5	52.0	108	6	US-11-051-453-58	Sequence 58, Appli	500	26	51.0	322	7	US-11-073-605-4	Sequence 4, Appli
428	26.5	52.0	109	6	US-10-771-257-64	Sequence 64, Appli	501	26	51.0	325	7	US-11-129-143-88	Sequence 88, Appli
429	26.5	52.0	109	6	US-10-834-397-16	Sequence 16, Appli	502	26	51.0	352	6	US-10-995-561-523	Sequence 523, App
430	26.5	52.0	109	7	US-11-127-677-62	Sequence 62, Appli	503	26	51.0	352	7	US-11-068-686-2	Sequence 2, Appli
431	26.5	52.0	110	6	US-10-834-397-30	Sequence 30, Appli	504	26	51.0	352	7	US-11-068-686-20	Sequence 20, Appli
432	26.5	52.0	110	6	US-10-834-397-47	Sequence 47, Appli	505	26	51.0	352	7	US-11-127-877-61	Sequence 61, Appli
433	26.5	52.0	112	7	US-11-127-933-15	Sequence 15, Appli	506	26	51.0	355	7	US-11-068-686-4	Sequence 4, Appli
434	26.5	52.0	112	7	US-11-127-903-15	Sequence 15, Appli	507	26	51.0	355	7	US-11-127-877-64	Sequence 64, Appli
435	26.5	52.0	128	7	US-11-051-453-60	Sequence 60, Appli	508	26	51.0	355	7	US-11-216-610-2	Sequence 2, Appli
436	26.5	52.0	131	6	US-10-721-763-27	Sequence 27, Appli	509	26	51.0	355	7	US-11-216-610-4	Sequence 4, Appli
437	26.5	52.0	235	7	US-11-086-289-16	Sequence 16, Appli	510	26	51.0	355	7	US-11-216-610-6	Sequence 6, Appli
438	26.5	52.0	245	7	US-11-054-515-1896	Sequence 1896, Ap	511	26	51.0	363	6	US-10-995-561-804	Sequence 804, App
439	26.5	52.0	246	7	US-11-054-515-1896	Sequence 1896, Ap	512	26	51.0	364	6	US-10-131-826A-186	Sequence 186, App
440	26.5	52.0	247	7	US-11-056-825-8	Sequence 8, Appli	513	26	51.0	364	6	US-10-793-6266-2626	Sequence 2626, Ap
441	26.5	52.0	247	7	US-11-056-825-4	Sequence 4, Appli	514	26	51.0	370	7	US-11-073-605-2	Sequence 2, Appli
442	26.5	52.0	251	7	US-11-054-515-1219	Sequence 1219, Ap	515	26	51.0	370	7	US-11-075-400-14	Sequence 14, Appli
443	26.5	52.0	252	7	US-11-054-515-1534	Sequence 1534, Ap	516	26	51.0	374	7	US-11-127-877-60	Sequence 60, Appli
444	26.5	52.0	307	7	US-11-000-463-332	Sequence 332, App	517	26	51.0	377	7	US-11-124-368A-209	Sequence 209, App
445	26.5	52.0	312	7	US-11-000-463-334	Sequence 334, App	518	26	51.0	377	7	US-11-124-368A-210	Sequence 210, App
446	26.5	52.0	384	7	US-11-000-463-804	Sequence 804, App	519	26	51.0	399	6	US-10-467-657-1672	Sequence 1672, Ap
447	26.5	52.0	384	7	US-11-000-463-805	Sequence 805, App	520	26	51.0	414	6	US-10-995-561-803	Sequence 803, App
448	26.5	52.0	384	7	US-11-000-463-806	Sequence 806, App	521	26	51.0	433	7	US-11-109-156-9	Sequence 9, Appli
449	26.5	52.0	384	7	US-11-000-463-807	Sequence 807, App	522	26	51.0	448	6	US-10-510-386-24	Sequence 24, Appli
450	26	51.0	11	6	US-10-850-635-48	Sequence 48, Appli	523	26	51.0	485	7	US-11-151-601-41	Sequence 41, Appli
451	26	51.0	11	6	US-11-152-846-19	Sequence 19, Appli	524	26	51.0	583	7	US-11-080-991-64	Sequence 64, Appli
452	26	51.0	15	7	US-11-069-834-10	Sequence 10, Appli	525	26	51.0	611	6	US-10-467-657-4656	Sequence 4656, App
453	26	51.0	70	7	US-11-000-463-265	Sequence 265, App	526	26	51.0	626	7	US-11-010-748A-1	Sequence 1, Appli
454	26	51.0	95	7	US-11-054-669-63	Sequence 63, Appli	527	26	51.0	633	6	US-10-821-234-1146	Sequence 1146, Ap
455	26	51.0	95	7	US-11-054-669-64	Sequence 64, Appli	528	26	51.0	633	6	US-10-467-657-1930	Sequence 1930, Ap
456	26	51.0	95	7	US-11-084-554-128	Sequence 128, App	529	26	51.0	970	6	US-10-467-657-5524	Sequence 5524, Ap
457	26	51.0	95	7	US-11-084-554-136	Sequence 136, App	530	26	51.0	1033	7	US-11-037-243-75	Sequence 75, Appli
458	26	51.0	95	7	US-11-061-848-40	Sequence 40, Appli	531	26	51.0	1170	7	US-11-080-026-2	Sequence 2, Appli
459	26	51.0	95	7	US-11-061-848-41	Sequence 41, Appli	532	26	51.0	1170	7	US-11-107-028-4	Sequence 4, Appli
460	26	51.0	106	6	US-10-850-635-10	Sequence 10, Appli	533	26	51.0	1278	6	US-10-995-561-952	Sequence 952, App
461	26	51.0	107	7	US-11-069-834-8	Sequence 8, Appli	534	26	51.0	1360	7	US-11-188-743-22	Sequence 22, Appli
462	26	51.0	108	6	US-10-925-366A-191	Sequence 191, App	535	26	51.0	1463	7	US-11-080-991-22	Sequence 22, Appli
463	26	51.0	108	6	US-10-925-366A-284	Sequence 284, App	536	26	51.0	1572	6	US-11-073-6266-2906	Sequence 2906, Ap

537	26	51.0	2340	7	US-11-052-554A-171	Sequence 171, App	610	25	49.0	341	6	US-10-515-481-9	Sequence 12, Appl
538	26	51.0	3056	7	US-11-109-156-20	Sequence 20, Appl	611	25	49.0	341	6	US-10-515-481-12	Sequence 19, Appl
539	26	51.0	3073	7	US-11-143-980-50	Sequence 50, Appl	612	25	49.0	344	6	US-10-995-561-524	Sequence 524, App
540	25.5	50.0	113	7	US-11-096-074-53	Sequence 53, Appl	613	25	49.0	344	6	US-10-995-561-525	Sequence 525, App
541	25.5	50.0	113	7	US-11-095-822-53	Sequence 53, Appl	614	25	49.0	347	6	US-10-467-657-2962	Sequence 2962, App
542	25.5	50.0	688	7	US-11-113-424-49	Sequence 49, Appl	615	25	49.0	351	6	US-10-729-121-2	Sequence 2, Appl
543	25	49.0	15	6	US-10-880-238-75	Sequence 75, Appl	616	25	49.0	354	7	US-11-108-528-72	Sequence 72, Appl
544	25	49.0	15	6	US-10-880-238-78	Sequence 78, Appl	617	25	49.0	354	7	US-11-108-528-74	Sequence 74, Appl
545	25	49.0	37	7	US-11-214-199-73	Sequence 73, Appl	618	25	49.0	369	6	US-10-467-657-7206	Sequence 1920, App
546	25	49.0	44	6	US-10-467-657-2078	Sequence 2078, Ap	619	25	49.0	385	7	US-11-074-176-192	Sequence 442, App
547	25	49.0	48	6	US-10-467-657-8897	Sequence 8897, Ap	620	25	49.0	402	6	US-10-485-513-422	Sequence 84, Appl
548	25	49.0	50	6	US-10-729-121-32	Sequence 32, Appl	621	25	49.0	407	7	US-11-129-143-84	Sequence 422, App
549	25	49.0	52	6	US-10-467-657-8354	Sequence 8354, Ap	622	25	49.0	426	6	US-10-454-437-70	Sequence 70, Appl
550	25	49.0	70	7	US-11-000-463-737	Sequence 737, App	623	25	49.0	426	6	US-10-454-437-72	Sequence 72, Appl
551	25	49.0	85	6	US-10-467-657-9150	Sequence 9150, Ap	624	25	49.0	427	6	US-10-485-788A-503	Sequence 503, App
552	25	49.0	94	7	US-11-097-812-9	Sequence 9, Appl	625	25	49.0	453	6	US-10-467-657-206	Sequence 206, App
553	25	49.0	94	7	US-11-097-812-169	Sequence 169, App	626	25	49.0	453	6	US-10-467-657-3626	Sequence 3626, App
554	25	49.0	95	7	US-11-054-663-62	Sequence 62, Appl	627	25	49.0	453	6	US-10-467-657-6400	Sequence 6400, Ap
555	25	49.0	95	7	US-11-061-848-39	Sequence 39, Appl	628	25	49.0	459	6	US-10-949-720-390	Sequence 390, App
556	25	49.0	95	7	US-11-061-848-60	Sequence 60, Appl	629	25	49.0	500	6	US-10-467-657-48	Sequence 48, App
557	25	49.0	103	6	US-10-821-234-1005	Sequence 1005, Ap	630	25	49.0	539	6	US-10-467-657-7736	Sequence 7736, Ap
558	25	49.0	105	7	US-11-155-775-48	Sequence 48, Appl	631	25	49.0	543	6	US-10-495-664-3	Sequence 3, Appl
559	25	49.0	108	7	US-11-097-812-44	Sequence 44, Appl	632	25	49.0	543	7	US-11-106-672A-10	Sequence 10, Appl
560	25	49.0	108	7	US-11-097-812-47	Sequence 47, Appl	633	25	49.0	545	7	US-11-065-943-63	Sequence 63, Appl
561	25	49.0	109	7	US-11-102-201-2	Sequence 2, Appl	634	25	49.0	545	7	US-11-065-943-65	Sequence 65, Appl
562	25	49.0	109	7	US-11-097-812-40	Sequence 40, Appl	635	25	49.0	545	7	US-11-065-943-67	Sequence 67, Appl
563	25	49.0	109	7	US-11-097-812-41	Sequence 41, Appl	636	25	49.0	545	7	US-11-065-943-69	Sequence 69, Appl
564	25	49.0	109	7	US-11-097-812-49	Sequence 49, Appl	637	25	49.0	545	7	US-11-065-943-71	Sequence 71, Appl
565	25	49.0	109	7	US-11-097-812-55	Sequence 55, Appl	638	25	49.0	545	7	US-11-065-943-77	Sequence 77, Appl
566	25	49.0	111	7	US-11-097-812-105	Sequence 105, Appl	639	25	49.0	545	7	US-11-065-943-81	Sequence 81, Appl
567	25	49.0	112	7	US-11-097-812-169	Sequence 169, App	640	25	49.0	545	7	US-11-065-943-81	Sequence 81, Appl
568	25	49.0	112	7	US-11-097-812-176	Sequence 176, App	641	25	49.0	545	7	US-11-065-943-83	Sequence 83, Appl
569	25	49.0	112	7	US-11-097-812-182	Sequence 182, App	642	25	49.0	545	7	US-11-065-943-85	Sequence 85, Appl
570	25	49.0	112	7	US-11-097-812-183	Sequence 183, App	643	25	49.0	545	7	US-11-065-943-87	Sequence 87, Appl
571	25	49.0	112	7	US-11-097-812-184	Sequence 184, App	644	25	49.0	545	7	US-11-065-943-89	Sequence 89, Appl
572	25	49.0	112	7	US-11-097-812-185	Sequence 185, App	645	25	49.0	545	7	US-11-065-943-91	Sequence 91, Appl
573	25	49.0	113	7	US-11-074-176-334	Sequence 334, App	646	25	49.0	545	7	US-11-065-943-93	Sequence 93, Appl
574	25	49.0	113	7	US-11-097-812-102	Sequence 102, App	647	25	49.0	545	7	US-11-065-943-95	Sequence 95, Appl
575	25	49.0	113	7	US-11-097-812-170	Sequence 170, App	648	25	49.0	545	7	US-11-065-943-97	Sequence 97, Appl
576	25	49.0	113	7	US-11-097-812-172	Sequence 172, App	649	25	49.0	545	7	US-11-065-943-99	Sequence 99, Appl
577	25	49.0	113	7	US-11-097-812-175	Sequence 175, App	650	25	49.0	545	7	US-10-850-816-2	Sequence 2, Appl
578	25	49.0	113	7	US-11-097-812-177	Sequence 177, App	651	25	49.0	554	6	US-10-850-816-4	Sequence 4, Appl
579	25	49.0	113	7	US-11-097-812-181	Sequence 181, App	652	25	49.0	554	6	US-10-850-816-6	Sequence 6, Appl
580	25	49.0	113	7	US-11-097-812-186	Sequence 186, App	653	25	49.0	554	6	US-10-850-816-6	Sequence 6, Appl
581	25	49.0	113	7	US-11-097-812-187	Sequence 187, App	654	25	49.0	560	6	US-10-763-712A-79	Sequence 79, Appl
582	25	49.0	113	7	US-11-097-812-188	Sequence 188, App	655	25	49.0	562	7	US-11-065-943-20	Sequence 20, Appl
583	25	49.0	113	7	US-11-097-812-204	Sequence 204, App	656	25	49.0	562	7	US-11-065-943-22	Sequence 22, Appl
584	25	49.0	115	7	US-11-097-812-28	Sequence 28, Appl	657	25	49.0	562	7	US-11-065-943-24	Sequence 24, Appl
585	25	49.0	115	7	US-11-097-812-35	Sequence 35, Appl	658	25	49.0	562	7	US-11-065-943-26	Sequence 26, Appl
586	25	49.0	116	7	US-11-074-176-124	Sequence 124, App	659	25	49.0	562	7	US-11-065-943-30	Sequence 30, Appl
587	25	49.0	119	7	US-11-097-812-134	Sequence 134, App	660	25	49.0	562	7	US-11-065-943-32	Sequence 32, Appl
588	25	49.0	119	7	US-11-097-812-148	Sequence 148, App	661	25	49.0	562	7	US-11-065-943-34	Sequence 34, Appl
589	25	49.0	119	7	US-11-097-812-152	Sequence 152, App	662	25	49.0	562	7	US-11-065-943-36	Sequence 36, Appl
590	25	49.0	126	6	US-10-467-657-892	Sequence 892, App	663	25	49.0	562	7	US-11-065-943-38	Sequence 38, Appl
591	25	49.0	161	6	US-10-793-626-2834	Sequence 2834, Ap	664	25	49.0	592	7	US-11-106-672A-14	Sequence 14, Appl
592	25	49.0	173	6	US-10-793-626-1070	Sequence 1070, Ap	665	25	49.0	604	6	US-10-467-657-2280	Sequence 2280, Ap
593	25	49.0	173	6	US-10-793-626-2702	Sequence 2702, Ap	666	25	49.0	636	6	US-10-485-517-170	Sequence 170, App
594	25	49.0	188	7	US-11-036-797-37	Sequence 37, Appl	667	25	49.0	644	6	US-10-821-234-1107	Sequence 1107, Ap
595	25	49.0	199	6	US-10-667-295-231	Sequence 31, App	668	25	49.0	678	6	US-10-055-877-202	Sequence 202, App
596	25	49.0	219	6	US-10-667-295-232	Sequence 232, App	669	25	49.0	687	6	US-10-055-877-201	Sequence 201, App
597	25	49.0	219	6	US-11-074-176-106	Sequence 106, App	670	25	49.0	802	6	US-10-873-528-75	Sequence 75, App
598	25	49.0	233	6	US-10-949-720-388	Sequence 388, App	671	25	49.0	832	7	US-11-065-943-100	Sequence 100, Appl
599	25	49.0	245	6	US-11-054-515-1844	Sequence 1844, Ap	672	25	49.0	832	7	US-11-007-797A-11	Sequence 11, Appl
600	25	49.0	252	7	US-10-793-626-1658	Sequence 1658, Ap	673	25	49.0	832	7	US-11-007-644B-11	Sequence 11, Appl
601	25	49.0	252	7	US-11-055-822-134	Sequence 134, App	674	25	49.0	892	6	US-10-507-278-3	Sequence 3, Appl
602	25	49.0	252	7	US-11-055-822-1120	Sequence 1120, Ap	675	25	49.0	904	6	US-10-507-278-5	Sequence 5, Appl
603	25	49.0	262	6	US-10-467-657-8100	Sequence 8100, Ap	676	25	49.0	1034	7	US-11-087-227-12	Sequence 12, Appl
604	25	49.0	306	7	US-11-052-554A-222	Sequence 222, App	677	25	49.0	1107	6	US-10-485-517-145	Sequence 145, App
605	25	49.0	322	7	US-11-052-554A-111	Sequence 131, App	678	25	49.0	1217	7	US-11-052-554A-9	Sequence 9, Appl
606	25	49.0	331	7	US-11-016-564-3	Sequence 36, Appl	679	25	49.0	1579	7	US-10-374-954-23	Sequence 23, Appl
607	25	49.0	333	6	US-10-949-720-396	Sequence 3, Appl	680	25	49.0	1861	6	US-10-374-954-23	Sequence 23, Appl
608	25	49.0	341	6	US-10-515-481-3	Sequence 6, Appl	681	25	49.0	1998	6	US-10-374-954-21	Sequence 21, Appl
609	25	49.0	341	6	US-10-515-481-6	Sequence 6, Appl	682	25	49.0	1998	6	US-10-374-954-21	Sequence 21, Appl

683	25	49.0	2009	6	US-10-374-954-2	Sequence 2, Appl1	756	24	47.1	399	6	US-10-793-626-2576	Sequence 2576, Ap
684	25	49.0	2015	7	US-11-052-554A-374	Sequence 374, App	757	24	47.1	418	6	US-10-485-517-174	Sequence 174, App
685	25	49.0	2261	6	US-10-995-561-600	Sequence 600, App	758	24	47.1	423	6	US-11-082-389-128	Sequence 128, App
686	25	49.0	2261	6	US-10-511-545-1	Sequence 1, Appl1	759	24	47.1	430	6	US-10-793-626-130	Sequence 130, App
687	25	49.0	2261	7	US-11-055-309A-9	Sequence 9, Appl1	760	24	47.1	430	6	US-10-517-939-80	Sequence 80, Appl
688	25	49.0	2261	7	US-11-055-309A-10	Sequence 10, Appl1	761	24	47.1	433	6	US-10-467-657-1434	Sequence 1434, Ap
689	24.5	48.0	12	7	US-11-125-837-7	Sequence 7, Appl1	762	24	47.1	433	7	US-11-167-856-16	Sequence 16, Appl1
690	24.5	48.0	91	7	US-11-144-248-22	Sequence 22, Appl1	763	24	47.1	438	7	US-11-067-121-19	Sequence 19, Appl1
691	24.5	48.0	91	7	US-11-144-222-22	Sequence 22, Appl1	764	24	47.1	440	6	US-10-821-234-1330	Sequence 1330, Ap
692	24.5	48.0	91	7	US-11-125-837-21	Sequence 21, Appl1	765	24	47.1	445	6	US-10-793-626-8858	Sequence 2858, Ap
693	24	47.1	130	7	US-11-125-837-21	Sequence 21, Appl1	766	24	47.1	452	6	US-10-624-932-28	Sequence 13, Appl
694	24	47.1	11	7	US-11-051-453-25	Sequence 25, Appl1	767	24	47.1	477	6	US-10-520-820-13	Sequence 106, App
695	24	47.1	16	6	US-10-485-788A-495	Sequence 495, App	768	24	47.1	498	6	US-10-524-647-108	Sequence 106, App
696	24	47.1	16	7	US-11-033-039-839	Sequence 839, App	769	24	47.1	508	7	US-11-075-185-26	Sequence 1093, Ap
697	24	47.1	29	7	US-11-041-103-8	Sequence 8, Appl1	770	24	47.1	509	6	US-10-821-234-1093	Sequence 1612, Ap
698	24	47.1	69	7	US-11-090-878-62	Sequence 62, Appl1	771	24	47.1	510	6	US-10-821-234-1612	Sequence 236, App
699	24	47.1	99	6	US-10-467-657-8622	Sequence 8622, Ap	772	24	47.1	512	6	US-10-517-939-236	Sequence 236, App
700	24	47.1	106	7	US-11-155-775-4	Sequence 4, Appl1	773	24	47.1	515	7	US-11-052-554A-255	Sequence 255, App
701	24	47.1	106	7	US-11-155-775-20	Sequence 20, Appl1	774	24	47.1	537	6	US-10-719-311-10	Sequence 10, Appl1
702	24	47.1	108	6	US-10-925-366A-93	Sequence 93, Appl1	775	24	47.1	539	6	US-10-878-556A-88	Sequence 88, Appl1
703	24	47.1	108	6	US-10-925-366A-141	Sequence 141, App	776	24	47.1	549	7	US-11-085-185-2	Sequence 2, Appl1
704	24	47.1	108	6	US-10-925-366A-154	Sequence 154, App	777	24	47.1	549	7	US-10-959-310-7	Sequence 7, Appl1
705	24	47.1	108	6	US-10-925-366A-167	Sequence 167, App	778	24	47.1	575	6	US-10-959-310-8	Sequence 8, Appl1
706	24	47.1	108	6	US-10-925-366A-168	Sequence 168, App	779	24	47.1	575	7	US-11-131-212-23	Sequence 23, Appl1
707	24	47.1	108	6	US-10-925-366A-171	Sequence 171, App	780	24	47.1	575	7	US-11-131-212-24	Sequence 24, Appl1
708	24	47.1	108	6	US-10-925-366A-182	Sequence 182, App	781	24	47.1	575	6	US-10-131-826A-46	Sequence 46, Appl1
709	24	47.1	108	6	US-10-925-366A-184	Sequence 184, App	782	24	47.1	594	7	US-11-012-762-4	Sequence 4, Appl1
710	24	47.1	108	6	US-10-925-366A-189	Sequence 189, App	783	24	47.1	601	6	US-10-467-657-7120	Sequence 7120, Ap
711	24	47.1	108	6	US-10-925-366A-201	Sequence 201, App	784	24	47.1	607	7	US-11-167-856-18	Sequence 18, Appl1
712	24	47.1	109	6	US-11-041-471-8	Sequence 8, Appl1	785	24	47.1	617	6	US-10-878-556A-67	Sequence 67, Appl1
713	24	47.1	112	7	US-11-054-669-113	Sequence 113, App	786	24	47.1	619	7	US-11-205-109-37	Sequence 37, Appl1
714	24	47.1	112	7	US-11-054-669-115	Sequence 115, App	787	24	47.1	621	7	US-11-184-380-26	Sequence 26, Appl1
715	24	47.1	125	7	US-11-155-775-14	Sequence 14, Appl1	788	24	47.1	623	6	US-10-719-311-12	Sequence 12, Appl1
716	24	47.1	128	6	US-10-510-386-78	Sequence 78, Appl1	789	24	47.1	623	6	US-10-719-311-11	Sequence 11, Appl1
717	24	47.1	168	6	US-10-793-626-724	Sequence 724, App	790	24	47.1	626	6	US-10-467-657-1772	Sequence 1772, Ap
718	24	47.1	172	6	US-10-793-626-1952	Sequence 1952, Ap	791	24	47.1	633	6	US-10-467-657-6628	Sequence 6628, Ap
719	24	47.1	178	6	US-10-821-234-1052	Sequence 1052, Ap	792	24	47.1	643	6	US-10-510-386-8	Sequence 8, Appl1
720	24	47.1	178	7	US-11-055-822-118	Sequence 118, App	793	24	47.1	654	7	US-11-120-308-52	Sequence 52, Appl1
721	24	47.1	178	7	US-11-055-822-488	Sequence 488, App	794	24	47.1	688	7	US-11-165-226-124	Sequence 124, App
722	24	47.1	197	7	US-11-090-878-54	Sequence 54, Appl1	795	24	47.1	711	6	US-10-510-386-10	Sequence 10, Appl1
723	24	47.1	197	7	US-11-120-308-46	Sequence 46, Appl1	796	24	47.1	711	6	US-10-821-234-1017	Sequence 1017, Ap
724	24	47.1	199	6	US-10-374-954-5	Sequence 5, Appl1	797	24	47.1	738	7	US-11-147-047-48	Sequence 48, Appl1
725	24	47.1	251	7	US-11-054-515-1310	Sequence 1310, Ap	798	24	47.1	770	7	US-11-070-627-10	Sequence 10, Appl1
726	24	47.1	253	6	US-10-467-657-8346	Sequence 8346, Ap	799	24	47.1	770	7	US-10-821-234-1271	Sequence 1271, Ap
727	24	47.1	257	6	US-10-467-657-5118	Sequence 5118, Ap	800	24	47.1	809	6	US-10-467-657-1106	Sequence 1106, Ap
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730	24	47.1	281	6	US-10-878-556A-27	Sequence 27, Appl1	803	24	47.1	844	6	US-10-453-372-856	Sequence 856, App
731	24	47.1	287	6	US-10-980-388-66	Sequence 66, Appl1	804	24	47.1	869	7	US-11-113-751-2	Sequence 2, Appl1
732	24	47.1	290	6	US-10-467-657-3190	Sequence 3190, Ap	805	24	47.1	896	7	US-11-192-219-3	Sequence 3, Appl1
733	24	47.1	291	7	US-11-032-797-6	Sequence 6, Appl1	806	24	47.1	897	6	US-10-821-234-1523	Sequence 1523, Ap
734	24	47.1	299	6	US-10-967-671-13	Sequence 13, Appl1	807	24	47.1	898	7	US-11-166-770-3	Sequence 3, Appl1
735	24	47.1	302	6	US-10-858-730-119	Sequence 119, App	808	24	47.1	923	7	US-11-192-219-4	Sequence 4, Appl1
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737	24	47.1	304	6	US-10-055-877-173	Sequence 173, App	810	24	47.1	932	7	US-11-103-959-13	Sequence 13, Appl1
738	24	47.1	304	7	US-11-033-039-824	Sequence 824, App	811	24	47.1	964	7	US-11-145-631-2	Sequence 2, Appl1
739	24	47.1	308	6	US-10-793-626-1732	Sequence 1732, Ap	812	24	47.1	1024	7	US-11-147-047-49	Sequence 49, Appl1
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748	24	47.1	369	7	US-11-055-822-116	Sequence 486, App	821	24	47.1	1476	6	US-10-647-956A-4	Sequence 4, Appl1
749	24	47.1	373	7	US-11-127-877-46	Sequence 46, Appl1	822	24	47.1	1970	6	US-10-821-234-1641	Sequence 1641, Ap
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752	24	47.1	392	6	US-10-467-657-2726	Sequence 2726, Ap	825	24	47.1	96	7	US-11-054-669-88	Sequence 135, App
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755	24	47.1	399	6	US-10-926-709-17	Sequence 17, Appl1	828	23.5	46.1	141	7	US-11-128-900-88	Sequence 88, Appl1

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832	23.5	46.1	235	7	US-11-128-900-65	Sequence 65, Appl	905	23	45.1	204	7	US-11-033-039-271	Sequence 271, App
833	23.5	46.1	253	7	US-11-054-515-1499	Sequence 1499, App	906	23	45.1	207	6	US-10-667-295-20	Sequence 20, Appl
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835	23	45.1	11	7	US-11-127-677-101	Sequence 101, App	908	23	45.1	208	6	US-10-878-556A-133	Sequence 133, App
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862	23	45.1	108	6	US-10-925-366A-152	Sequence 152, App	935	23	45.1	243	7	US-11-054-515-1935	Sequence 1935, App
863	23	45.1	108	6	US-10-925-366A-156	Sequence 156, App	936	23	45.1	243	7	US-11-054-515-1943	Sequence 1943, App
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874	23	45.1	116	6	US-10-467-657-9026	Sequence 9026, App	947	23	45.1	247	7	US-11-054-515-1177	Sequence 1177, App
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881	23	45.1	142	6	US-10-526-716-4	Sequence 4, Appl	954	23	45.1	248	7	US-11-054-515-1778	Sequence 1778, App
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23 45.1 270 6 US-10-841-956A-5 Sequence 5, Appl
23 45.1 271 6 US-10-793-626-678 Sequence 678, App
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23 45.1 290 6 US-10-793-626-3024 Sequence 3024, Ap
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23 45.1 293 6 US-10-841-956A-9 Sequence 9, Appl
23 45.1 295 6 US-10-873-528-195 Sequence 195, App
23 45.1 296 6 US-10-954-468-9 Sequence 9, Appl
23 45.1 301 7 US-11-074-176-362 Sequence 362, App
23 45.1 302 6 US-10-793-626-1144 Sequence 1144, Ap
23 45.1 303 7 US-11-080-991-72 Sequence 72, Appl
23 45.1 303 7 US-11-087-719-71 Sequence 71, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 13, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Prestia, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-Oct-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-Feb-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1CID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-665-658-13

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Best Local Similarity 100.0%; Pred. No. 5,4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-665-658-59
; Sequence 59, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Prestia, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-Nov-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-Oct-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-Feb-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1CID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
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RESULT 3
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; Sequence 49, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 49
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-49

Query Match          100.0%; Score 51; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
      |||||
      24 RASKTISKYLA 34

RESULT 4
US-11-107-028-51
; Sequence 51, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-107-028-51

Query Match          100.0%; Score 51; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
      |||||
      24 RASKTISKYLA 34

RESULT 5
US-10-665-658-1
; Sequence 1, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-Nov-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-Oct-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-Feb-2001

ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-665-658-1

Query Match          100.0%; Score 51; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.00073;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
      |||||
      24 RASKTISKYLA 34

RESULT 6
US-10-665-658-2
; Sequence 2, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
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1      PRIOR APPLICATION DATA:
2      APPLICATION NUMBER: 60/031971
3      FILING DATE: 27-NOV-1996
4      APPLICATION NUMBER: 08/974899
5      FILING DATE: 20-NOV-1997
6      APPLICATION NUMBER: 03/420745
7      FILING DATE: 20-OCT-1999
8      APPLICATION NUMBER: 03/975798
9      FILING DATE: 28-FEB-2001
10     ATTORNEY/AGENT INFORMATION:
11     NAME: Tan, Lee K.
12     REGISTRATION NUMBER: 39,447
13     REFERENCE/DOCKET NUMBER: P1014R1CIDIC
14     TELECOMMUNICATION INFORMATION:
15     TELEPHONE: 650/225-4462
16     TELEFAX: 650/952-9881
17     INFORMATION FOR SEQ ID NO: 2:
18     SEQUENCE CHARACTERISTICS:
19     LENGTH: 108 amino acids
20     TYPE: Amino acid
21     TOPOLOGY: linear
22
23     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
24     GS-10-665-658-2

```

Query Match	100.0%;	Score 51;	DB 6;	Length 108;
Best Local Similarity	100.0%;	Pred. No. 0.00073;		
Matches	11;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qy	1	RASKTISKYLA	11	
Db	24	RASKTISKYLA	34	

```

RESULT 7
US-10-771-257-32
; Sequence 32. Application US/10771257
; Publication No. US20050288864A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
; APPLICANT: Cattaneo, Antonino
; APPLICANT: Maritan, Amos
; APPLICANT: Vainilin, Michela
; APPLICANT: Rabbitts, Terrence H
; APPLICANT: Setlami, Giovanni
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2272
; CURRENT APPLICATION NUMBER: US/10/771,257
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/GB02/03512
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0119004.0
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: GB 0121577.1
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: GB 0200928.0
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: GB 0203569.9
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: IT RM2001A00063
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-257-32

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Query Match	78.4%;	Score 40;	DB 6;	Length 108;
Best Local Similarity	72.7%;	Pred. No. 0.13;		
Matches	8;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;

```
Qy      1 RASKTISKYLA 11
Db      24 RASRAIAKYLA 34
```

```

RESULT 8
US-11-127-677-32
; Sequence 32, Application US/11/127677
; Publication NO. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127, 677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scfv
US-11-127-677-32

```

Query Match	78.4%	Score 40;	DB 7;	Length 108;
Best Local Similarity	72.7%	Pred. No. 0.13;		
Matches	8;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY	1	RASKTISKYLA	11
		: :	
Db	24	RASPAIAKYLA	34

RESULT 9
 US-10-665-658-3
 Sequence 3, Application US/10665658
 Publication NO. US20050276801A1
 GENERAL INFORMATION:
 APPLICANT: Jardieu, Paula M.
 Prestea, Leonard G.
 TITLE OF INVENTION: Humanized Anti-CD14 Antibodies
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 City: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/665,658
 FILING DATE: 19-Sep-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/031971
 FILING DATE: 27-NOV-1996
 APPLICATION NUMBER: 08/974899
 FILING DATE: 20-NOV-1997
 APPLICATION NUMBER: 09/420745
 FILING DATE: 20-OCT-1999
 APPLICATION NUMBER: 09/975798

```

; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1CID1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 108 amino acids
;         TYPE: Amino Acid
;         TOPOLOGY: Linear
;     SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-665-658-3

Query Match      74.5%; Score 38; DB 6; Length 108;
Best Local Similarity 72.7%; Pred. No. 0.33;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 10
US-11-120-338-3
; Sequence 3, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: MALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-3

Query Match      74.5%; Score 38; DB 7; Length 108;
Best Local Similarity 72.7%; Pred. No. 0.33;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 11
US-11-106-820-3
; Sequence 3, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
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```

; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-820-3

Query Match      74.5%; Score 38; DB 7; Length 108;
Best Local Similarity 72.7%; Pred. No. 0.33;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 12
US-11-096-046-5
; Sequence 5, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE
; APPLICANT: FIVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954R1US
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-5

Query Match      74.5%; Score 38; DB 7; Length 109;
Best Local Similarity 72.7%; Pred. No. 0.33;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASKTISKYLA 11
        |||::|||
Db      24 RASQISINYLA 34

RESULT 13
US-11-093-274-10
; Sequence 10, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutler, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; SOFTWARE: PatentIn version 3.2
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-10
```

Query Match 72.5% Score 37; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.039;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
Db 1 RASQSVSSYLA 11

RESULT 14
US-11-093-274-11
; Sequence 11, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutler, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-11

Query Match 72.5% Score 37; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.039;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
Db 1 RASQSVSSYLA 11

RESULT 15
US-11-093-274-12
; Sequence 12, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutler, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-12

Query Match 72.5% Score 37; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.039;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
Db 1 RASQSVSSYLA 11

Db 1 RASQSVSSYLA 11

RESULT 16
US-11-051-453-19
; Sequence 19, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BARCOCCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; FILE REFERENCE: M01-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-19

Query Match 72.5% Score 37; DB 7; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.039;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
Db 1 RASQSVSSYLA 11

RESULT 17
US-11-093-274-33
; Sequence 33, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutler, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-33

Query Match 72.5% Score 37; DB 7; Length 94;
Best Local Similarity 63.6%; Pred. No. 0.45;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
Db 1 RASQSVSSYLA 11

Db 24 RASQSVSYLA 34
 |||::| |||

RESULT 18
 US-11-054-669-86
 ; Sequence 86, Application US/11054669
 ; Publication No. US20050261480A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Foote, Jefferson
 ; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
 ; FILE REFERENCE: 30219/US/3
 ; CURRENT APPLICATION NUMBER: US/11/054,669
 ; PRIOR FILING DATE: 2005-02-08
 ; PRIOR FILING DATE: 2002-07-12
 ; PRIOR FILING DATE: 2001-07-12
 ; PRIOR FILING DATE: 2001-07-12
 ; NUMBER OF SEQ ID NOS: 124
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 86
 ; LENGTH: 95
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-054-669-86

Query Match 72.5%; Score 37; DB 7; Length 95;
 Best Local Similarity 63.6%; Pred. No. 0.46;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 |||::| |||

Db 24 RASQSVSYLA 34

RESULT 19
 US-11-084-554-138
 ; Sequence 138, Application US/11084554
 ; Publication No. US20050260679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kellermann, Strid-AI
 ; APPLICANT: Green, Larry L.
 ; APPLICANT: Korver, Wouter
 ; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
 ; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
 ; FILE REFERENCE: ABGENIX.100A
 ; CURRENT APPLICATION NUMBER: US/11/084,554
 ; CURRENT FILING DATE: 2005-03-17
 ; PRIOR FILING DATE: 2004-03-19
 ; PRIOR FILING DATE: 2004-05-24
 ; PRIOR FILING DATE: 2004-05-24
 ; NUMBER OF SEQ ID NOS: 266
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 138
 ; LENGTH: 95
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-084-554-138

Query Match 72.5%; Score 37; DB 7; Length 95;
 Best Local Similarity 63.6%; Pred. No. 0.46;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 |||::| |||

Db 24 RASQSVSYLA 34

RESULT 20
 US-11-061-848-52
 ; Sequence 52, Application US/11061848
 ; Publication No. US20050288491A1

; GENERAL INFORMATION:
 ; APPLICANT: Wilson, David S.
 ; APPLICANT: Nock, Steffen
 ; APPLICANT: Larrick, James W.
 ; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
 ; FILE REFERENCE: 186280/US
 ; CURRENT APPLICATION NUMBER: US/11/061,848
 ; CURRENT FILING DATE: 2005-02-17
 ; PRIOR FILING DATE: 2004-02-17
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 52
 ; LENGTH: 95
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-061-848-52

Query Match 72.5%; Score 37; DB 7; Length 95;
 Best Local Similarity 63.6%; Pred. No. 0.46;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 |||::| |||

Db 24 RASQSVSYLA 34

RESULT 21
 US-11-061-848-65
 ; Sequence 65, Application US/11061848
 ; Publication No. US20050288491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wilson, David S.
 ; APPLICANT: Nock, Steffen
 ; APPLICANT: Larrick, James W.
 ; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
 ; FILE REFERENCE: 186280/US
 ; CURRENT APPLICATION NUMBER: US/11/061,848
 ; CURRENT FILING DATE: 2005-02-17
 ; PRIOR FILING DATE: 2004-02-17
 ; NUMBER OF SEQ ID NOS: 78
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 65
 ; LENGTH: 95
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-061-848-65

Query Match 72.5%; Score 37; DB 7; Length 95;
 Best Local Similarity 63.6%; Pred. No. 0.46;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
 |||::| |||

Db 24 RASQSVSYLA 34

RESULT 22
 US-11-061-848-66
 ; Sequence 66, Application US/11061848
 ; Publication No. US20050288491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wilson, David S.
 ; APPLICANT: Nock, Steffen
 ; APPLICANT: Larrick, James W.
 ; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
 ; FILE REFERENCE: 186280/US
 ; CURRENT APPLICATION NUMBER: US/11/061,848
 ; CURRENT FILING DATE: 2005-02-17
 ; PRIOR FILING DATE: 2004-02-17
 ; NUMBER OF SEQ ID NOS: 78

SOFTWARE: PatentIn version 3.3
SEQ ID NO 66
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
US-11-061-848-66

Query Match 72.5%; Score 37; DB 7; Length 95;
Best Local Similarity 63.6%; Pred. No. 0.46;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
|||::|
Db 24 RASQSVSSYLA 34

RESULT 23
US-11-040-159-17
Sequence 17, Application US/11040159
Publication No. US2005025552A1
GENERAL INFORMATION:
APPLICANT: Flynn, Peter
APPLICANT: Luehrs, Kenneth
APPLICANT: Balinc, Robert F.
APPLICANT: Her, Jeng-Horng
APPLICANT: Bebbington, Christopher R.
APPLICANT: Yarranton, Geoffrey T.
APPLICANT: Kalobios, Inc.
TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
TITLE OF INVENTION: Binding Determinants
FILE REFERENCE: 021167-001730US
CURRENT APPLICATION NUMBER: US/11/040,159
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 60/537,364
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/546,216
PRIOR FILING DATE: 2004-02-23
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: V-region of
US-11-040-159-17

Query Match 72.5%; Score 37; DB 7; Length 107;
Best Local Similarity 63.6%; Pred. No. 0.52;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
|||::|
Db 24 RASQSVSSYLA 34

RESULT 24
US-11-093-274-24
Sequence 24, Application US/11093274
Publication No. US20050266008A1
GENERAL INFORMATION:
APPLICANT: Graziano, Robert
APPLICANT: Cardarelli, Josephine M.
APPLICANT: Kempe, Thomas
APPLICANT: Cutler, Beth
APPLICANT: Srinivasan, Mohan
TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
FILE REFERENCE: 04280/1201101-US1
CURRENT APPLICATION NUMBER: US/11/093,274
CURRENT FILING DATE: 2005-03-28
PRIOR APPLICATION NUMBER: 60/557,741
PRIOR FILING DATE: 2004-03-29

NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.2
SEQ ID NO 24
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-11-093-274-24

Query Match 72.5%; Score 37; DB 7; Length 107;
Best Local Similarity 63.6%; Pred. No. 0.52;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
|||::|
Db 24 RASQSVSSYLA 34

RESULT 25
US-11-093-274-22
Sequence 22, Application US/11093274
Publication No. US20050266008A1
GENERAL INFORMATION:
APPLICANT: Graziano, Robert
APPLICANT: Cardarelli, Josephine M.
APPLICANT: Kempe, Thomas
APPLICANT: Cutler, Beth
APPLICANT: Srinivasan, Mohan
TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
FILE REFERENCE: 04280/1201101-US1
CURRENT APPLICATION NUMBER: US/11/093,274
CURRENT FILING DATE: 2005-03-28
PRIOR APPLICATION NUMBER: 60/557,741
PRIOR FILING DATE: 2004-03-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-11-093-274-22

Query Match 72.5%; Score 37; DB 7; Length 108;
Best Local Similarity 63.6%; Pred. No. 0.53;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RASKTISKYLA 11
|||::|
Db 24 RASQSVSSYLA 34

RESULT 26
US-11-093-274-23
Sequence 23, Application US/11093274
Publication No. US20050266008A1
GENERAL INFORMATION:
APPLICANT: Graziano, Robert
APPLICANT: Cardarelli, Josephine M.
APPLICANT: Kempe, Thomas
APPLICANT: Cutler, Beth
APPLICANT: Srinivasan, Mohan
TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
FILE REFERENCE: 04280/1201101-US1
CURRENT APPLICATION NUMBER: US/11/093,274
CURRENT FILING DATE: 2005-03-28
PRIOR APPLICATION NUMBER: 60/557,741
PRIOR FILING DATE: 2004-03-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-11-093-274-23

Query Match 72.5%; Score 37; DB 7; Length 108;
Best Local Similarity 63.6%; Pred. No. 0.53;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||::|
Db 24 RASQSVSSYLA 34

RESULT 27

US-11-051-453-5
; Sequence 5, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MJI-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-5

Query Match 72.5%; Score 37; DB 7; Length 108;
Best Local Similarity 63.6%; Pred. No. 0.53;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||::|
Db 24 RASQSVSSYLA 34

RESULT 28

US-10-721-763-31
; Sequence 31, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCF
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-721-763-31

Query Match 72.5%; Score 37; DB 6; Length 128;
Best Local Similarity 63.6%; Pred. No. 0.64;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||::|
Db 44 RASQSVSSYLA 54

RESULT 29

US-11-051-453-50
; Sequence 50, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MJI-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 50
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-50

Query Match 72.5%; Score 37; DB 7; Length 128;
Best Local Similarity 63.6%; Pred. No. 0.64;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASKTISKYLA 11
|||::|
Db 44 RASQSVSSYLA 54

RESULT 30

US-11-128-900-16
; Sequence 16, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: US 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087

```
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-16
```

```
Query Match          72.5%; Score 37; DB 7; Length 139;
Best Local Similarity 63.6%; Pred. No. 0.71;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

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QY 1 RASKTISKYLA 11
    |||::|||
Db 16 RASQSVSYLA 26
```

```
RESULT 31
US-11-128-900-90
; Sequence 90, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PPI DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-90
```

```
Query Match          72.5%; Score 37; DB 7; Length 139;
Best Local Similarity 63.6%; Pred. No. 0.71;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RASKTISKYLA 11
    |||::|||
Db 16 RASQSVSYLA 26
```

```
RESULT 32
US-11-128-900-91
; Sequence 91, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
```

```
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PPI DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-91
```

```
Query Match          72.5%; Score 37; DB 7; Length 142;
Best Local Similarity 63.6%; Pred. No. 0.72;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RASKTISKYLA 11
    |||::|||
Db 19 RASQSVSYLA 29
```

```
RESULT 33
US-11-128-900-21
; Sequence 21, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PPI DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-21
```

```
Query Match          72.5%; Score 37; DB 7; Length 146;
Best Local Similarity 63.6%; Pred. No. 0.75;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

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QY 1 RASKTISKYLA 11
    |||::|||
Db 19 RASQSVSYLA 29
```

```
RESULT 34
US-11-128-900-93
; Sequence 93, Application US/11128900
```



```
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN E.
/ APPLICANT: HANKE, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PFI DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ PRIOR FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 93
/ LENGTH: 146
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-93
```

```
Query Match          72.5%; Score 37; DB 7; Length 146;
Best Local Similarity 63.6%; Pred. No. 0.75;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RASKTISKYLA 11
    |||::|||
Db 19 RASQSVSYLA 29
```

```
RESULT 35
US-11-128-900-17
/ Sequence 17, Application US/11128900
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN E.
/ APPLICANT: HANKE, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PFI DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ PRIOR FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 17
/ LENGTH: 234
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-17
```

```
Query Match          72.5%; Score 37; DB 7; Length 234;
Best Local Similarity 63.6%; Pred. No. 1.3;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

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QY 1 RASKTISKYLA 11
    |||::|||
Db 44 RASQSVSYLA 54
```

```
RESULT 36
US-11-128-900-69
/ Sequence 69, Application US/11128900
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN E.
/ APPLICANT: HANKE, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PFI DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ PRIOR FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 69
/ LENGTH: 234
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-69
```

```
Query Match          72.5%; Score 37; DB 7; Length 234;
Best Local Similarity 63.6%; Pred. No. 1.3;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 RASKTISKYLA 11
    |||::|||
Db 44 RASQSVSYLA 54
```

```
RESULT 37
US-11-054-515-1049
/ Sequence 1049, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruden et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
/ FILE REFERENCE: PFS23P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
```

; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1049

Query Match 72.5%; Score 37; DB 7; Length 251;
Best Local Similarity 63.6%; Pred. No. 1.4;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYLA 11
|||:|:|
Db 166 RASQSVSYLA 176

RESULT 38
US-11-064-174-44
; Sequence 44, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain 113
US-11-064-174-44

Query Match 70.6%; Score 36; DB 7; Length 107;
Best Local Similarity 70.0%; Pred. No. 0.84;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
|||:|:|
Db 23 RASQSVSYLA 32

RESULT 39
US-11-064-174-169
; Sequence 169, Application US/11064174
; Publication No. US2005028252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/11/064,174
; PRIOR FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550

; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 169
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH39
US-11-064-174-169

Query Match 70.6%; Score 36; DB 7; Length 107;
Best Local Similarity 70.0%; Pred. No. 0.84;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
|||:|:|
Db 23 RASQSVSYLA 32

RESULT 40
US-11-127-932-12
; Sequence 12, Application US/11127932
; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular scfv
US-11-127-932-12

Query Match 70.6%; Score 36; DB 7; Length 108;
Best Local Similarity 70.0%; Pred. No. 0.85;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYL 10
|||:|:|
Db 24 RASQSVSYLA 33

RESULT 41
US-11-127-932-13
; Sequence 13, Application US/11127932
; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1

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/ SEQ ID NO 13
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: anti-RAS intracellular scfv
US-11-127-932-13
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Query Match          70.6%; Score 36; DB 7; Length 108;
Best Local Similarity 70.0%; Pred. No. 0.85;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RASKTISKYL 10
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Db      24 RASQGISRYL 33
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RESULT 42

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US-11-064-174-181
/ Sequence 181, Application US/11064174
/ Publication No. US2005028252A1
/ GENERAL INFORMATION:
/ APPLICANT: Siegel, Donald L.
/ TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
/ TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
/ FILE REFERENCE: 09596-42U2
/ CURRENT APPLICATION NUMBER: US/11/064,174
/ CURRENT FILING DATE: 2005-02-22
/ PRIOR APPLICATION NUMBER: US/09/240,274
/ PRIOR FILING DATE: 1999-01-29
/ PRIOR APPLICATION NUMBER: 60/081,380
/ PRIOR FILING DATE: 1998-04-10
/ PRIOR APPLICATION NUMBER: 60/028,550
/ PRIOR FILING DATE: 1996-10-11
/ NUMBER OF SEQ ID NOS: 224
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 181
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-11-064-174-181
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Query Match          70.6%; Score 36; DB 7; Length 108;
Best Local Similarity 70.0%; Pred. No. 0.85;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RASKTISKYL 10
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Db      23 RASQGISRYL 32
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RESULT 43

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US-11-127-903-12
/ Sequence 12, Application US/11127903
/ Publication No. US20050288492A1
/ GENERAL INFORMATION:
/ APPLICANT: Medical Research Council
/ APPLICANT: Rabbits, Terence H
/ APPLICANT: Tanaka, Tomoyuki
/ TITLE OF INVENTION: Anti-activated RAS Antibodies
/ FILE REFERENCE: 18396/2482
/ CURRENT APPLICATION NUMBER: US/11/127,903
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: PCT/GB03/04953
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: GB 0226728.4
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: GB 0226729.2
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: GB 0316680.8
/ PRIOR FILING DATE: 2003-07-16
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/ PRIOR APPLICATION NUMBER: GB 0226723.5
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: GB 0226731.8
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: GB 0226727.6
/ PRIOR FILING DATE: 2002-11-15
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 12
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: anti-RAS intracellular antibody
US-11-127-903-12
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Query Match          70.6%; Score 36; DB 7; Length 108;
Best Local Similarity 70.0%; Pred. No. 0.85;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RASKTISKYL 10
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Db      24 RASQGISRYL 33
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RESULT 44

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US-11-127-903-13
/ Sequence 13, Application US/11127903
/ Publication No. US20050288492A1
/ GENERAL INFORMATION:
/ APPLICANT: Medical Research Council
/ APPLICANT: Rabbits, Terence H
/ APPLICANT: Tanaka, Tomoyuki
/ TITLE OF INVENTION: Anti-activated RAS Antibodies
/ FILE REFERENCE: 18396/2482
/ CURRENT APPLICATION NUMBER: US/11/127,903
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: PCT/GB03/04953
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: GB 0226728.4
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: GB 0226729.2
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: GB 0316680.8
/ PRIOR FILING DATE: 2003-07-16
/ PRIOR APPLICATION NUMBER: GB 0226723.5
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: GB 0226731.8
/ PRIOR FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: GB 0226727.6
/ PRIOR FILING DATE: 2002-11-15
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 13
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: anti-RAS intracellular antibody
US-11-127-903-13
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Query Match          70.6%; Score 36; DB 7; Length 108;
Best Local Similarity 70.0%; Pred. No. 0.85;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RASKTISKYL 10
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Db      24 RASQGISRYL 33
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RESULT 45
US-11-127-932-16
/ Sequence 16, Application US/11127932
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; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular scFv
US-11-127-932-16

Query Match          70.6%; Score 36; DB 7; Length 109;
Best Local Similarity 70.0%; Pred. No. 0.86;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYTL 10
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Db 25 RASQSIISRYL 34

RESULT 46
US-11-127-932-17
; Sequence 17, Application US/11127932
; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 25
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular scFv
US-11-127-932-17

Query Match          70.6%; Score 36; DB 7; Length 109;
Best Local Similarity 70.0%; Pred. No. 0.86;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASKTISKYTL 10
   |||::|||:|
Db 25 RASQSIISRYL 34

RESULT 47
US-11-127-932-20
; Sequence 20, Application US/11127932
; Publication No. US20050276800A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
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; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intrabodies
; FILE REFERENCE: 18396/2472
; CURRENT APPLICATION NUMBER: US/11/127,932
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04943
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 25
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; SEQ ID NO 20
; LENGTH: 109
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular scFv
US-11-127-932-20
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Query Match          70.6%; Score 36; DB 7; Length 109;
Best Local Similarity 70.0%; Pred. No. 0.86;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RASKTISKYTL 10
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Db 25 RASQSIISRYL 34
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RESULT 48
US-11-127-903-16
; Sequence 16, Application US/11127903
; Publication No. US20050288492A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Anti-activated RAS Antibodies
; FILE REFERENCE: 18396/2482
; CURRENT APPLICATION NUMBER: US/11/127,903
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04953
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226728.4
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0316680.8
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: GB 0226723.5
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226731.8
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular antibody
US-11-127-903-16
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Query Match          70.6%; Score 36; DB 7; Length 109;
Best Local Similarity 70.0%; Pred. No. 0.86;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RASKTISKYTL 10
   |||::|||:|
Db 25 RASQSIISRYL 34
```

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RESULT 49
US-11-127-903-17
; Sequence 17, Application US/11127903
; Publication No. US20050288492A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Anti-activated RAS Antibodies
; FILE REFERENCE: 18396/2482
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04953
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226728.4
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0316680.8
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: GB 0226723.5
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226731.8
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular antibody
US-11-127-903-17

Query Match          70.6%; Score 36; DB 7; Length 109;
Best Local Similarity 70.0%; Pred. No. 0.86;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASKTISKYL 10
      |||:|:|
Db      25 RASQISRYL 34

RESULT 50
US-11-127-903-20
; Sequence 20, Application US/11127903
; Publication No. US20050288492A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Anti-activated RAS Antibodies
; FILE REFERENCE: 18396/2482
; CURRENT APPLICATION NUMBER: US/11/127,903
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04953
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226728.4
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0316680.8
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: GB 0226723.5
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226731.8
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226727.6
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 53
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: anti-RAS intracellular antibody
US-11-127-903-20

Query Match          70.6%; Score 36; DB 7; Length 109;
Best Local Similarity 70.0%; Pred. No. 0.86;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASKTISKYL 10
      |||:|:|
Db      25 RASQISRYL 34
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:46:53 ; Search time 43.803 Seconds
(without alignments)
70.215 Million cell updates/sec

Title: US-10-665-658-14
Perfect score: 32
Sequence: 1 SGSTIQS 7

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Searched: 2443163 seqs, 439378781 residues

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Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	32	100.0	107	9	ADV66159
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9	32	100.0	107	9	AAE62455
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39	29	90.6	109	2	AAZ29449
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43	29	90.6	109	6	ABU59499
44	29	90.6	109	6	AAE39082
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49	29	90.6	1377	3	AAE41151
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56	29	90.6	1892	4	AAW79884
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58	29	90.6	2275	7	ADG31684
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65	28	87.5	17	2	AD184068
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73	28	87.5	18	2	AAW24034
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76	28	87.5	61	4	AAW59911
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78	28	87.5	67	4	AAU18857
79	28	87.5	67	4	AAW94949
80	28	87.5	67	4	AAW96644
81	28	87.5	80	4	AAW24279
82	28	87.5	82	4	ADW87137
83	28	87.5	110	4	AAW75578
84	28	87.5	171	5	ABW54067
85	28	87.5	186	4	ABW70425
86	28	87.5	191	8	ADY13068
87	28	87.5	223	4	ABG06419
88	28	87.5	232	8	ADN71920
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90	28	87.5	294	7	ABW85551
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92	28	87.5	304	6	ABW70276
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94	28	87.5	361	8	ADW93198
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97	28	87.5	435	8	ADN24254

AAV17961	Mouse scf
AAV17959	Mouse scf
AAV10863	S11-VGF2
ADZ83409	C-termina
ADW66089	Anti-CD3-
ADW66123	Anti-CD3-
ADW66125	Anti-CD3-
ADZ83427	Deimmuniz
AAV10864	S11-scVEG
ADW66113	Anti-CD3-
ADRO3420	Humanised
ADRO3421	Humanised
AAO22075	Human pro
ADP59199	Human pol
AAZ29449	Human 11g
AAV77752	Human 11g
AAV30309	Human 11g
ABU13786	Human 11g
ABU59499	Human 11g
AAE39082	Human 11g
ABU38629	Protein e
ABO74075	Pseudomon
ABE63332	Drosophila
AAW58376	Human b7a
AAE41151	Human ORP
ABR41958	Human HMG
ADG33264	Human nov
ABG09044	Novel hum
AAW78900	Human pro
AAW78899	Human pro
AAW79883	Human pro
AAW79884	Human pro
ABG09042	Novel hum
ADG31684	Human nov
AAW07864	Reovirus
AAW38270	Reo3R-bin
AAW38275	Reo3R-bin
AAW07865	Dimerisin
AAW24035	VL-Fil pe
AAW24039	VL-Fil pe
AD184068	Monoclonal
AD184072	Monoclonal
AAW91552	Monoclonal
AAW38268	Reo3R-bin
AAW38272	Reo3R-bin
AAW38269	Reo3R-bin
AAW07866	Dimerisin
AAW24043	VL-Fil pe
AAW24034	VL-Fil pe
ADJ84069	Monoclonal
ADJ84087	Anti-rece
AAW59911	Propionib
ABW56430	Novel pro
AAU18857	Human rep
AAW94949	Human exc
AAW96644	Human kid
AAW24279	Anti-huma
ADW87137	Human col
AAW75578	Human col
ABW54067	Lactococc
ABW70425	Drosophila
ADY13068	Novel hum
ABG06419	Novel hum
ADN71920	Mouse MAP
ADW93196	Plant ful
ABW85551	Human pro
AAW47072	Immunogen
ABW70276	Photofab
ADW68893	Plant ful
ADW93198	Plant ful
AAW70389	Hypertens
ADW79090	Plant ful
ADN24254	Bacterial

98	28	87.5	454	5	ABP73979	Abp73979	Candida a	171	27	84.4	593	2	AAE63208	AAE63208	CryIA(a) I
99	28	87.5	472	8	ADY05388	Ady05388	Plant ful	172	27	84.4	593	2	AAE97660	AAE97660	Bacillus
100	28	87.5	488	8	ABE48381	ABE48381	I. ricini	173	27	84.4	593	2	AAE97661	AAE97661	Bacillus
101	28	87.5	512	7	ADG74270	Adg74270	Mouse fti	174	27	84.4	594	2	AAE37267	AAE37267	Truncated
102	28	87.5	572	2	AAW31273	AAW31273	Mouse fti	175	27	84.4	594	2	AAE63209	AAE63209	CryIA(b) I
103	28	87.5	572	8	ADG29338	Adg29338	Mouse GPC	176	27	84.4	609	8	ADH29181	ADH29181	Delta end
104	28	87.5	572	8	ADG29338	Adg29338	Mouse GPC	177	27	84.4	609	8	ADH29186	ADH29186	Delta end
105	28	87.5	572	6	ADZ13020	Adz13020	Murine ca	178	27	84.4	609	8	ADH29185	ADH29185	Delta end
106	28	87.5	574	6	ABU55902	Abu55902	Human pro	179	27	84.4	609	8	ADH29183	ADH29183	Delta end
107	28	87.5	574	6	AAE34056	AAE34056	FZD7 prot	180	27	84.4	609	8	ADH29184	ADH29184	Delta end
108	28	87.5	574	8	ADG74269	Adg74269	Human fti	181	27	84.4	609	8	ADH29182	ADH29182	Delta end
109	28	87.5	574	8	ADN03982	Adn03982	AntiIpbort	182	27	84.4	610	1	AAE60094	AAE60094	Sequence
110	28	87.5	574	8	ADG29337	Adg29337	Human GPC	183	27	84.4	610	6	AAO27314	AAO27314	Bacillus
111	28	87.5	574	8	ADG18261	Adg18261	Human sof	184	27	84.4	614	2	AAE81466	AAE81466	Bacillus
112	28	87.5	574	8	ADG59264	Adg59264	Frizled	185	27	84.4	614	2	AAE65297	AAE65297	Bacillus
113	28	87.5	574	8	ADU06307	Adu06307	Novel dro	186	27	84.4	614	3	AAE54828	AAE54828	Synthetic
114	28	87.5	574	9	ADZ13023	Adz13023	Human can	187	27	84.4	614	3	AAE76918	AAE76918	Synthetic
115	28	87.5	574	9	ABE28131	ABE28131	Human Pri	188	27	84.4	614	5	AAE808173	AAE808173	Bacillus
116	28	87.5	587	7	ABM86414	ABM86414	Rice abio	189	27	84.4	614	8	AEA37440	AEA37440	Endotoxin
117	28	87.5	587	7	ADR86300	ADR86300	Aspergill	190	27	84.4	615	4	AAE18416	AAE18416	Amino aci
118	28	87.5	654	8	ADS44314	ADS44314	Bacterial	191	27	84.4	615	3	AAE18416	AAE18416	Amino aci
119	28	87.5	655	8	ADY05078	Ady05078	Plant ful	192	27	84.4	615	4	AAE83924	AAE83924	Amino aci
120	28	87.5	655	7	ABM85550	ABM85550	Mouse pro	193	27	84.4	615	4	AAE02360	AAE02360	Insectici
121	28	87.5	693	8	ABM85550	ABM85550	Drosophil	194	27	84.4	615	4	AAE02425	AAE02425	Insectici
122	28	87.5	713	4	ABE65949	ABE65949	Drosophil	195	27	84.4	615	5	ABE76305	ABE76305	CryIAb cr
123	28	87.5	732	4	ABE65949	ABE65949	Drosophil	196	27	84.4	615	7	ABW01161	ABW01161	Bacillus
124	28	87.5	834	8	ADT56040	ADT56040	Plant pol	197	27	84.4	617	7	ADG45013	ADG45013	Modified
125	28	87.5	1046	5	ABE54658	ABE54658	Lactococc	198	27	84.4	617	8	AAE02542	AAE02542	Modified
126	28	87.5	1046	8	ADG29335	ADG29335	Bacterial	199	27	84.4	617	8	AAE02542	AAE02542	Modified
127	28	87.5	1346	4	ABE62770	ABE62770	Drosophil	200	27	84.4	619	4	ABE70023	ABE70023	Truncated
128	28	87.5	1398	4	ABE60535	ABE60535	Drosophil	201	27	84.4	622	2	AAE37266	AAE37266	Modified
129	28	87.5	1602	2	AAW64453	AAW64453	Rat brain	202	27	84.4	648	2	AAE15356	AAE15356	Modified
130	28	87.5	1602	7	ADG62931	ADG62931	Rat Prote	203	27	84.4	648	3	AAE12777	AAE12777	truncated
131	28	87.5	2110	3	AAE84528	AAE84528	Vriulence	204	27	84.4	648	3	AAE83905	AAE83905	truncated
132	28	87.5	2110	5	ABP54460	ABP54460	Pasturel	205	27	84.4	655	2	AAE15798	AAE15798	Amino aci
133	28	87.5	2110	5	ADM77465	ADM77465	Rat fibro	206	27	84.4	663	3	AAE07212	AAE07212	Fission y
134	27	84.4	12	7	ADC44614	ADC44614	Humalised	207	27	84.4	714	3	AAE32994	AAE32994	Bacillus
135	27	84.4	14	5	AU81919	AU81919	Bacillus	208	27	84.4	724	2	AAE46232	AAE46232	Bacillus
136	27	84.4	14	5	AU81919	AU81919	Bacillus	209	27	84.4	789	4	AAE41735	AAE41735	Human pol
137	27	84.4	54	6	ABM48709	ABM48709	Propionib	210	27	84.4	824	3	AAE42174	AAE42174	Human pol
138	27	84.4	54	6	ABM48709	ABM48709	Propionib	211	27	84.4	939	2	AAE04104	AAE04104	Human pol
139	27	84.4	71	6	ABU41588	ABU41588	Protein e	212	27	84.4	942	4	AAE39949	AAE39949	Novel hum
140	27	84.4	77	6	ABU43149	ABU43149	Propionib	213	27	84.4	958	7	ADG71272	ADG71272	Novel hum
141	27	84.4	77	6	ABM39668	ABM39668	Propionib	214	27	84.4	958	7	ADG71272	ADG71272	Novel hum
142	27	84.4	93	4	AU02027	AU02027	B. thurin	215	27	84.4	958	7	ADG69962	ADG69962	Human hea
143	27	84.4	129	4	AU02027	AU02027	Human car	216	27	84.4	1022	7	AAE04105	AAE04105	PJH2 gene
144	27	84.4	129	8	ADG45827	ADG45827	Human car	217	27	84.4	1140	1	AAE82525	AAE82525	Bacterial
145	27	84.4	137	2	AAW46843	AAW46843	Bacillus	218	27	84.4	1150	2	AAE62541	AAE62541	Bacterial
146	27	84.4	137	2	AAW46843	AAW46843	Bacillus	219	27	84.4	1150	2	AAE62541	AAE62541	Bacterial
147	27	84.4	137	2	AAW46843	AAW46843	Bacillus	220	27	84.4	1150	2	AAE62541	AAE62541	Bacterial
148	27	84.4	137	2	AAW46843	AAW46843	Bacillus	221	27	84.4	1150	9	AAE81462	AAE81462	Bacillus
149	27	84.4	137	2	AAW46843	AAW46843	Bacillus	222	27	84.4	1152	9	AAE81461	AAE81461	Amino aci
150	27	84.4	137	2	AAW46843	AAW46843	Bacillus	223	27	84.4	1152	9	AAE81461	AAE81461	Amino aci
151	27	84.4	137	2	AAW46843	AAW46843	Bacillus	224	27	84.4	1154	2	AAE21455	AAE21455	Sequence
152	27	84.4	137	2	AAW46843	AAW46843	Bacillus	225	27	84.4	1155	1	AAE60043	AAE60043	Sequence
153	27	84.4	137	2	AAW46843	AAW46843	Bacillus	226	27	84.4	1155	1	AAE60043	AAE60043	Sequence
154	27	84.4	137	2	AAW46843	AAW46843	Bacillus	227	27	84.4	1155	1	AAE60043	AAE60043	Sequence
155	27	84.4	137	2	AAW46843	AAW46843	Bacillus	228	27	84.4	1155	1	AAE60043	AAE60043	Sequence
156	27	84.4	137	2	AAW46843	AAW46843	Bacillus	229	27	84.4	1155	1	AAE60043	AAE60043	Sequence
157	27	84.4	137	2	AAW46843	AAW46843	Bacillus	230	27	84.4	1155	1	AAE60043	AAE60043	Sequence
158	27	84.4	137	2	AAW46843	AAW46843	Bacillus	231	27	84.4	1155	1	AAE60043	AAE60043	Sequence
159	27	84.4	137	2	AAW46843	AAW46843	Bacillus	232	27	84.4	1155	1	AAE60043	AAE60043	Sequence
160	27	84.4	137	2	AAW46843	AAW46843	Bacillus	233	27	84.4	1155	1	AAE60043	AAE60043	Sequence
161	27	84.4	137	2	AAW46843	AAW46843	Bacillus	234	27	84.4	1155	1	AAE60043	AAE60043	Sequence
162	27	84.4	137	2	AAW46843	AAW46843	Bacillus	235	27	84.4	1155	1	AAE60043	AAE60043	Sequence
163	27	84.4	137	2	AAW46843	AAW46843	Bacillus	236	27	84.4	1155	1	AAE60043	AAE60043	Sequence
164	27	84.4	137	2	AAW46843	AAW46843	Bacillus	237	27	84.4	1155	1	AAE60043	AAE60043	Sequence
165	27	84.4	137	2	AAW46843	AAW46843	Bacillus	238	27	84.4	1155	1	AAE60043	AAE60043	Sequence
166	27	84.4	137	2	AAW46843	AAW46843	Bacillus	239	27	84.4	1155	1	AAE60043	AAE60043	Sequence
167	27	84.4	137	2	AAW46843	AAW46843	Bacillus	240	27	84.4	1155	1	AAE60043	AAE60043	Sequence
168	27	84.4	137	2	AAW46843	AAW46843	Bacillus	241	27	84.4	1155	1	AAE60043	AAE60043	Sequence
169	27	84.4	137	2	AAW46843	AAW46843	Bacillus	242	27	84.4	1155	1	AAE60043	AAE60043	Sequence
170	27	84.4	137	2	AAW46843	AAW46843	Bacillus	243	27	84.4	1155	1	AAE60043	AAE60043	Sequence

244	27	84.4	1155	2	AAW76713	AAW76713	B. thurin	317	26	81.2	321	3	AAQ04632	AAQ04632	Arabidops
245	27	84.4	1155	2	AAW6705	AAW6705	Plasmiid p	318	26	81.2	321	3	AAQ48343	AAQ48343	Arabidops
246	27	84.4	1155	2	AAW49878	AAW49878	Bacillus	319	26	81.2	335	4	ABG02013	ABG02013	Novel hum
247	27	84.4	1155	2	AAW54074	AAW54074	Bt2 cryot	320	26	81.2	335	4	ABG28044	ABG28044	Novel hum
248	27	84.4	1155	2	AAW62668	AAW62668	Protein 8	321	26	81.2	338	3	AAQ13048	AAQ13048	Arabidops
249	27	84.4	1155	2	AAW79262	AAW79262	Bacillus	322	26	81.2	341	3	AAV95843	AAV95843	Autocontlg
250	27	84.4	1155	2	AAW49768	AAW49768	Bacillus	323	26	81.2	342	3	AAQ48342	AAQ48342	Arabidops
251	27	84.4	1155	2	AAW83393	AAW83393	Bacillus	324	26	81.2	342	3	AAQ04631	AAQ04631	Human nov
252	27	84.4	1155	3	AAW85146	AAW85146	B. thurin	325	26	81.2	354	4	AAW79389	AAW79389	Human pro
253	27	84.4	1155	3	AAW821987	AAW821987	Bacillus	326	26	81.2	354	4	AAV95654	AAV95654	Arabidops
254	27	84.4	1155	3	AAW79133	AAW79133	Amino act	327	26	81.2	372	3	AAQ13721	AAQ13721	Arabidops
255	27	84.4	1155	5	AAE25792	AAE25792	Bacillus	328	26	81.2	374	7	ADM26508	ADM26508	Hypether
256	27	84.4	1155	8	ADH74767	ADH74767	Transgeni	329	26	81.2	384	5	AAW92630	AAW92630	Herbicida
257	27	84.4	1155	8	ADY59856	ADY59856	Bacillus	330	26	81.2	405	2	AAW89251	AAW89251	Mouse PTP
258	27	84.4	1156	2	AAV33351	AAV33351	Plasmiid p	331	26	81.2	406	3	AAQ13720	AAQ13720	Arabidops
259	27	84.4	1156	4	AAW74298	AAW74298	B. thuring	332	26	81.2	407	3	AAQ13719	AAQ13719	Arabidops
260	27	84.4	1165	2	AAW84738	AAW84738	Native cr	333	26	81.2	409	8	ADM57191	ADM57191	A. thalian
261	27	84.4	1176	2	AAW71675	AAW71675	cty-1-1 g	334	26	81.2	409	8	AAQ13047	AAQ13047	Arabidops
262	27	84.4	1176	1	AAW81255	AAW81255	Sequence	335	26	81.2	416	3	AAQ04630	AAQ04630	Arabidops
263	27	84.4	1176	1	AAW81014	AAW81014	Sequence	336	26	81.2	419	3	AAQ48341	AAQ48341	Mouse PTP
264	27	84.4	1176	1	AAW92060	AAW92060	Sequence	337	26	81.2	420	2	AAW89249	AAW89249	Mouse PTP
265	27	84.4	1176	2	AAW25827	AAW25827	Crystral p	338	26	81.2	426	2	AAW89250	AAW89250	Mouse PTP
266	27	84.4	1176	2	AAW53786	AAW53786	Crystral d	339	26	81.2	438	4	AAW89250	AAW89250	Mouse PTP
267	27	84.4	1176	2	AAW09401	AAW09401	Bacillus	340	26	81.2	463	2	ADM5839	ADM5839	Plant pol
268	27	84.4	1176	2	ADR89418	ADR89418	cty1Aa. 1	341	26	81.2	482	8	ADT55839	ADT55839	Herbicida
269	27	84.4	1176	9	ADY59855	ADY59855	Bacillus	342	26	81.2	521	5	ABW93293	ABW93293	Xenopus S
270	27	84.4	1177	1	AAW70184	AAW70184	Plasmiid p	343	26	81.2	549	5	AAW14287	AAW14287	Human del
271	27	84.4	1177	1	AAW70187	AAW70187	Plasmiid p	344	26	81.2	552	2	AAW14287	AAW14287	Human del
272	27	84.4	1177	1	AAW62084	AAW62084	Bacillus	345	26	81.2	552	3	AAW70071	AAW70071	Human Sma
273	27	84.4	1180	2	AAW60337	AAW60337	Insectici	346	26	81.2	552	3	AAW169622	AAW169622	Human Sma
274	27	84.4	1180	2	AAW13309	AAW13309	Modified	347	26	81.2	552	5	ABW80354	ABW80354	DCP4 (del
275	27	84.4	1181	5	AAW25794	AAW25794	Bacillus	348	26	81.2	552	5	ABW53786	ABW53786	Human Sma
276	27	84.4	1181	5	AAW25796	AAW25796	Bacillus	349	26	81.2	552	7	ADC64233	ADC64233	Human Sma
277	27	84.4	1181	5	AAW25795	AAW25795	Bacillus	350	26	81.2	552	7	ADW60584	ADW60584	Rat Prote
278	27	84.4	1181	5	AAW25793	AAW25793	Bacillus	351	26	81.2	552	9	ADW606835	ADW606835	Cyclin-de
279	27	84.4	1181	8	ADH74769	ADH74769	Transgeni	352	26	81.2	587	4	ABW67608	ABW67608	Cyclin-de
280	27	84.4	1181	8	ADH74777	ADH74777	Transgeni	353	26	81.2	590	5	ABW50070	ABW50070	Listeria
281	27	84.4	1181	8	ADH74773	ADH74773	Transgeni	354	26	81.2	592	2	AAW15483	AAW15483	Protein e
282	27	84.4	1181	8	ADH74775	ADH74775	Transgeni	355	26	81.2	609	4	ABW40480	ABW40480	Novel hum
283	27	84.4	1202	1	AAW90717	AAW90717	Bacillus	356	26	81.2	673	8	ADR86258	ADR86258	Aspergill
284	26	81.2	35	4	AAW88333	AAW88333	Human imm	357	26	81.2	698	8	ADM61489	ADM61489	Human KPP
285	26	81.2	40	6	ABW25307	ABW25307	SAC Isola	358	26	81.2	730	8	ADM30558	ADM30558	Bacterial
286	26	81.2	40	6	ABW25305	ABW25305	SAC Isola	359	26	81.2	744	6	ABW17437	ABW17437	Protein e
287	26	81.2	60	2	AAW28126	AAW28126	Staphyloc	360	26	81.2	765	7	ABW08670	ABW08670	Pseudomon
288	26	81.2	78	4	AAW91418	AAW91418	Human imm	361	26	81.2	798	2	AAW85025	AAW85025	Smad4-gre
289	26	81.2	97	4	AAW814895	AAW814895	Human ner	362	26	81.2	808	2	AAW85013	AAW85013	Smad4-gre
290	26	81.2	109	4	AAW86648	AAW86648	Human imm	363	26	81.2	819	6	AAW30331	AAW30331	Human MAP
291	26	81.2	115	9	ADY50082	ADY50082	Endotheli	364	26	81.2	819	9	ADW12640	ADW12640	Human ste
292	26	81.2	130	4	ABW14400	ABW14400	Novel hum	365	26	81.2	820	9	ADW80357	ADW80357	Cyclin-de
293	26	81.2	148	8	ADW181993	ADW181993	Deleted i	366	26	81.2	820	6	AAW30332	AAW30332	Human MAP
294	26	81.2	159	4	AAW01630	AAW01630	Human pol	367	26	81.2	820	9	ADW80357	ADW80357	Human MAP
295	26	81.2	192	5	ABW53745	ABW53745	Lactococc	368	26	81.2	829	8	ADW80357	ADW80357	Human MAP
296	26	81.2	212	6	ADW76325	ADW76325	M18-L 11g	369	26	81.2	859	8	ADW65117	ADW65117	Mouse Rho
297	26	81.2	233	8	ABW38881	ABW38881	Protein e	370	26	81.2	859	8	ADW61885	ADW61885	Human NOV
298	26	81.2	234	6	AAW64819	AAW64819	OWU10 Sc	371	26	81.2	955	8	ADR86411	ADR86411	Human NOV
299	26	81.2	239	6	ABW84449	ABW84449	Human NOV	372	26	81.2	970	5	ABW27418	ABW27418	Streptococ
300	26	81.2	239	7	ADW49085	ADW49085	Human NOV	373	26	81.2	1009	5	ADW39774	ADW39774	Human myo
301	26	81.2	240	4	AAW45992	AAW45992	Human MUC	374	26	81.2	1193	5	ABW90860	ABW90860	Herbicida
302	26	81.2	240	4	AAW46004	AAW46004	Human MUC	375	26	81.2	1287	4	ABW67246	ABW67246	Drosophill
303	26	81.2	240	4	AAW45991	AAW45991	Human MUC	376	26	81.2	1291	2	AAW59912	AAW59912	Amino act
304	26	81.2	245	8	ADW71214	ADW71214	Plant ful	377	26	81.2	1444	4	ABW15667	ABW15667	Novel hum
305	26	81.2	248	8	ADW79549	ADW79549	Plant ful	378	26	81.2	1453	6	ABW17103	ABW17103	Protein e
306	26	81.2	251	7	ABW73906	ABW73906	Staphyloc	379	26	81.2	1497	3	ABW95535	ABW95535	M. xanthu
307	26	81.2	251	7	ABW72323	ABW72323	Staphyloc	380	26	81.2	1703	6	ABW63930	ABW63930	Drosophill
308	26	81.2	258	6	ABW72323	ABW72323	Bacterial	381	26	81.2	2103	6	ABW16769	ABW16769	Protein e
309	26	81.2	280	8	ADW29946	ADW29946	Sequence	382	26	81.2	2261	6	ABW18914	ABW18914	Pathogen
310	26	81.2	280	8	ADW26700	ADW26700	Protein e	383	26	81.2	2271	6	ABW16000	ABW16000	Protein e
311	26	81.2	305	3	AAW858229	AAW858229	Lung canc	384	26	81.2	2271	6	ABW16000	ABW16000	Protein e
312	26	81.2	310	6	ABW73447	ABW73447	Staphyloc	385	26	81.2	2271	6	ABW16000	ABW16000	Protein e
313	26	81.2	315	3	AAW13049	AAW13049	Arabidops	386	26	81.2	2271	6	ABW16000	ABW16000	Protein e
314	26	81.2	319	5	AAW78405	AAW78405	Human pro	387	26	81.2	2271	6	ABW16000	ABW16000	Protein e
315	26	81.2	319	5	AAW15253	AAW15253	Human RNA	388	26	81.2	2271	6	ABW16000	ABW16000	Protein e
316	26	81.2	319	8	ABW82290	ABW82290	Tumour-as	389	26	81.2	2271	6	ABW16000	ABW16000	Protein e

390	26	81.2	2283	6	ABP56876	Staphyloc	463	25	78.1	154	3	AAG08082	Aag08082	Arabidops
391	26	81.2	2344	4	AAU37120	Staphyloc	464	25	78.1	154	4	AAU66842	AAU66842	Propionib
392	26	81.2	3079	2	AAAS9926	GAP prote	465	25	78.1	154	6	ABP76786	ABP76786	N. gonorr
393	26	81.2	3079	8	ADN19371	Bacterial	466	25	78.1	154	6	ABP80607	ABP80607	N. gonorr
394	26	81.2	4829	8	AAAB97833	Human apo	467	25	78.1	154	6	ABM63361	ABM63361	Propionib
395	25	78.1	8	8	ADM43415	Synthetic	468	25	78.1	155	5	ABM89284	ABM89284	Human pol
396	25	78.1	17	7	AAW24036	VL-A12 pe	469	25	78.1	158	7	ADBE63801	ADBE63801	Rat prote
397	25	78.1	17	7	ADJ84073	Monoclonal	470	25	78.1	158	7	ADBE63799	ADBE63799	Rat prote
398	25	78.1	18	2	AAAP1553	Monoclonal	471	25	78.1	158	7	ADBE63803	ADBE63803	Rat prote
399	25	78.1	18	2	AAAP38273	Reo3r-bin	472	25	78.1	158	7	ADBE63797	ADBE63797	Rat prote
400	25	78.1	18	2	AAAO7667	Dimerisin	473	25	78.1	158	7	ADDA6409	ADDA6409	Rat prote
401	25	78.1	18	2	AAW24044	VL-A12 pe	474	25	78.1	159	2	AAI29505	AAI29505	Human lun
402	25	78.1	18	7	ADJ84086	Anti-1-rece	475	25	78.1	159	3	AAAB4444	AAAB4444	Human lun
403	25	78.1	20	9	ADY32519	Viral dis	476	25	78.1	159	7	AAE13785	AAE13785	Human lun
404	25	78.1	32	8	ABO58286	Human gen	477	25	78.1	159	4	ADDE6406	ADDE6406	Human lun
405	25	78.1	43	2	AAAY35944	Extended	478	25	78.1	159	7	ADDE87660	ADDE87660	Human lun
406	25	78.1	43	2	ADP19252	Human sec	479	25	78.1	160	8	ADPE51204	ADPE51204	Bet v 1 a
407	25	78.1	43	7	ADC78297	Human mlg	480	25	78.1	161	4	AAAG73540	AAAG73540	Human col
408	25	78.1	48	3	AAAG25678	Arabidops	481	25	78.1	162	7	ABO67523	ABO67523	Novel hum
409	25	78.1	48	3	AAU20240	Human nov	482	25	78.1	162	7	ABO67523	ABO67523	Klebsiell
410	25	78.1	50	5	ABP29304	Streptoco	483	25	78.1	169	3	AAAG08081	AAAG08081	Arabidops
411	25	78.1	51	5	ABP29304	Human ORF	484	25	78.1	169	3	AAAG43268	AAAG43268	Arabidops
412	25	78.1	59	7	ADFS9304	Human pol	485	25	78.1	170	4	AAW79600	AAW79600	Human pro
413	25	78.1	60	2	AAAR78447	Deduced f	486	25	78.1	172	4	ABG28041	ABG28041	Human hum
414	25	78.1	61	6	ADAI1807	Human nov	487	25	78.1	176	4	ABU52739	ABU52739	Human bra
415	25	78.1	70	4	AAAB00411	Human nov	488	25	78.1	179	3	AAAG43267	AAAG43267	Arabidops
416	25	78.1	73	4	AAAB88890	Human lmm	489	25	78.1	179	3	AAAG08080	AAAG08080	Arabidops
417	25	78.1	74	4	AAUS5829	Propionib	490	25	78.1	179	8	ADK90689	ADK90689	Thale cre
418	25	78.1	74	6	AAW52348	Propionib	491	25	78.1	186	6	ABM69585	ABM69585	Photorhab
419	25	78.1	76	4	AAW82841	Human lmm	492	25	78.1	193	6	ADK90088	ADK90088	Plant ful
420	25	78.1	78	4	AAU41107	Propionib	493	25	78.1	196	7	ABO83280	ABO83280	Pseudomon
421	25	78.1	78	4	AAU62439	Propionib	494	25	78.1	201	5	ABU52177	ABU52177	Helicobac
422	25	78.1	78	6	ABM37626	Propionib	495	25	78.1	211	4	ABU52765	ABU52765	Human sig
423	25	78.1	78	6	ABM58958	Propionib	496	25	78.1	213	3	AAAG29246	AAAG29246	Arabidops
424	25	78.1	80	5	ABP31962	Human gly	497	25	78.1	221	4	ADT60187	ADT60187	Plant pol
425	25	78.1	84	2	AAAY13157	Human sec	498	25	78.1	223	6	ABU36940	ABU36940	Anti-CD40
426	25	78.1	84	2	ABG26581	Novel hum	499	25	78.1	223	7	ABO68505	ABO68505	Pseudomon
427	25	78.1	85	6	ABU49245	Protein e	500	25	78.1	227	5	ABU51273	ABU51273	Helicobac
428	25	78.1	87	4	ABG16805	Novel hum	501	25	78.1	227	5	ABU51273	ABU51273	Helicobac
429	25	78.1	94	4	ABG23470	Novel hum	502	25	78.1	232	5	ABU51216	ABU51216	Helicobac
430	25	78.1	96	3	AAAG00956	Human sec	503	25	78.1	232	8	ADRA4495	ADRA4495	SnsAG4 an
431	25	78.1	99	4	ABG25273	Novel hum	504	25	78.1	236	4	AAAD25283	AAAD25283	Human pro
432	25	78.1	100	5	ABG32636	Human l1	505	25	78.1	236	7	ADDF60460	ADDF60460	Human con
433	25	78.1	103	6	ABM69963	Phocorhab	506	25	78.1	252	5	ABP69201	ABP69201	Human pol
434	25	78.1	106	4	AAO04148	Human pol	507	25	78.1	252	7	ABO74565	ABO74565	Pseudomon
435	25	78.1	106	4	ABG26832	Novel hum	508	25	78.1	254	8	ADSA4885	ADSA4885	Bacterial
436	25	78.1	108	3	AAAB41391	Human ORF	509	25	78.1	264	5	ABP65018	ABP65018	Human pro
437	25	78.1	109	4	AAU58650	Propionib	510	25	78.1	264	8	ADT09001	ADT09001	Plant ful
438	25	78.1	109	6	ABM55169	Propionib	511	25	78.1	265	8	ADH31310	ADH31310	Saccharom
439	25	78.1	111	4	AAU54152	Propionib	512	25	78.1	271	8	AAU87132	AAU87132	Novel gen
440	25	78.1	111	6	ABM50671	Propionib	513	25	78.1	271	8	ADU54447	ADU54447	Novel hum
441	25	78.1	111	8	ADN47160	Thermococ	514	25	78.1	272	9	AEA21114	AEA21114	Novel hum
442	25	78.1	112	4	ABG09278	Novel hum	515	25	78.1	273	6	ABM73459	ABM73459	Staphyloc
443	25	78.1	114	4	ABG23473	Novel hum	516	25	78.1	273	7	ADH80418	ADH80418	Human HER
444	25	78.1	125	4	AAO08279	Human pol	517	25	78.1	273	7	ADH80420	ADH80420	Human HER
445	25	78.1	128	8	ADX65950	Plant ful	518	25	78.1	277	8	ADY07146	ADY07146	Plant ful
446	25	78.1	134	7	ABM89077	Rice abio	519	25	78.1	278	5	ABM55081	ABM55081	Laccococ
447	25	78.1	135	5	ABM89159	Human pol	520	25	78.1	278	8	ADN27332	ADN27332	Bacterial
448	25	78.1	137	7	ADBE5087	Human pro	521	25	78.1	283	6	ABU20564	ABU20564	Protein e
449	25	78.1	140	3	AAAB12152	Hydrophob	522	25	78.1	287	8	ADT28923	ADT28923	Sarcocyst
450	25	78.1	140	4	AAW78616	Human pro	523	25	78.1	287	8	ADRA4491	ADRA4491	Sarcocyst
451	25	78.1	140	5	ABM89972	Human pol	524	25	78.1	296	4	AAAG54677	AAAG54677	Arabidops
452	25	78.1	140	8	ADL82969	Human PRO	525	25	78.1	296	3	AAW25235	AAW25235	Human pro
453	25	78.1	140	8	ADPS5174	Human PRO	526	25	78.1	303	8	ADY13627	ADY13627	Plant ful
454	25	78.1	140	8	ADP23362	HUO polyP	527	25	78.1	308	7	ADP93467	ADP93467	Neisseria
455	25	78.1	140	8	ADT87990	Human reg	528	25	78.1	312	4	ABG15011	ABG15011	Novel hum
456	25	78.1	147	2	AAAY29506	Human lun	529	25	78.1	315	7	AAAY91403	AAAY91403	Human sec
457	25	78.1	147	2	AAAB44445	Human lun	530	25	78.1	315	7	ADOC31748	ADOC31748	Human nov
458	25	78.1	147	7	AAE13786	Human lun	531	25	78.1	319	8	ADY08317	ADY08317	Plant ful
459	25	78.1	147	7	ADDE6407	Human lun	532	25	78.1	322	8	ADY09824	ADY09824	Plant ful
460	25	78.1	147	7	ADDE87661	Human lun	533	25	78.1	324	4	ABG15077	ABG15077	Novel hum
461	25	78.1	152	4	AAU28293	Novel hum	534	25	78.1	327	5	ABG77435	ABG77435	Selected
462	25	78.1	154	3	AAAG33269	Arabidops	535	25	78.1	331	4	ABG09623	ABG09623	Novel hum

536	25	78.1	332	6	ABM67365	Abm67365	Phototrab	609	25	78.1	476	5	ABG32633	Abg32633	Human	LI
537	25	78.1	336	6	ABU49870	Abu49870	Protein e	610	25	78.1	476	6	ABG74360	Abg74360	Human	UBX
538	25	78.1	338	6	ABM97060	Abm97060	M. xanthu	611	25	78.1	476	7	ADF03921	Adf03921	Bacterial	
539	25	78.1	340	6	ABU39271	Abu39271	Protein e	612	25	78.1	477	4	ABG13336	Abg13336	Novel	hum
540	25	78.1	340	7	ADC19714	Adc19714	H. influe	613	25	78.1	477	5	ABM79940	Abm79940	Human	mem
541	25	78.1	343	2	AAW20333	AAw20333	H. pylori	614	25	78.1	483	4	ADC27792	Adc27792	Human	nov
542	25	78.1	343	2	AAW24634	AAw24634	H. pylori	615	25	78.1	483	8	ADS27090	Ads27090	Bacterial	
543	25	78.1	344	6	ADA36897	Ada36897	Acinetoba	616	25	78.1	485	6	ABP77208	Abp77208	N. gonorr	
544	25	78.1	349	2	ABBS2608	Abbs2608	Bacterich	617	25	78.1	491	5	ABBA8200	Abba8200	Mouse	cal
545	25	78.1	350	2	AAAR42426	AAar42426	Bovine ro	618	25	78.1	500	6	AAK34903	AAk34903	Listeria	
546	25	78.1	350	3	AAIY5936	AAiy5936	Bovine ro	619	25	78.1	503	4	ABU39375	Abu39375	Protein e	
547	25	78.1	350	3	AAAB99067	AAab99067	Human G-P	620	25	78.1	503	6	ABBE2834	Abbe2834	Rice	abio
548	25	78.1	350	5	ABBO9278	Abbo9278	G protein	621	25	78.1	505	7	ABM88005	Abm88005	Rice	abio
549	25	78.1	350	5	ABM77787	Abm77787	Amino aci	622	25	78.1	514	7	ADM05662	Adm05662	Human	pro
550	25	78.1	350	6	ABU61595	Abu61595	Rat rod t	623	25	78.1	517	5	ABU65106	Abu65106	Human	NOV
551	25	78.1	350	7	ABR82633	AbR82633	C. elegan	624	25	78.1	517	8	ADN61863	Adn61863	Human	nov
552	25	78.1	350	7	ADC09613	Adc09613	Human G-P	625	25	78.1	519	4	AAU12276	AAu12276	Human	PRO
553	25	78.1	350	7	ADJ68622	Adj68622	Human hea	626	25	78.1	519	4	AAW39125	AAw39125	Human	pol
554	25	78.1	350	8	ADN06142	Adn06142	Bovine Gc	627	25	78.1	519	5	ABR01703	AbR01703	Human	bte
555	25	78.1	350	8	ADU60732	Adu60732	Human G-P	628	25	78.1	519	5	ABU65105	Abu65105	Human	NOV
556	25	78.1	354	6	ABU61596	Abu61596	Gustduct	629	25	78.1	519	6	ABO17720	AbO17720	Novel	hum
557	25	78.1	355	4	AAE03127	AAe03127	Human gen	630	25	78.1	519	6	ABU80974	Abu80974	Human	hum
558	25	78.1	358	2	AAW39262	AAw39262	A. cellu	631	25	78.1	519	6	ABU66674	Abu66674	Human	PRO
559	25	78.1	358	6	ABU25808	Abj25808	Aspergill	632	25	78.1	519	6	ABU59755	Abu59755	Novel	sec
560	25	78.1	358	6	ABJ26408	Abj26408	Aspergill	633	25	78.1	519	6	ABO24945	AbO24945	Human	sec
561	25	78.1	359	5	ABG93141	Abg93141	S. cerevi	634	25	78.1	519	6	ABU11861	Abu11861	Human	sec
562	25	78.1	359	5	ABR52869	AbR52869	Protein s	635	25	78.1	519	6	ABU66950	Abu66950	Human	sec
563	25	78.1	359	7	ADK62344	Adk62344	Disease t	636	25	78.1	519	6	ADA45729	Ada45729	Novel	hum
564	25	78.1	359	8	ADA33824	Ada33824	Bacterial	637	25	78.1	519	6	ADA76160	Ada76160	Human	PRO
565	25	78.1	359	8	AEA48956	Aea48956	Amino aci	638	25	78.1	519	6	ADAL18810	Ada18810	Human	PRO
566	25	78.1	360	9	ADW17803	Adw17803	Pinus rad	639	25	78.1	519	6	ADA61433	Ada61433	Homo	sapi
567	25	78.1	362	9	ADW18489	Adw18489	Pinus rad	640	25	78.1	519	6	ADBI19218	Adbi19218	Novel	hum
568	25	78.1	370	6	ABU45367	Abu45367	Protein e	641	25	78.1	519	6	ADB27759	Adb27759	Human	PRO
569	25	78.1	374	7	ADC46713	Adc46713	Thalecres	642	25	78.1	519	6	ADA86238	Ada86238	Novel	hum
570	25	78.1	374	7	ADD30694	Add30694	Plant yle	643	25	78.1	519	6	ADB15802	Adb15802	Human	PRO
571	25	78.1	374	8	AD143933	Ad143933	Plant tira	644	25	78.1	519	6	ADA77588	Ada77588	Human	PRO
572	25	78.1	374	8	ADO02035	Ado02035	Thalecres	645	25	78.1	519	6	ADA67383	Ada67383	Human	PRO
573	25	78.1	375	2	AAAR26327	AAar26327	Asymetri	646	25	78.1	519	6	ADB30390	Adb30390	Novel	hum
574	25	78.1	375	5	AAAR98068	AAar98068	Arthrobac	647	25	78.1	519	6	ADA85686	Ada85686	Novel	hum
575	25	78.1	375	8	ADK70251	Adk70251	Arthrobac	648	25	78.1	519	6	ADA96898	Ada96898	Human	PRO
576	25	78.1	377	5	ABM05716	Abm05716	Human tira	649	25	78.1	519	6	ADA79202	Ada79202	Human	PRO
577	25	78.1	377	9	ADY17857	Ady17857	PRO Polyp	650	25	78.1	519	6	ADA87341	Ada87341	Novel	hum
578	25	78.1	378	4	ABG13510	Abg13510	Novel hum	651	25	78.1	519	6	ADBI1653	Adbi1653	Human	PRO
579	25	78.1	385	5	ADW14458	Adw14458	Mouse gua	652	25	78.1	519	6	ADA91635	Ada91635	Novel	hum
580	25	78.1	388	4	AABS1345	AAbs1345	Mouse HS-	653	25	78.1	519	6	ADB14698	Adb14698	Human	PRO
581	25	78.1	390	4	ABBS1032	Abbs1032	Drosophi	654	25	78.1	519	6	ADB18659	Adb18659	Novel	hum
582	25	78.1	398	8	ADX92527	Adx92527	Plant ful	655	25	78.1	519	6	ADA93874	Ada93874	Human	PRO
583	25	78.1	400	8	ADQ39214	Adq39214	Human mayo	656	25	78.1	519	6	ADBI19770	Adbi19770	Novel	hum
584	25	78.1	401	7	ADF09521	Adf09521	Human pap	657	25	78.1	519	6	ADB13082	Adb13082	Human	PRO
585	25	78.1	403	2	AAAR26882	AAar26882	Streptomy	658	25	78.1	519	6	ABO43253	AbO43253	Novel	hum
586	25	78.1	404	8	ADK66871	Adk66871	Plant ful	659	25	78.1	519	6	ADA74336	Ada74336	Human	PRO
587	25	78.1	406	8	ADT58182	Adt58182	Plant pol	660	25	78.1	519	6	ADB24569	Adb24569	Human	PRO
588	25	78.1	414	3	AAAG29245	AAag29245	Arabidops	661	25	78.1	519	6	ADA82093	Ada82093	Human	PRO
589	25	78.1	415	6	ABU11494	Abu11494	Human MDD	662	25	78.1	519	6	ADA75056	Ada75056	Human	PRO
590	25	78.1	425	5	ADT60049	Adt60049	Plant pol	663	25	78.1	519	6	ADA85134	Ada85134	Novel	hum
591	25	78.1	435	6	ABU19738	Abu19738	Protein e	664	25	78.1	519	6	ADA84582	Ada84582	Novel	hum
592	25	78.1	435	8	ADN99855	Adn99855	Novel hum	665	25	78.1	519	6	ADB29838	Adb29838	Human	PRO
593	25	78.1	441	7	ADBE08447	Adbe08447	Novel pro	666	25	78.1	519	6	ADA80366	Ada80366	Human	PRO
594	25	78.1	441	4	ABBB66122	Abbb66122	Drosophi	667	25	78.1	519	6	ADA75608	Ada75608	Human	PRO
595	25	78.1	444	4	AAU38966	AAu38966	Drosophi	668	25	78.1	519	6	ADA46833	Ada46833	Human	PRO
596	25	78.1	444	7	ADC35880	Adc35880	Drosophi	669	25	78.1	519	6	ADB25129	Adb25129	Human	PRO
597	25	78.1	450	5	ABU11337	Abj11337	Yeast sel	670	25	78.1	519	6	ADA93305	Ada93305	Human	PRO
598	25	78.1	458	2	ADJ21009	Adj21009	Bacterial	671	25	78.1	519	6	ADB26655	Adb26655	Human	PRO
599	25	78.1	461	2	AAIY38793	AAiy38793	Neisseria	672	25	78.1	519	6	ADB30942	Adb30942	Human	PRO
600	25	78.1	461	8	AAIY38794	AAiy38794	N. gonorr	673	25	78.1	519	6	ADA80870	Ada80870	Homo	sapi
601	25	78.1	461	8	AAIY38793	AAiy38793	Novel S.	674	25	78.1	519	6	ADB24017	Adb24017	Human	PRO
602	25	78.1	461	9	AEA59263	AAe59263	Streptoco	675	25	78.1	519	6	ADA86346	Ada86346	Human	PRO
603	25	78.1	461	9	ABBA49406	ABba49406	N. gonorr	676	25	78.1	519	6	ADA80918	Ada80918	Human	PRO
604	25	78.1	461	8	ABBA49404	ABba49404	N. gonorr	677	25	78.1	519	6	ADA95794	Ada95794	Human	PRO
605	25	78.1	462	8	ADY12802	Ady12802	Plant ful	678	25	78.1	519	6	ADB26103	Adb26103	Human	PRO
606	25	78.1	462	8	ADW14450	Adw14450	Human gua	679	25	78.1	519	6	ADB21588	Adb21588	Novel	hum
607	25	78.1	474	6	ABU41026	Abu41026	Protein e	680	25	78.1	519	7	ADA77367	Ada77367	Human	PRO
608	25	78.1	474	7	ABM86533	Abm86533	Rice abio	681	25	78.1	519	7	ADBI18107	Adbi18107	Human	PRO

682	25	78.1	519	7	ADa86790	AdA86790	Novel	hum	755	25	78.1	519	7	ADD79859	AdD79859	Human	PRO
683	25	78.1	519	7	ADa87893	AdA87893	Novel	hum	756	25	78.1	519	7	ADD92896	AdD92896	Human	PRO
684	25	78.1	519	7	ADa46281	AdA46281	Novel	hum	757	25	78.1	519	7	ADD19316	AdD19316	Human	PRO
685	25	78.1	519	7	ADb28311	AdB28311	Human	PRO	758	25	78.1	519	7	ADb18764	AdB18764	Human	PRO
686	25	78.1	519	7	ADb28863	AdB28863	Human	PRO	759	25	78.1	519	7	ADb42960	AdB42960	Human	PRO
687	25	78.1	519	7	ADa76815	AdA76815	Human	PRO	760	25	78.1	519	7	ADb95749	AdB95749	Human	PRO
688	25	78.1	519	7	ADa88445	AdA88445	Novel	hum	761	25	78.1	519	7	ADb22635	AdB22635	Human	PRO
689	25	78.1	519	7	ADa97450	AdA97450	Human	PRO	762	25	78.1	519	7	ADb78753	AdB78753	Human	PRO
690	25	78.1	519	7	ADb27207	AdB27207	Human	PRO	763	25	78.1	519	7	ADb32703	AdB32703	Novel	hum
691	25	78.1	519	7	ADb22140	AdB22140	Novel	hum	764	25	78.1	519	7	ADb42395	AdB42395	Human	PRO
692	25	78.1	519	7	ADa66831	AdA66831	Human	PRO	765	25	78.1	519	7	ADb80411	AdB80411	Human	PRO
693	25	78.1	519	7	ADb22692	AdB22692	Human	PRO	766	25	78.1	519	7	ADb89439	AdB89439	Human	PRO
694	25	78.1	519	7	ADb23465	AdB23465	Human	PRO	767	25	78.1	519	7	ADb40723	AdB40723	Human	PRO
695	25	78.1	519	7	ADa92187	AdA92187	Novel	hum	768	25	78.1	519	7	ADb04522	AdB04522	Human	PRO
696	25	78.1	519	7	ADb15250	AdB15250	Human	PRO	769	25	78.1	519	7	ADb92651	AdB92651	Human	PRO
697	25	78.1	519	7	ADb38502	AdB38502	Novel	hum	770	25	78.1	519	7	ADb21360	AdB21360	Novel	hum
698	25	78.1	519	7	ADb37950	AdB37950	Novel	hum	771	25	78.1	519	7	ADb23001	AdB23001	Novel	hum
699	25	78.1	519	7	ADb66422	AdB66422	Novel	hum	772	25	78.1	519	7	ADb97336	AdB97336	Human	PRO
700	25	78.1	519	7	ADb89502	AdB89502	Human	PRO	773	25	78.1	519	7	ADb80400	AdB80400	Human	PRO
701	25	78.1	519	7	ADb90234	AdB90234	Human	PRO	774	25	78.1	519	7	ADb79848	AdB79848	Human	PRO
702	25	78.1	519	7	ADb39335	AdB39335	Novel	hum	775	25	78.1	519	7	ADb55140	AdB55140	Novel	hum
703	25	78.1	519	7	ADb46958	AdB46958	Novel	hum	776	25	78.1	519	7	ADb55692	AdB55692	Novel	hum
704	25	78.1	519	7	ADb86565	AdB86565	Human	PRO	777	25	78.1	519	7	ADb163911	AdB163911	Novel	hum
705	25	78.1	519	7	ADb77170	AdB77170	Novel	hum	778	25	78.1	519	7	ADb164860	AdB164860	Novel	hum
706	25	78.1	519	7	ADb34327	AdB34327	Human	PRO	779	25	78.1	519	7	ADb81773	AdB81773	Novel	hum
707	25	78.1	519	7	ADb35431	AdB35431	Human	PRO	780	25	78.1	519	7	ADb81221	AdB81221	Novel	hum
708	25	78.1	519	7	ADb33775	AdB33775	Human	PRO	781	25	78.1	519	7	ADb82390	AdB82390	Novel	hum
709	25	78.1	519	7	ADb34879	AdB34879	Human	PRO	782	25	78.1	519	7	ADb15789	AdB15789	Novel	hum
710	25	78.1	519	7	ADb35983	AdB35983	Human	PRO	783	25	78.1	519	7	ADb16418	AdB16418	Novel	hum
711	25	78.1	519	7	ADb46378	AdB46378	Novel	hum	784	25	78.1	519	7	ADb15237	AdB15237	Novel	hum
712	25	78.1	519	7	ADb50251	AdB50251	Novel	hum	785	25	78.1	519	7	ADb14685	AdB14685	Novel	hum
713	25	78.1	519	7	ADb71798	AdB71798	Novel	hum	786	25	78.1	519	7	ADb163359	AdB163359	Novel	hum
714	25	78.1	519	7	ADb59777	AdB59777	Novel	hum	787	25	78.1	519	8	ADb80947	AdB80947	Novel	hum
715	25	78.1	519	7	ADb52784	AdB52784	Novel	hum	788	25	78.1	519	8	ADb76395	AdB76395	Human	PRO
716	25	78.1	519	7	ADb57138	AdB57138	Novel	hum	789	25	78.1	519	8	ADb87759	AdB87759	Human	PRO
717	25	78.1	519	7	ADb60329	AdB60329	Novel	hum	790	25	78.1	519	8	ADb86163	AdB86163	Human	PRO
718	25	78.1	519	7	ADb50804	AdB50804	Novel	hum	791	25	78.1	519	8	ADb75611	AdB75611	Human	PRO
719	25	78.1	519	7	ADb65331	AdB65331	Human	PRO	792	25	78.1	519	8	ADb23187	AdB23187	Human	PRO
720	25	78.1	519	7	ADb54429	AdB54429	Novel	hum	793	25	78.1	519	8	ADb23739	AdB23739	Human	PRO
721	25	78.1	519	7	ADb53390	AdB53390	Novel	hum	794	25	78.1	519	8	ADb24382	AdB24382	Human	PRO
722	25	78.1	519	7	ADb58913	AdB58913	Novel	hum	795	25	78.1	519	8	ADb87207	AdB87207	Human	PRO
723	25	78.1	519	7	ADb55791	AdB55791	Novel	hum	796	25	78.1	519	8	ADb89073	AdB89073	Human	PRO
724	25	78.1	519	7	ADb58361	AdB58361	Novel	hum	797	25	78.1	519	8	ADb18212	AdB18212	Human	PRO
725	25	78.1	519	7	ADb03035	AdB03035	Novel	hum	798	25	78.1	519	8	ADb88521	AdB88521	Human	PRO
726	25	78.1	519	7	ADb90027	AdB90027	Novel	hum	799	25	78.1	519	8	ADb94541	AdB94541	Human	PRO
727	25	78.1	519	7	ADb69446	AdB69446	Human	PRO	800	25	78.1	519	8	ADb90952	AdB90952	Human	PRO
728	25	78.1	519	7	ADb48335	AdB48335	Human	PRO	801	25	78.1	519	8	ADb95093	AdB95093	Human	PRO
729	25	78.1	519	7	ADb09864	AdB09864	Human	PRO	802	25	78.1	519	8	ADb93203	AdB93203	Human	PRO
730	25	78.1	519	7	ADb04439	AdB04439	Novel	hum	803	25	78.1	519	8	ADb34784	AdB34784	Human	PRO
731	25	78.1	519	7	ADb80395	AdB80395	Novel	hum	804	25	78.1	519	8	ADb92099	AdB92099	Novel	hum
732	25	78.1	519	7	ADb10902	AdB10902	Human	PRO	805	25	78.1	519	8	ADb90400	AdB90400	Human	PRO
733	25	78.1	519	7	ADb47783	AdB47783	Human	PRO	806	25	78.1	519	8	ADb91547	AdB91547	Human	PRO
734	25	78.1	519	7	ADb79843	AdB79843	Novel	hum	807	25	78.1	519	8	ADb02126	AdB02126	Human	PRO
735	25	78.1	519	7	ADb09312	AdB09312	Human	PRO	808	25	78.1	519	8	ADb21912	AdB21912	Novel	hum
736	25	78.1	519	7	ADb41025	AdB41025	Novel	hum	809	25	78.1	519	8	ADb19982	AdB19982	Human	PRO
737	25	78.1	519	7	ADb52164	AdB52164	Human	PRO	810	25	78.1	519	8	ADb97888	AdB97888	Human	PRO
738	25	78.1	519	7	ADb52904	AdB52904	Human	PRO	811	25	78.1	519	8	ADb24105	AdB24105	Novel	hum
739	25	78.1	519	7	ADb53456	AdB53456	Novel	hum	812	25	78.1	519	8	ADb98459	AdB98459	Human	PRO
740	25	78.1	519	7	ADb51612	AdB51612	Human	PRO	813	25	78.1	519	8	ADb03290	AdB03290	Human	PRO
741	25	78.1	519	7	ADb02411	AdB02411	Human	PRO	814	25	78.1	519	8	ADb99011	AdB99011	Human	PRO
742	25	78.1	519	7	ADb01845	AdB01845	Human	PRO	815	25	78.1	519	8	ADb16596	AdB16596	Human	PRO
743	25	78.1	519	7	ADb54027	AdB54027	Novel	hum	816	25	78.1	519	8	ADb05055	AdB05055	Human	PRO
744	25	78.1	519	7	ADb92344	AdB92344	Human	PRO	817	25	78.1	519	8	ADb19322	AdB19322	Human	PRO
745	25	78.1	519	7	ADb91240	AdB91240	Human	PRO	818	25	78.1	519	8	ADb13159	AdB13159	Human	PRO
746	25	78.1	519	7	ADb03854	AdB03854	Human	PRO	819	25	78.1	519	8	ADb08216	AdB08216	Novel	hum
747	25	78.1	519	7	ADb32151	AdB32151	Novel	hum	820	25	78.1	519	8	ADb15386	AdB15386	Human	PRO
748	25	78.1	519	7	ADb22083	AdB22083	Human	PRO	821	25	78.1	519	8	ADb96784	AdB96784	Human	PRO
749	25	78.1	519	7	ADb79307	AdB79307	Human	PRO	822	25	78.1	519	8	ADb05969	AdB05969	Human	PRO
750	25	78.1	519	7	ADb41843	AdB41843	Human	PRO	823	25	78.1	519	8	ADb23553	AdB23553	Novel	hum
751	25	78.1	519	7	ADb17660	AdB17660	Human	PRO	824	25	78.1	519	8	ADb03842	AdB03842	Human	PRO
752	25	78.1	519	7	ADb91792	AdB91792	Human	PRO	825	25	78.1	519	8	ADb244743	AdB244743	Novel	hum
753	25	78.1	519	7	ADb33255	AdB33255	Novel	hum	826	25	78.1	519	8	ADb07040	AdB07040	Novel	hum
754	25	78.1	519	7	ADb33807	AdB33807	Novel	hum	827	25	78.1	519	8	ADb07592	AdB07592	Novel	hum

682	25	78.1	519	7	ADb33807	AdB33807	Novel	hum	827	25	78.1	519	8	ADb07592	AdB07592	Novel	hum
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828	25	78.1	519	8	ADG55087	Adg55087	Novel	hum	901	25	78.1	589	7	ADD95087	Adg55087	Murine gu
829	25	78.1	519	8	ADG60751	Adg60751	Novel	hum	902	25	78.1	589	8	ADJ76217	Adj76217	Maier ge
830	25	78.1	519	8	ADG61855	Adg61855	Novel	hum	903	25	78.1	589	8	ADM67201	Adm67201	Murine ad
831	25	78.1	519	8	ADG82056	Adg82056	Human	PRO	904	25	78.1	589	8	ADU59655	Adus9655	Guanylate
832	25	78.1	519	8	ADG57295	Adg57295	Novel	hum	905	25	78.1	591	5	ABB91362	Abb91362	Herbicida
833	25	78.1	519	8	ADG56743	Adg56743	Novel	hum	906	25	78.1	591	7	ADBS8059	Adbs8059	Rat Prote
834	25	78.1	519	8	ADG55639	Adg55639	Novel	hum	907	25	78.1	591	8	ADU59508	Adus9508	Rat guany
835	25	78.1	519	8	ADG55839	Adg55839	Novel	hum	908	25	78.1	591	7	ADU59656	Adus9656	Guanylate
836	25	78.1	519	8	ADG70765	Adg70765	Novel	hum	909	25	78.1	592	2	AAy41039	Aay41039	Human lun
837	25	78.1	519	8	ADG57847	Adg57847	Novel	hum	910	25	78.1	592	2	AAy05369	Aay05369	Human HCM
838	25	78.1	519	8	ADG53431	Adg53431	Novel	hum	911	25	78.1	592	3	AAb11324	Aab11324	Human lun
839	25	78.1	519	8	ADG71317	Adg71317	Novel	hum	912	25	78.1	592	4	AAm39547	Aam39547	Human pol
840	25	78.1	519	8	ADG81504	Adg81504	Human	PRO	913	25	78.1	592	5	AAu85547	Aau85547	Clone #20
841	25	78.1	519	8	ADH30466	Adh30466	Human	PRO	914	25	78.1	592	5	ABb74956	Abb74956	Human lun
842	25	78.1	519	8	ADH11833	Adh11833	Novel	hum	915	25	78.1	592	5	ABp61876	Abp61876	Human lun
843	25	78.1	519	8	ADG52255	Adg52255	Novel	hum	916	25	78.1	592	6	ABU69519	Abu69519	Human lun
844	25	78.1	519	8	ADG53983	Adg53983	Novel	hum	917	25	78.1	592	6	ABU66422	Abu66422	Lung canc
845	25	78.1	519	8	ADG80952	Adg80952	Human	PRO	918	25	78.1	592	7	ADbA8259	AdbA8259	Human lun
846	25	78.1	519	8	ADG56191	Adg56191	Novel	hum	919	25	78.1	592	7	ADc47052	Adc47052	GBPI amin
847	25	78.1	519	8	ADH12457	Adh12457	Novel	hum	920	25	78.1	592	7	ADd18940	Add18940	Human dis
848	25	78.1	519	8	ADG61303	Adg61303	Novel	hum	921	25	78.1	592	7	ADBS8061	Adbs8061	Human pro
849	25	78.1	519	8	ADH28390	Adh28390	Human	PRO	922	25	78.1	592	7	ADBS5077	Adbs5077	Human gua
850	25	78.1	519	8	ADG54535	Adg54535	Novel	hum	923	25	78.1	592	7	ADBS3458	Adbs3458	Human gua
851	25	78.1	519	8	ADG58575	Adg58575	Novel	hum	924	25	78.1	592	7	ADBS3464	Adbs3464	Human lun
852	25	78.1	519	8	ADH80999	Adh80999	Novel	hum	925	25	78.1	592	7	ADH36823	Adh36823	Human lun
853	25	78.1	519	8	ADG09742	Adg09742	Novel	hum	926	25	78.1	592	7	ADH47328	Adh47328	Human lun
854	25	78.1	519	8	ADH15213	Adh15213	Novel	hum	927	25	78.1	592	8	ADMS6626	Adms6626	Human lun
855	25	78.1	519	8	ADG09090	Adg09090	Novel	hum	928	25	78.1	592	8	ADN03843	Adn03843	Human lun
856	25	78.1	519	8	ADH14545	Adh14545	Novel	hum	929	25	78.1	592	8	ADJ21247	Adj21247	Human lun
857	25	78.1	519	8	ADH18140	Adh18140	Novel	hum	930	25	78.1	592	8	ADU59646	Adus9646	Guanylate
858	25	78.1	519	8	ADJ63421	Adj63421	Novel	hum	931	25	78.1	592	8	ADU98318	Adus98318	Lung tumo
859	25	78.1	519	8	ADJ77316	Adj77316	Human	PRO	932	25	78.1	592	9	ADV70254	Adv70254	Tumor-ass
860	25	78.1	519	8	ADJ65438	Adj65438	Human	PRO	933	25	78.1	592	9	ADY14749	Ady14749	PRO polyp
861	25	78.1	519	8	ADM27574	Adm27574	Human	PRO	934	25	78.1	592	9	ADY14747	Ady14747	PRO polyp
862	25	78.1	519	8	ADM42298	Adm42298	Human	PRO	935	25	78.1	592	9	ADY19046	Ady19046	PRO polyp
863	25	78.1	519	8	ADM61861	Adm61861	Human	nov	936	25	78.1	592	9	ADY19636	Ady19636	PRO polyp
864	25	78.1	519	8	ADM28160	Adm28160	Human	PRO	937	25	78.1	592	9	ADZ10049	Adz10049	Human bre
865	25	78.1	519	8	ADH95642	Adh95642	Human	PRO	938	25	78.1	592	9	AEA23607	Aea23607	Human PRO
866	25	78.1	519	8	ADH96194	Adh96194	Novel	hum	939	25	78.1	592	9	AEA23686	Aea23686	Human PRO
867	25	78.1	519	8	ADH32146	Adh32146	Novel	hum	940	25	78.1	592	9	AEA23623	Aea23623	Human PRO
868	25	78.1	519	8	ADT03130	Adt03130	Human	PRO	941	25	78.1	592	9	AEb10126	Aeb10126	Cancer re
869	25	78.1	519	8	ADZ03181	Adz03181	Human	sec	942	25	78.1	597	4	ABG30278	Abg30278	Novel hum
870	25	78.1	519	2	AEb13927	Aeb13927	Cancer ce		943	25	78.1	597	4	ABG14867	Abg14867	Novel hum
871	25	78.1	521	2	AAb89927	Aab89927	A. cellu1		944	25	78.1	597	6	ABP79344	Abp79344	N. gonorr
872	25	78.1	521	4	AAb48787	Aab48787	Acidothet		945	25	78.1	597	6	ABP79342	Abp79342	Mouse fri
873	25	78.1	521	4	AAb48788	Aab48788	Acidothet		946	25	78.1	605	9	ADM14456	Adm14456	Mouse gua
874	25	78.1	521	4	ADM04082	Adm04082	Human pro		948	25	78.1	611	4	ABG05291	Abg05291	Novel hum
875	25	78.1	535	7	ADD24922	Add24922	Xanthomon		949	25	78.1	613	4	ABG08445	Abg08445	Novel hum
876	25	78.1	537	4	AAm40911	Aam40911	Human	pol	950	25	78.1	615	9	AEb37354	Aeb37354	L. pneumo
877	25	78.1	537	4	ADP60436	Adp60436	Human	con	951	25	78.1	615	9	AEb40674	Aeb40674	L. pneumo
878	25	78.1	546	7	ABG10021	Abg10021	Novel	hum	952	25	78.1	619	7	AAE10890	Aae10890	Rickettsi
879	25	78.1	546	8	ADM87619	Adm87619	Human	EST	953	25	78.1	619	7	ADc12742	Adc12742	Human GPC
880	25	78.1	550	8	ADS21203	Ads21203	Bacterial		954	25	78.1	620	3	AAy51847	Aay51847	Murine mg
881	25	78.1	551	8	ADN12022	Adn12022	Mini-PP2		955	25	78.1	620	7	ADP74024	Adp74024	Mouse pur
882	25	78.1	553	5	ABG32632	Abg32632	Human	l1	956	25	78.1	620	8	ADU59654	Adus9654	Purine GB
883	25	78.1	553	5	ADH17180	Adh17180	Pig	NOVX	957	25	78.1	624	8	ADBS7023	Adbs7023	E. coli K
884	25	78.1	553	6	ABG74359	Abg74359	Human	UBX	958	25	78.1	624	9	ADY73685	Ady73685	Becherich
885	25	78.1	553	6	ADX83234	Adx83234	Human	TEG	959	25	78.1	626	8	ADJ27174	Adj27174	Human TRI
886	25	78.1	558	7	ADJ71136	Adj71136	Human	int	960	25	78.1	627	4	ABG30135	Abg30135	Novel hum
887	25	78.1	558	8	ADU50318	Adu50318	Oil-assoc		961	25	78.1	630	6	ABJ26539	Abj26539	Aspergill1
888	25	78.1	558	8	ADR32352	Adr32352	Thale cre		962	25	78.1	630	6	ADb67046	Adb67046	Human lun
889	25	78.1	558	8	ADP72631	Adp72631	Rat recep		963	25	78.1	633	7	ADb14370	Adb14370	Human int
890	25	78.1	562	3	AAy69508	Aay69508	Acidothet		964	25	78.1	633	7	ADBS8300	Adbs8300	Human lun
891	25	78.1	562	5	AAU79549	Aau79549	A. cellu1		965	25	78.1	633	8	ADL91498	Adl91498	Human imm
892	25	78.1	579	2	ADG74258	Adg74258	Fruit fly		966	25	78.1	633	8	ADP67801	Adp67801	Novel hum
893	25	78.1	579	2	AAW18301	Aaw18301	Photorhab		967	25	78.1	640	5	ABG31804	Abg31804	Human int
894	25	78.1	579	2	AAW56574	Aaw56574	Toxin Tcd		968	25	78.1	640	8	ADJ70677	Adj70677	Human hea
895	25	78.1	580	4	AAm39548	Aam39548	Human	pol	969	25	78.1	640	8	ADJ91502	Adj91502	Human imm
896	25	78.1	580	4	ABG25757	Abg25757	Novel	hum	970	25	78.1	646	6	ABR41788	Abz41788	Human DIT
897	25	78.1	580	4	ADBE09035	Adbe09035	Novel	pro	971	25	78.1	646	8	ADY09213	Ady09213	Plant ful
898	25	78.1	585	9	AEa55076	Aea55076	Mouse fri		972	25	78.1	647	6	ADa55556	Ada55556	Human pro
899	25	78.1	589	3	AAy51844	Aay51844	Murine em		973	25	78.1					

974	25	78.1	648	4	ABG22526	Abg22526	Novel hum
975	25	78.1	648	8	ABM64879	Abm64879	Human dia
976	25	78.1	650	7	ADDe7047	Adde7047	Human lun
977	25	78.1	650	7	ADDe8301	Adde8301	Human lun
978	25	78.1	661	4	ABG09285	Abg09285	Novel hum
979	25	78.1	668	8	ABM64877	Abm64877	Human dia
980	25	78.1	674	9	ABM64448	Abm64448	Human gna
981	25	78.1	675	9	ADW11236	Adw11236	Human cal
982	25	78.1	685	2	AAW31274	Aaw31274	Mouse fri
983	25	78.1	685	2	ADG74272	Adg74272	Mouse fri
984	25	78.1	685	8	ADO29340	Ado29340	Mouse GPC
985	25	78.1	685	9	ADX16341	Adx16341	Mouse fri
986	25	78.1	689	8	ADU01133	Adu01133	Human pro
987	25	78.1	689	8	ADU15515	Adu15515	Novel hum
988	25	78.1	690	9	ABE31363	Aeb31363	Human pro
989	25	78.1	694	2	AAW31267	Aaw31267	Drosophill
990	25	78.1	694	4	ABE71797	AbE71797	Drosophill
991	25	78.1	694	5	AAU74823	Aau74823	Human REP
992	25	78.1	694	6	ABU55903	Abu55903	Human pro
993	25	78.1	694	6	AAE34057	Aae34057	Human pro
994	25	78.1	694	7	ADB75330	Adb75330	Prostate
995	25	78.1	694	7	ADG74271	Adg74271	Human fri
996	25	78.1	694	7	ADN40026	Adn40026	Cancer/an
997	25	78.1	694	8	ADM67157	Adm67157	Human pro
998	25	78.1	694	8	ADO29339	Ado29339	Human GPC
999	25	78.1	694	8	ADO22266	Ado22266	Human FZD
1000	25	78.1	694	8	ADR46693	Adr46693	Cancer-as

ALIGNMENTS

RESULT 1
AAW62015

ID AAW62015 standard; peptide; 7 AA.

XX AAW62015;

DT 01-OCT-1998 (first entry)

XX Light chain variable region complementarity determining region 2.

XX Complementarity determining region; light chain variable region;
 KW humanised antibody; MWM24F(ab)-8; anti-CD11a antibody;
 KM human CD11a I domain; MWM24 epitope; alpha subunit;
 KW lymphocyte function-associated antigen 1; LFA-1; immunoassay;
 KM in vivo imaging; diagnosis; CD11a-associated disease.

XX Mus sp.

OS Homo sapiens.

XX WO9823761-A1.

PN 04-JUN-1998.

PD 20-OCT-1997; 97WO-US019041.

PF 27-NOV-1996; 96US-00757205.

PR (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;

PI WPI; 1998-322737/28.

XX New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
 PT also to treat conditions such as immunological or inflammatory disease.

XX Claim 8; Page 2; 66pp; English.

CC AAW62014-16 represent complementarity determining regions of the light
 CC chain variable region of humanised antibody MWM24F(ab)-8. The fragments
 CC were used to make a humanised anti-CD11a antibody that binds specifically

CC to the human CD11a I domain (MWM24 epitope). CD11a refers to the alpha
 CC subunit of lymphocyte function-associated antigen 1 (LFA-1) from any
 CC mammal. The humanised anti-CD11a antibodies are used to determine
 CC presence of CD11a in usual immunoassays or by in vivo imaging,
 CC particularly for diagnosis of CD11a-associated diseases (typically immune
 CC responses and inflammation such as psoriasis, Crohn's disease, rheumatoid
 CC arthritis, transplant rejection, leukaemia, etc
 XX

SQ Sequence 7 AA;

Query Match 100.0%; Score 32; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
 |||||
 Db 1 SGGTLOS 7

RESULT 2
AAW82341

ID AAW82341 standard; peptide; 7 AA.

XX AAW82341;

DT 22-JUN-2000 (first entry)

XX Humanised anti-CD11a antibody light chain CDR2 SEQ ID NO:14.

XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
 KW antitumour; antiviral; inflammation; immunological response; LFA-1;
 KW lymphocyte function-associated antigen 1; psoriasis; rhinitis; eczema;
 KM inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KW viral infection; transplant rejection; graft rejection.

XX Homo sapiens.

OS Mus sp.

XX US6037454-A.

PN 14-MAR-2000.

PD 20-NOV-1997; 97US-00974899.

PF 27-NOV-1996; 96US-0031971P.

PR (GETH) GENENTECH INC.

XX Jardieu PM, Presta LG;

PI WPI; 2000-282241/24.

XX New humanized anti-CD11a antibody, useful for treating or preventing e.g.
 PT inflammation and transplant rejection, contains human heavy variable
 PT region complementarity determining regions.

XX Claim 4; Col 57-58; 38pp; English.

CC The present invention describes a humanised anti-CD11a antibody (Ab) that
 CC binds specifically to the human CD11a I-domain. The Ab has anti-
 CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
 CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
 CC involved in leucocyte adhesion associated with inflammatory and
 CC immunological responses. The Ab are used: (i) optionally when coupled to
 CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
 CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
 CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
 CC rhinitis, leukaemia, viral infections and many others, also for
 CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
 CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
 CC to active anticancer agent; and (v) for affinity chromatography. The Ab
 CC retain about the same activity in adhesion and mixed lymphocyte response
 CC assays as the murine antibodies from which they are derived. The murine

CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
 CC between Jurkat cells (expressing LFA-1) and normal epidermal
 CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
 CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
 CC sequence represents the light chain variable region CDR2 of the humanised
 CC anti-CD11a Ab
 CC XX
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 32; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTLOS 7
 DB 1 SGSTLOS 7
 RESULT 3
 ADG39002
 ID ADG39002 standard; peptide; 7 AA.
 AC ADG39002;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Humanised Mouse anti-CD11a antibody light chain variable region CDR2.
 XX
 KW Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
 KW VL; cluster of differentiation 11a; mixed lymphocyte response assay;
 KW Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
 KW ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
 KW psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
 KW diabetes mellitus; prodrug activating enzyme; humanised;
 KW complementarity determining region; CDR.
 KW XX
 OS Synthetic.
 OS Mus sp.
 OS XX
 PN US2003207336-A1.
 PD 06-NOV-2003.
 XX
 PF 28-FEB-2001; 2001US-00795798.
 XX
 PR 27-NOV-1996; 96US-0031971P.
 PR 20-NOV-1997; 97US-00974899.
 PR 20-OCT-1999; 99US-00420745.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta IG;
 XX
 DR WPI; 2004-051511/05.
 PT Humanized anti-CD11a antibody useful for treating lymphocyte function-
 PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
 PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
 XX
 PS Claim 8; SEQ ID NO 14; 43pp; English.
 CC The invention relates to a Humanised anti-cluster of differentiation
 CC (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
 CC a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
 CC inhibition (IC50) (nm) value of not more than 1 nM in mixed lymphocyte
 CC response assay or for preventing adhesion of Jurkat cells to normal human
 CC epidermal keratinocytes expressing intercellular adhesion molecule (ICAM
 CC -1. Also included are a kit comprising the antibody and instructions for
 CC use to detect the CD11a protein, an isolated nucleic acid encoding the
 CC antibody, a vector comprising the nucleic acid, a host cell comprising
 CC the vector and producing the antibody by culturing the cell so that the
 CC antibody is expressed. The antibody binds to epitope MHM24 on CD11a. The

CC antibody is useful for determining the presence of CD11a protein and for
 CC treating lymphocyte function-associated antigen 1 mediated disorder such
 CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
 CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
 CC and diabetes mellitus. The antibody is useful when conjugated to a
 CC prodrug activating enzyme, or as an affinity purification agent. The
 CC present sequence is a CDR (complementarity determining region) of the
 CC light chain variable region (VL) of the humanised mouse anti-CD11a I
 CC domain monoclonal antibody MHM24.
 CC XX
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 32; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTLOS 7
 DB 1 SGSTLOS 7
 RESULT 4
 ADR03418
 ID ADR03418 standard; peptide; 7 AA.
 AC ADR03418;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MHM24 CDR-L2 peptide.
 XX
 KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; Rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MHM24; variable light chain;
 KW VL; murine; human; fusion protein; complementarity determining region;
 KW CDR.
 KW XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 OS XX
 PN US2004146507-A1.
 PD 29-JUL-2004.
 XX
 PF 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardieu PM, Presta IG;
 XX
 DR WPI; 2004-552640/53.
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 55; 54pp; English.
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful

CC for treating and preventing infectious diseases such as human
CC immunodeficiency virus (HIV) and rhinovirus infections; inflammatory skin
CC disease such as psoriasis; inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis; adult respiratory distress syndrome;
CC allergic diseases such as eczema and asthma; autoimmune diseases such as
CC rheumatoid arthritis; systemic lupus erythematosus (SLE); diabetes
CC mellitus; Reynaud's syndrome; immunological diseases such as
CC tuberculosis; sarcoidosis; polymyositis and chronic obstructive pulmonary
CC disease (COPD); CNS inflammatory disorder; skin hypersensitivity
CC disorders such as poison ivy and poison oak; B-cell malignancies such as
CC chronic lymphocytic leukaemia and hairy cell leukaemia; graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is humanised murine anti-human CD14 monoclonal antibody
CC (MH24) CDR-L2 peptide. This sequence is used in the exemplification of
CC the invention.

SQ Sequence 7 AA;
XX

Query Match 100.0%; Score 32; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTLOS 7
Db 1 SGGTLOS 7

RESULT 5
AB07177
ID ABB07177 standard; protein; 101 AA.
XX
AC ABB07177;
XX
DT 13-MAR-2002 (first entry)
XX
DE Mouse 09 antibody kappa light chain 2 variable region.
XX
KM Neuromodulatory; central nervous system; CNS; SHIGM22; LYM 22; AKUR4;
KM ebvH1GM M6119D10; ebv H1GM CB2B68; CB21E12; CB21E17; MS119E5; virucide;
KM antiParkinsonian; neuroprotective; nootropic; vulnerary; mouse.
XX
OS Mus sp.
XX
PN WO200185797-A1.
XX
PD 15-NOV-2001.
XX
PF 30-MAY-2000; 2000WO-US014902.
XX
PR 10-MAY-2000; 2000US-00568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2002-066596/09.
XX
DR N-PSDB; ABA94224.
XX
PT Novel neuromodulatory agent (a human IGM monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX
PS Disclosure; Fig 36A-B; 219pp; English.

CC The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca2+
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody SHIGM22 (LYM 22), ebvH1GM M6119D10, ebv H1GM
CC CB2B68, AKUR4, CB21E12, CB21E7 or MS119E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in

CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within
CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEM) or for treating a human being having multiple sclerosis, or a post-
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neural disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture. (I)
CC is also useful for stimulating remyelination of CNS axons. The antibodies
CC are useful for preventing infection by a bacterium, virus or like
CC pathogen that causes demyelination or other neurodegenerative condition
CC in a subject. Methods where (I) is administered to a patient are useful
CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC disease, CNS diseases, and other conditions in the CNS where nerves are
CC damaged as by trauma. The present sequence represents the mouse 09
CC antibody kappa light chain 2 variable region
XX

SQ Sequence 101 AA;
XX

Query Match 100.0%; Score 32; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGTLOS 7
Db 50 SGGTLOS 56

RESULT 6
AD126670
ID AD126670 standard; protein; 101 AA.
XX
AC AD126670;
XX
DT 15-APR-2004 (first entry)
XX
DE Mouse anti oligodendrocyte antibody 09 V kappa 2 protein.
XX
KM Mouse; antibody; IGM; remyelination; neuronal growth; autoantibody;
KM demyelination disease; multiple sclerosis; central nervous system; CNS;
KM axon; glial cell proliferation;
KM Theiler's murine encephalomyelitis virus infection; CNS injury;
KM spinal cord injury.
XX
OS Mus sp.
XX
PN US2003185827-A1.
XX
PD 02-OCT-2003.
XX
PF 13-NOV-2001; 2001US-00010729.
XX
PR 29-APR-1994; 94US-00236520.
PR 08-AUG-1996; 96US-00692084.
PR 07-JAN-1997; 97US-00779784.
PR 28-MAY-1999; 99US-00328862.
PR 30-MAY-2000; 2000US-00580787.
PR 05-DEC-2000; 2000US-00730473.
XX
PA (MAYO-) MAYO FOUND.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2004-119219/12.
XX
DR N-PSDB; AD126671.
XX
PT New human immunoglobulin M antibody for treating or preventing a
PT demyelinating disease of the central nervous system in a human or
PT domestic animal, such as multiple sclerosis.
XX
PS Example 11; Fig 54; 159pp; English.
XX

CC The invention relates to an antibody (1) produced by injecting an
 CC immunocompetent host with an antibody peptide, and harvesting the
 CC antibody, where the peptide comprises a human anti-IgM antibody fragment
 CC given in the specification, or active fragments. Also included are
 CC stimulating remyelination of central nervous system (CNS) axons in a
 CC mammal (comprising administering a monoclonal antibody, or mixtures,
 CC monomers, active fragments, or recombinant antibodies derived from it,
 CC characterised by their ability to bind structures and cells within the
 CC CNS, including oligodendrocytes), stimulating the proliferation of glial
 CC cells in CNS axons in a mammal (comprising administering a monoclonal
 CC antibody, or mixtures, monomers, active fragments, or recombinant
 CC antibodies derived from it, characterised by their ability to bind
 CC structures and cells within the CNS), treating or preventing a
 CC demyelinating disease of the CNS in a mammal (comprising administering a
 CC monoclonal antibody, or mixtures, monomers, active fragments, or
 CC recombinant antibodies derived from it, characterised by their ability to
 CC bind structures and cells within the CNS, and to stimulate remyelination
 CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
 CC cells from mixed cell culture, stimulating remyelination of CNS axons in
 CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 CC antibody/or a peptide analogue, hapten, or active fragment of it, where
 CC the DNA sequence consists of a sequence encoding an anti-IgM antibody), a
 CC probe capable of screening for the antibody, an assay for screening drugs
 CC and other agents for the ability to modulate the production or mimic the
 CC activities of mAb SH1G42, SH1G46, or combinations of them, a
 CC recombinant virus transformed with recombinant antibody nucleic acids or
 CC vector, imaging a portion of the CNS using the antibody and diagnosing or
 CC monitoring demyelination and/or remyelination of the CNS comprising using
 CC CNS image. The antibody is used to stimulate remyelination of CNS axons,
 CC and to stimulate the proliferation of glial cells in CNS axons,
 CC optionally in vitro. The antibody is used to treat or prevent a
 CC demyelinating disease of the CNS in a human or domestic animal, such as
 CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 CC preferably the mammal is a mouse infected with Strain DA of Theiler's
 CC murine encephalomyelitis virus. The antibody is used to treat a spinal
 CC cord injury and used to screen drugs and other agents for the ability to
 CC modulate the production or mimic the activities of the antibody. The
 CC antibody can be used to image a portion of the CNS which can be used to
 CC diagnose or monitor demyelination and/or remyelination of the CNS. The
 CC present sequence is a variable region of a mouse anti-IgM antibody (or
 CC fragment).

XX
 XX
 SQ Sequence 101 AA;

Query Match 100.0%; Score 32; DB 8; Length 101;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQS 7
 |||||
 DB 50 SGGSTLQS 56

RESULT 7

ADV66159
 ADV66159 standard; protein; 107 AA.

AC ADV66159;

XX 24-FEB-2005 (first entry)

DE Human EpcAM-specific antibody light chain variable domain - SEQ ID 82.

XX bispecific single chain antibody; epithelial cell adhesion molecule;

KW EpcAM; tumor; cancer; cytostatic; light chain variable region.

XX Unidentified.

OS
 PN WO2004106383-A1.

XX 09-DEC-2004.

PD 26-MAY-2004; 2004WO-EP005687.
 PF

XX 31-MAY-2003; 2003BP-00012133.
 PR 31-MAY-2003; 2003BP-00012134.
 XX (MICR-) MICROMET AG.
 PA Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkneri-Schuetz U, Baerle P;
 XX WPI: 2005-021271/02.
 DR N-PSDB; ADV66158.
 PT New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 XX disease, such as an epithelial or minimal residual cancer.
 PS Claim 10; SEQ ID NO 82; 227pp; English.
 XX The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EpcAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents an antibody
 CC light chain variable domain that is specific for human EpcAM.

XX
 XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 32; DB 9; Length 107;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQS 7
 |||||
 DB 50 SGGSTLQS 56

RESULT 8

ADV283517
 ADV283517 standard; protein; 107 AA.

AC ADV283517;

XX 14-JUL-2005 (first entry)

DE AntispCam single chain antibody SEQ ID NO 139.

XX neoplasm; inflammation; immune disorder; infection; allergy;

KW graft versus host disease; Cytostatic; Antiinflammatory;
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
 KW EpcAM; antibody.

XX Synthetic.

OS
 PN WO2005040220-A1.

XX 06-MAY-2005.

XX 15-OCT-2004; 2004WO-EP011646.

XX 16-OCT-2003; 2003BP-00023581.

XX (MICR-) MICROMET AG.

XX Hofmeister R, Kohleisen B, Lenkneri-Schuetz U, Itin C, Baerle P;
 PI Carr FJ, Hamilton AA, Williams S;

XX WPI: 2005-333494/34.

DR N-PSDB; AD283516.

XX New cytotoxicity active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding

PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.
XX
XX Example 8; SEQ ID NO 139; 639pp; English.
XX
XX The invention relates to a cytotoxically active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,
CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of an anti-EpCam single chain antibody.
XX
SQ Sequence 107 AA;
XX
Query Match 100.0%; Score 32; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SGGSTLOS 7
| | | | |
Db 50 SGGSTLOS 56
XX
RESULT 9
ID AEA62455 standard; protein; 107 AA.
XX
XX AEA62455;
XX
XX 25-AUG-2005 (first entry)
XX
XX Mouse 1B3 anti-C35 antibody kappa chain variable region.
XX
XX C35 antigen; cell growth; cancer; cytostatic; apoptosis; immunotherapy;
XX hyperproliferation; antibody; light chain variable region.
XX
XX Mus sp.
XX
XX WO2005055936-A2.
XX
XX 23-JUN-2005.
XX
XX 06-DEC-2004; 2004WO-US040573.
XX
XX 04-DEC-2003; 2003US-0526572P.
XX
XX 23-DEC-2003; 2003US-0531688P.
XX
XX (VACC-) VACCINEX INC.
XX
XX Evans EE, Paris MJ, Sahasrabudhe DM, Smith ES, Zauderer M;
XX
XX MPI; 2005-458501/46.
XX
XX N-PSDB; AEA62454.
XX
XX Killing cancer cells, by administering apoptosis-inducing therapy and
PT administering antibody specific for intracellular, cancer-associated
PT protein other than C35, or antibody specific for C35.
XX
XX
XX Disclosure; SEQ ID NO 10; 255pp; English.
XX
XX The invention relates to killing (M1) cancer cells, comprising
CC administering an apoptosis-inducing therapy to cancer cells, and
CC administering to the cells an antibody specific for an intracellular,

CC cancer-associated protein, provided that the protein is not C35 antigen,
CC where protein becomes exposed on the cell surface in cells undergoing
CC apoptosis, where the antibody is conjugated to or complexed with a toxin.
CC The non-C35 antigen protein is a premethylated protein. Also included are an
CC isolated antibody (I) specific for C35 (chosen from an antibody
CC comprising the VH region encoded by clone 1B3G, the VL region encoded by
CC clone 1B3K, the VH region encoded by clone 1P2G, the VL region encoded by
CC clone 1P2K, the VH region encoded by clone H0009, the VL region encoded
CC by clone L0010, an antibody comprising at least one of CDR1 or CDR2 of
CC the VH region encoded by AEA62495, an antibody comprising at least one of
CC CDR1 or CDR2 of the VH region encoded by AEA62499, an antibody comprising
CC at least one of CDR1, CDR2, or CDR3 of the VL region encoded by
CC AEA62497, a chimeric antibody, or a humanized antibody), a polynucleotide
CC encoding the antibody, a vector comprising the polynucleotide, a host
CC cell comprising the vector and a composition comprising the antibody and
CC a carrier. The method is useful for killing cancer cells in a mammal
CC preferably human in need of eradication of smaller tumors and/or
CC micrometastases, or in need of cancer treatment for C35-associated cancer
CC chosen from breast cancer, ovarian cancer, bladder cancer, lung cancer,
CC prostate cancer, pancreatic cancer, colon cancer, melanoma and other
CC hyperproliferative disorders. The antibody is useful for detecting,
CC diagnosing or monitoring C35-associated cancers. The antibody comprises a
CC chimeric antibody comprising human immunoglobulin constant regions fused
CC to the variable regions of mouse anti-C35 antibodies (named 1P2, 1B3, MAb
CC 165 and MAb 171). The present sequence represents a kappa chain variable
CC region of a mouse anti-C35 antibody.
XX
SQ Sequence 107 AA;
XX
Query Match 100.0%; Score 32; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 SGGSTLOS 7
| | | | |
Db 50 SGGSTLOS 56
XX
RESULT 10
ID AAW62017 standard; peptide; 108 AA.
XX
XX AAW62017;
XX
XX 01-OCT-1998 (first entry)
XX
XX light chain variable region of humanised anti-CD11a antibody.
XX
XX
XX Complementarity determining region; light chain variable region;
XX humanised antibody; MMW24F(ab)-8; anti-CD11a antibody;
XX human CD11a I domain; MMW24 epitope; alpha subunit;
XX lymphocyte function-associated antigen 1; LFA-1; immunoassay;
XX in vivo imaging; diagnosis; CD11a-associated disease.
XX
XX Mus sp.
XX
XX Homo sapiens.
XX
XX WO9823761-A1.
XX
XX 04-JUN-1998.
XX
XX 20-OCT-1997; 97WO-US019041.
XX
XX 27-NOV-1996; 96US-00757205.
XX
XX (GETH) GENENTECH INC.
XX
XX Jardiou PM, Presta IG;
XX
XX MPI; 1998-322737/28.
XX
XX New humanised anti-CD11a antibody - used in immunoassays for CD11a, and
PT also to treat conditions such as immunological or inflammatory disease.
PT

XX Claim 9; Page 48; 66pp; English.
 PS
 XX
 CC The present sequence represents the light chain variable region of a
 CC humanised anti-CD1a antibody that binds specifically to the human CD1a
 CC I domain (MHM24 epitope). CD1a refers to the alpha subunit of lymphocyte
 CC function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-
 CC CD1a antibodies are used to determine presence of CD1a in usual
 CC immunosays or by in vivo imaging, particularly for diagnosis of CD1a-
 CC associated diseases (typically immune responses and inflammation such as
 CC psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
 CC leukaemia, etc
 CC
 SQ Sequence 108 AA;
 Query Match 100.0%; Score 32; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGTLOS 7
 Db 50 SGGTLOS 56
 RESULT 11
 AAM63528
 ID AAM63528 standard; protein; 108 AA.
 AC AAM63528;
 XX
 DT 06-OCT-1998 (first entry)
 XX
 DE Murine MHM24 light chain.
 XX
 KM Antibody mutant production; species-dependent antibody; malignancy;
 KM infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KM intercellular adhesion molecule-1; inflammatory disease; CD1a; therapy;
 KM autoimmune disease; transplant rejection; tumour cell invasion;
 KM human immune deficiency virus infection; light chain.
 XX
 OS Mus sp.
 XX
 PN WO9823746-A1.
 XX
 PD 04-JUN-1998.
 XX
 PF 29-OCT-1997; 97WO-US020169.
 XX
 PR 27-NOV-1996; 96US-00756150.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardiou PM, Presta LG;
 XX
 DR WPI; 1998-322726/28.
 XX
 PT Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD1a.
 XX
 PS Disclosure; Page 52-53; 71pp; English.
 XX
 CC This sequence represents the light chain of the murine antibody MHM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD1a (lymphocyte function-associated antigen

CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use
 CC
 SQ Sequence 108 AA;
 Query Match 100.0%; Score 32; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGTLOS 7
 Db 50 SGGTLOS 56
 RESULT 12
 AAM63529
 ID AAM63529 standard; protein; 108 AA.
 AC AAM63529;
 XX
 DT 06-OCT-1998 (first entry)
 XX
 DE Humanised MHM24 light chain.
 XX
 KM Antibody mutant production; species-dependent antibody; malignancy;
 KM infection; haematopoiesis; lymphocyte function-associated antigen-1;
 KM intercellular adhesion molecule-1; inflammatory disease; CD1a; therapy;
 KM autoimmune disease; transplant rejection; tumour cell invasion;
 KM human immune deficiency virus infection; light chain.
 XX
 OS Synthetic.
 XX
 PN WO9823746-A1.
 XX
 PD 04-JUN-1998.
 XX
 PF 29-OCT-1997; 97WO-US020169.
 XX
 PR 27-NOV-1996; 96US-00756150.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Jardiou PM, Presta LG;
 XX
 DR WPI; 1998-322726/28.
 XX
 PT Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD1a.
 XX
 PS Disclosure; Page 53; 71pp; English.
 XX
 CC This sequence represents the light chain of the humanised antibody MHM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoiesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD1a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use

```

XX SQ Sequence 108 AA;
Query Match 100.0%; Score 32; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
   |||||
Db 50 SGSTLOS 56

RESULT 13
AA82344
ID AAY82344 standard; protein; 108 AA.
XX AC AAY82344;
XX DT 22-JUN-2000 (first entry)
XX DE Murine MHM24 light chain amino acid sequence SEQ ID NO:1.
XX KW Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
XX KW antitumour; antiviral; inflammation; immunological response; LFA-1;
XX KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
XX KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
XX KW viral infection; transplant rejection; graft rejection.
XX OS Mus sp.
XX PN US6037454-A.
XX PD 14-MAR-2000.
XX PF 20-NOV-1997; 97US-00974899.
XX PR 27-NOV-1996; 96US-0031971P.
XX PA (GENTH ) GENENTECH INC.
XX PI Jardieu PM, Presta LG;
XX DR WPI; 2000-282241/24.
XX PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.
XX PT inflammation and transplant rejection, contains human heavy variable
XX PT region complementarily determining regions.
XX PS Example; Fig 1; 38pp; English.
XX CC The present invention describes a humanised anti-CD11a antibody (Ab) that
XX CC binds specifically to the human CD11a I-domain. The Ab has anti-
XX CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
XX CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
XX CC involved in leucocyte adhesion associated with inflammatory and
XX CC immunological responses. The Ab are used: (i) optionally when coupled to
XX CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
XX CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
XX CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
XX CC rhinitis, leukaemia, viral infections and many others, also for
XX CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
XX CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
XX CC to active anticancer agent; and (v) for affinity chromatography. The Ab
XX CC retain about the same activity in adhesion and mixed lymphocyte response
XX CC assays as the murine antibodies from which they are derived. The murine
XX CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
XX CC between Jurkat cells (expressing LFA-1) and normal epidermal
XX CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
XX CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
XX CC sequence represents the amino acid sequence of murine MHM24 light chain,
XX CC which is used in the exemplification of the present invention
XX CC Sequence 108 AA;

```

```

Query Match 100.0%; Score 32; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
   |||||
Db 50 SGSTLOS 56

RESULT 14
AA82343
ID AAY82343 standard; protein; 108 AA.
XX AC AAY82343;
XX DT 22-JUN-2000 (first entry)
XX DE Humanised anti-CD11a antibody light chain variable region SEQ ID NO:2.
XX KW Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
XX KW antitumour; antiviral; inflammation; immunological response; LFA-1;
XX KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
XX KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
XX KW viral infection; transplant rejection; graft rejection.
XX OS Homo sapiens.
XX PN US6037454-A.
XX PD 14-MAR-2000.
XX PF 20-NOV-1997; 97US-00974899.
XX PR 27-NOV-1996; 96US-0031971P.
XX PA (GENTH ) GENENTECH INC.
XX PI Jardieu PM, Presta LG;
XX DR WPI; 2000-282241/24.
XX PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.
XX PT inflammation and transplant rejection, contains human heavy variable
XX PT region complementarily determining regions.
XX PS Claim 5; Fig 1; 38pp; English.
XX CC The present invention describes a humanised anti-CD11a antibody (Ab) that
XX CC binds specifically to the human CD11a I-domain. The Ab has anti-
XX CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
XX CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
XX CC involved in leucocyte adhesion associated with inflammatory and
XX CC immunological responses. The Ab are used: (i) optionally when coupled to
XX CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
XX CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
XX CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
XX CC rhinitis, leukaemia, viral infections and many others, also for
XX CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
XX CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
XX CC to active anticancer agent; and (v) for affinity chromatography. The Ab
XX CC retain about the same activity in adhesion and mixed lymphocyte response
XX CC assays as the murine antibodies from which they are derived. The murine
XX CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
XX CC between Jurkat cells (expressing LFA-1) and normal epidermal
XX CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
XX CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
XX CC sequence represents the light chain variable region of the humanised anti-
XX CC CD11a Ab
XX CC Sequence 108 AA;

```

Query Match 100.0%; Score 32; DB 3; Length 108; ..
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
|||
50 SGGSTLOS 56

DB

RESULT 15

ADG38989
ID ADG38989 standard; protein; 108 AA.

AC ADG38989;

DT 26-FEB-2004 (first entry)

DE Mouse anti-CD11a antibody light chain variable region.

XX Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
XX VL; cluster of differentiation 11a; mixed lymphocyte response assay;
XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; prodng activating enzyme.

OS Mus sp.

PN US2003207336-A1.

PD 06-NOV-2003.

PF 28-FEB-2001; 2001US-00795798.

PR 27-NOV-1996; 96US-0031971P.

PR 20-NOV-1997; 97US-00974899.

PR 20-OCT-1999; 99US-00420745.

PA (GENTH) GENENTECH INC.

PI Jardiou PM, Presta LG;

PT MPI; 2004-051511/05.

PT Humanized anti-CD11a antibody useful for treating lymphocyte function-
PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

XX Example; SEQ ID NO 1; 43pp; English.

XX The invention relates to a Humanised anti-cluster of differentiation
XX (CD11a) antibody having specificity to human CD11a I-domain or CD11a with
XX a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
XX inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
XX response assay or for preventing adhesion of Jurkat cells to normal human
XX epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
XX -1. Also included are a kit comprising the antibody and instructions for
XX use to detect the CD11a protein, an isolated nucleic acid encoding the
XX antibody, a vector comprising the nucleic acid, a host cell comprising the
XX the vector and producing the antibody by culturing the cell so that the
XX antibody is expressed. The antibody binds to epitope MM24 on CD11a. The
XX antibody is useful for determining the presence of CD11a protein and for
XX treating lymphocyte function-associated antigen 1 mediated disorder such
XX as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
XX rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
XX and diabetes mellitus. The antibody is useful when conjugated to a
XX prodng activating enzyme, or as an affinity purification agent. The
XX present sequence is the light chain variable region (VL) of the wild-type
XX mouse anti-CD11a I domain monoclonal antibody MM24.

XX Sequence 108 AA;
SQ

Query Match 100.0%; Score 32; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
|||
50 SGGSTLOS 56

DB

RESULT 16

ADG38990
ID ADG38990 standard; protein; 108 AA.

AC ADG38990;

DT 26-FEB-2004 (first entry)

DE Humanised Mouse anti-CD11a antibody light chain variable region.

XX Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
XX VL; cluster of differentiation 11a; mixed lymphocyte response assay;
XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; prodng activating enzyme; humanised.

OS Synthetic.

PN US2003207336-A1.

PD 06-NOV-2003.

PF 28-FEB-2001; 2001US-00795798.

PR 27-NOV-1996; 96US-0031971P.

PR 20-NOV-1997; 97US-00974899.

PR 20-OCT-1999; 99US-00420745.

PA (GENTH) GENENTECH INC.

PI Jardiou PM, Presta LG;

PT MPI; 2004-051511/05.

PT Humanized anti-CD11a antibody useful for treating lymphocyte function-
PT associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
PT ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

XX Claim 9; SEQ ID NO 2; 43pp; English.

XX The invention relates to a Humanised anti-cluster of differentiation
XX (CD11a) antibody having specificity to human CD11a I-domain or CD11a with
XX a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
XX inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte
XX response assay or for preventing adhesion of Jurkat cells to normal human
XX epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
XX -1. Also included are a kit comprising the antibody and instructions for
XX use to detect the CD11a protein, an isolated nucleic acid encoding the
XX antibody, a vector comprising the nucleic acid, a host cell comprising the
XX the vector and producing the antibody by culturing the cell so that the
XX antibody is expressed. The antibody binds to epitope MM24 on CD11a. The
XX antibody is useful for determining the presence of CD11a protein and for
XX treating lymphocyte function-associated antigen 1 mediated disorder such
XX as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
XX rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
XX and diabetes mellitus. The antibody is useful when conjugated to a
XX prodng activating enzyme, or as an affinity purification agent. The
XX present sequence is the light chain variable region (VL) of the humanised
XX mouse anti-CD11a I domain monoclonal antibody MM24.

XX Sequence 108 AA;
SQ

Query Match 100.0%; Score 32; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
 |||||
 50 SGSTLOS 56

Db

RESULT 17
 AD126700
 ID AD126700 standard; protein; 108 AA.
 AC AD126700;
 DT 15-APR-2004 (first entry)
 DE Mouse anti Igm antibody O1 kappa light chain protein.
 XX
 XX Mouse; antibody; Igm; remyelination; neuronal growth; autoantibody;
 XX demyelination disease; multiple sclerosis; central nervous system; CNS;
 XX axon; glial cell proliferation;
 XX Theiler's murine encephalomyelitis virus infection; CNS injury;
 XX spinal cord injury.
 XX
 XX Mus sp.
 XX
 XX US2003185827-A1.
 XX
 XX 02-OCT-2003.
 XX
 XX 13-NOV-2001; 2001US-00010729.
 XX
 XX 29-APR-1994; 94US-00236520.
 XX 08-AUG-1996; 96US-00692084.
 XX 07-JAN-1997; 97US-00779784.
 XX 28-MAY-1999; 99US-0032862.
 XX 30-MAY-2000; 2000US-00580787.
 XX 05-DEC-2000; 2000US-00730473.
 XX
 XX (MAYO-) MAYO FOUND.
 XX
 XX Rodriguez M, Miller DJ, Pease LR;
 XX
 XX WPI; 2004-119219/12.
 XX N-PSDB; AD126701.
 XX
 XX New human immunoglobulin M antibody for treating or preventing a
 XX demyelinating disease of the central nervous system in a human or
 XX domestic animal, such as multiple sclerosis.
 XX
 XX Example 19; Fig 68; 159pp; English.
 XX
 XX The invention relates to an antibody (1) produced by injecting an
 XX immunocompetent host with an antibody peptide, and harvesting the
 XX antibody, where the peptide comprises a human anti-igm antibody fragment
 XX given in the specification, or active fragments. Also included are
 XX stimulating remyelination of central nervous system (CNS) axons in a
 XX mammal (comprising administering a monoclonal antibody, or mixtures,
 XX monomers, active fragments, or recombinant antibodies derived from it,
 XX characterised by their ability to bind structures and cells within the
 XX CNS, including oligodendrocytes), stimulating the proliferation of glial
 XX cells in CNS axons in a mammal (comprising administering a monoclonal
 XX antibody, or mixtures, monomers, active fragments, or recombinant
 XX antibodies derived from it, characterised by their ability to bind
 XX structures and cells within the CNS), treating or preventing a
 XX demyelinating disease of the CNS in a mammal (comprising administering a
 XX monoclonal antibody, or mixtures, monomers, active fragments, or
 XX recombinant antibodies derived from it, characterised by their ability to
 XX bind structures and cells within the CNS, and to stimulate remyelination
 XX of axons of the CNS), stimulating, in vitro, the proliferation of glial
 XX cells from mixed cell culture, stimulating remyelination of CNS axons in

a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 antibody (or a peptide analogue, hapten, or active fragment of it, where
 the DNA sequence consists of a sequence encoding an anti Igm antibody), a
 probe capable of screening for the antibody, an assay for screening drugs
 and other agents for the ability to modulate the production or mimic the
 activities of mAb shlgm22, shlgm46, or combinations of them, a
 recombinant virus transformed with recombinant antibody nucleic acids or
 vector, imaging a portion of the CNS using the antibody and diagnosing or
 monitoring demyelination and/or remyelination of the CNS comprising using
 CNS image. The antibody is used to stimulate remyelination of CNS axons,
 and to stimulate the proliferation of glial cells in CNS axons,
 optionally in vitro. The antibody is used to treat or prevent a
 demyelinating disease of the CNS in a human or domestic animal, such as
 multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 preferably the mammal is a mouse infected with Strain DA of Theiler's
 murine encephalomyelitis virus. The antibody is used to treat a spinal
 cord injury and used to screen drugs and other agents for the ability to
 modulate the production or mimic the activities of the antibody. The
 antibody can be used to image a portion of the CNS which can be used to
 diagnose or monitor demyelination and/or remyelination of the CNS. The
 present sequence is a variable region of a mouse anti-igm antibody (or
 fragment).

SQ Sequence 108 AA;

Query Match 100.0%; Score 32; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
 |||||
 50 SGSTLOS 56

Db

RESULT 18
 ADR03365
 ID ADR03365 standard; protein; 108 AA.
 XX
 XX ADR03365;
 XX
 XX 21-OCT-2004 (first entry)
 XX
 XX Humanised MHM24 F(ab)-8 antibody variable light chain protein.
 XX
 XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
 XX rhinovirus infection; inflammatory skin disease; psoriasis;
 XX inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 XX adult respiratory distress syndrome; allergic disease; eczema; asthma;
 XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 XX SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 XX tuberculosis; sarcoidosis; polymyositis;
 XX chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 XX skin hypersensitivity disorder; poison ivy; poison oak;
 XX B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 XX graft versus host disease; cancer; gene therapy;
 XX murine anti-human CD11a monoclonal antibody; MHM24; variable light chain;
 XX VL; murine; human; fusion protein.
 XX
 XX Mus sp.
 XX Homo sapiens.
 XX Chimeric.
 XX
 XX US2004146507-A1.
 XX
 XX 29-JUL-2004.
 XX
 XX 03-DEC-2003; 2003US-00727737.
 XX
 XX 27-NOV-1996; 96US-0031945P.
 XX 20-NOV-1997; 97US-00975329.
 XX
 XX (GENTH) GEMENTECH INC.
 XX

PI Jardiou PM, Presta LG;
 XX WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 2; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD1a monoclonal antibody
 CC (MHM24) F(ab)-8 variable light chain protein. This sequence is used in
 CC the exemplification of the invention.
 XX
 SQ Sequence 108 AA;
 XX
 Query Match 100.0%; Score 32; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGSTLQS 7
 Db 50 SGGSTLQS 56
 XX
 RESULT 19
 ADR03364
 ID ADR03364 standard; protein; 108 AA.
 XX
 AC ADR03364;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Murine MHM24 antibody variable light chain protein.
 XX
 KW CD1a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD1a monoclonal antibody; MHM24; variable light chain;
 KW VJ; murine.
 XX
 OS Mus sp.
 XX
 XX US2004146507-A1.
 XX
 XX 29-JUL-2004.
 XX
 XX 03-DEC-2003; 2003US-00727737.
 XX
 XX 27-NOV-1996; 96US-0031945P.
 XX
 XX 20-NOV-1997; 97US-00975329.
 PR

XX (GETH) GENENTECH INC.
 XX
 PA Jardiou PM, Presta LG;
 XX WPI; 2004-552640/53.
 XX
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 1; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is murine anti-human CD1a monoclonal antibody (MHM24)
 CC variable light chain protein. This sequence is used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 108 AA;
 XX
 Query Match 100.0%; Score 32; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGSTLQS 7
 Db 50 SGGSTLQS 56
 XX
 RESULT 20
 ADM38457
 ID ADM38457 standard; protein; 108 AA.
 XX
 AC ADM38457;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE CD1a light chain variable region #2.
 XX
 KW monoclonal antibody; CD1a; light-chain variable region;
 KW heavy-chain variable region.
 KW Homo sapiens.
 XX
 OS CN1439651-A.
 XX
 XX 03-SEP-2003.
 XX
 XX 20-FEB-2002; 2002CN-00110866.
 XX
 XX 20-FEB-2002; 2002CN-00110866.
 XX
 XX (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
 XX
 XX Wang H, Wang J;
 XX WPI; 2004-169719/17.
 XX
 XX Recombinant human CD1a monoclonal antibody and its preparation and
 XX medicinal composition.
 PT

XX Claim 1; Page 14; 16pp; Chinese.
PS
XX
CC The present invention relates to a recombinant monoclonal antibody for
CC human CD1a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
CC No.5 in light-chain variable region and the amino acid sequence shown by
CC SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
CC bioactivity and the expression in host cell are greatly increased. The
CC DNA molecule for coding the antibody, its preparation process and the
CC medicinal composition containing it are also disclosed. The present
CC sequence represents a light chain variable region of human CD1a.
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 32; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTLOS 7
Db 50 SGGSTLOS 56
RESULT 21
ADX80645
ID ADX80645 standard; protein; 108 AA.
AC ADX80645;
XX
DT 05-MAY-2005 (first entry)
XX
DE Humanized CD1a variable light chain amino acid sequence, seq id 5.
XX
KW Protein purification; leaching; protein A affinity chromatography; CD1a;
KW antibody.
XX
OS Synthetic.
XX
PN US2005038231-A1.
XX
PD 17-FEB-2005.
XX
PF 24-JUN-2004; 2004US-00877532.
XX
PR 28-JUL-2003; 2003US-0490500P.
XX
XX (GETH) GENENTECH INC.
XX
XX Fahrner RL, Laverdiere A, McDonald PJ, O'leary RM;
XX WPI; 2005-172327/18.
XX
XX Purifying a protein, e.g. antibody or immunoadhesin, comprises reducing
XX the temperature of a composition subjected to protein A affinity
XX chromatography to 3-20 degrees C, where protein A leaching is reduced.
XX
PS Disclosure; SEQ ID NO 5; 27pp; English.
XX
XX The invention relates to a method of purifying a protein which comprises
XX a CH2/CH3 region by protein A affinity chromatography. The method
XX involves reducing the temperature of a composition comprising the protein
XX and one or more impurities subjected to protein A affinity chromatography
XX to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably
XX the protein is antibody. The antibody is selected from Trastuzumab,
XX humanized 2C4, humanized CD1a antibody, and humanized VEGF antibody.
XX Preferably, the antibody binds HER2 antigen, where the antibody is
XX Trastuzumab or humanized 2C4. The protein is an immunoadhesin,
XX specifically a TNP receptor immunoadhesin. The methods are useful for
XX purifying a protein, which comprises a CH2/CH3 region by protein A
XX affinity chromatography and for reducing leaching of protein A during
XX protein A affinity chromatography. The current sequence represents the
XX variable light chain amino acid sequence of CD1a.

SQ Sequence 108 AA;
Query Match 100.0%; Score 32; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTLOS 7
Db 50 SGGSTLOS 56
RESULT 22
ADW38453
ID ADW38453 standard; protein; 109 AA.
AC ADW38453;
XX
DT 24-MAR-2005 (first entry)
XX
DE CD1a light chain variable region #1.
XX
KW monoclonal antibody; CD1a; light-chain variable region;
KW heavy-chain variable region.
XX
OS Homo sapiens.
XX
PN CN1439651-A.
XX
PD 03-SEP-2003.
XX
PF 20-FEB-2002; 2002CN-00110866.
XX
PR 20-FEB-2002; 2002CN-00110866.
XX
XX (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX
XX Wang H, Wang J;
XX
XX WPI; 2004-169719/17.
XX
DR N-PsDB; ADW38455.
XX
XX Recombinant human CD1a monoclonal antibody and its preparation and
XX medicinal composition.
XX
PS Claim 1; Page 12; 16pp; Chinese.
XX
XX The present invention relates to a recombinant monoclonal antibody for
XX human CD1a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
XX No.5 in light-chain variable region and the amino acid sequence shown by
XX SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
XX bioactivity and the expression in host cell are greatly increased. The
XX DNA molecule for coding the antibody, its preparation process and the
XX medicinal composition containing it are also disclosed. The present
XX sequence represents a light chain variable region of human CD1a.
XX
SQ Sequence 109 AA;
Query Match 100.0%; Score 32; DB 8; Length 109;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTLOS 7
Db 50 SGGSTLOS 56
RESULT 23
ADP11669
ID ADP11669 standard; protein; 214 AA.
AC ADP11669;
XX
XX 26-FEB-2004 (first entry)
DT

XX anti-CD11a rhumAb light chain amino acid sequence #SEQ ID 3.
 DE Purifying; target protein; non-affinity purification;
 XX high-performance tangential flow filtration; HPTFF; pharmaceutical;
 KW diagnostic; therapeutic; antibody.
 XX Synthetic.
 OS WO2003102132-A2.
 PN 11-DEC-2003.
 XX 25-APR-2003; 2003WO-US013054.
 PF 26-APR-2002; 2002US-0375953P.
 PR (GETH) GENENTECH INC.
 PA Fahner RL, Follman D, Lebreton B, Van Reis R;
 XX WPI, 2004-043096/04.
 DR Purifying target protein from mixture containing host cell protein
 PT involves subjecting mixture to non-affinity purification, high-
 PT performance tangential flow filtration and isolating purified protein.
 XX disclosure; SEQ ID NO 3; 77pp; English.
 PS
 XX The invention relates to a method for purifying a target protein from a
 CC mixture containing a host cell protein. This method comprises subjecting
 CC the mixture to a non-affinity purification followed by high-performance
 CC tangential flow filtration (HPTFF) and isolating the protein in a purity
 CC containing less than 100 parts/million (ppm) of the host cell protein,
 CC where the method of the invention includes no affinity purification
 CC process. The method of the invention is useful for purifying a target
 CC protein from a mixture containing a host cell protein, and is useful for
 CC incorporating the isolated protein into a pharmaceutical formulation.
 CC Proteins purified using the method of the invention are useful in a
 CC pharmaceutical respect, and are also useful in various diagnostic and
 CC therapeutic purposes. The method of the invention is efficient in
 CC purifying a target protein from a mixture containing a host cell protein,
 CC and may also be effectively performed at low cost. The current sequence
 CC represents the anti-CD11a rhumAb light chain amino acid sequence. This
 CC particular protein was used to demonstrate the method of the invention.
 CC
 SQ Sequence 214 AA;
 XX
 XX
 Query Match 100.0%; Score 32; DB 8; Length 214;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGSTLQS 7
 DB 50 SGGSTLQS 56
 XX
 RESULT 24
 AAY17957
 ID AAY17957 standard; protein; 242 AA.
 XX
 AC AAY17957;
 XX
 DT 04-AUG-1999 (first entry)
 XX
 DE Mouse scFV fragment 3-1.
 XX
 KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
 KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.
 OS Mus sp.
 XX
 PN WO925818-A1.

XX 27-MAY-1999.
 PD 16-NOV-1998; 98WO-EP007313.
 XX
 PF 17-NOV-1997; 97EP-00120096.
 PR (KUFE/) KUFER P.
 PA Kufner P, Raum T, Borschert K, Zetcl F, Lutterbuese R;
 XX WPI, 1999-338004/28.
 DR N-PSDB; AAX77240.
 XX
 PT Phage display system for identification of binding site domains retaining
 PT capacity to bind an epitope.
 XX
 PS Claim 27; Fig 6.3; 152pp; English.
 XX
 CC The invention relates to a method of identifying binding site domains
 CC (BSD) that retain the capacity of binding to a predetermined epitope when
 CC positioned C-terminal of at least one further domain in a recombinant bi-
 CC or multivalent polypeptide. The method comprises (a) testing a panel of
 CC BSD displayed on the surface of a biological display system as part of a
 CC fusion protein for binding to a predetermined epitope, where the fusion
 CC protein comprises an additional domain positioned N-terminal of the BSD
 CC and an amino acid sequence that mediates anchoring of the fusion protein
 CC to the surface of the display system; and (b) identifying a BSD that
 CC binds to the predetermined epitope. The method is useful to identify bi-
 CC or multivalent polypeptides that comprise antibody binding sites capable
 CC of efficiently binding to the corresponding antigen. The polypeptides or
 CC antibodies identified by the method are useful therapeutically and
 CC diagnostically, for e.g. cancer and autoimmune diseases. scFv-antibody
 CC fragments that bind independently of their position within bifunctional
 CC single-chain fusion proteins can be isolated from combinatorial antibody
 CC libraries using the new in vitro method. Sequences AAY17957-965 represent
 CC mouse scFV fragments
 XX
 SQ Sequence 242 AA;
 XX
 XX
 Query Match 100.0%; Score 32; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGSTLQS 7
 DB 185 SGGSTLQS 191
 XX
 RESULT 25
 AAY17961
 ID AAY17961 standard; protein; 242 AA.
 XX
 AC AAY17961;
 XX
 DT 04-AUG-1999 (first entry)
 XX
 DE Mouse scFV fragment 4-4.
 XX
 KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
 KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.
 OS Mus sp.
 XX
 PN WO925818-A1.
 XX
 PD 27-MAY-1999.
 XX
 PF 16-NOV-1998; 98WO-EP007313.
 XX
 PR 17-NOV-1997; 97EP-00120096.
 PA (KUFE/) KUFER P.
 XX

```

XX Kufer P, Raum T, Borschert K, Zetcl F, Lutterbuese R;
XX WPI, 1999-338004/28.
XX N-PSDB; AAX77244.
XX Phase display system for identification of binding site domains retaining
XX capacity to bind an epitope.
XX Claim 27, Fig 6.7, 152pp; English.
XX The invention relates to a method of identifying binding site domains
XX (BSD) that retain the capacity of binding to a predetermined epitope when
XX positioned C-terminal of at least one further domain in a recombinant bi-
XX or multivalent polypeptide. The method comprises (a) testing a panel of
XX BSD displayed on the surface of a biological display system as part of a
XX fusion protein for binding to a predetermined epitope, where the fusion
XX protein comprises an additional domain positioned N-terminal of the BSD
XX and an amino acid sequence that mediates anchoring of the fusion protein
XX to the surface of the display system; and (b) identifying a BSD that
XX binds to the predetermined epitope. The method is useful to identify bi-
XX or multivalent polypeptides that comprise antibody binding sites capable
XX of efficiently binding to the corresponding antigen. The polypeptides or
XX antibodies identified by the method are useful therapeutically and
XX diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
XX fragments that bind independently of their position within bifunctional
XX single-chain fusion proteins can be isolated from combinatorial antibody
XX libraries using the new in vitro method. Sequences AAY17957-965 represent
XX mouse scFv fragments
SQ Sequence 242 AA;

Query Match 100.0%; Score 32; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 185 SGGSTLOS 191

RESULT 26
AAY17959
ID AAY17959 standard; protein; 242 AA.
AC AAY17959;
AC AAY17959;
DE 04-AUG-1999 (first entry)
DE Mouse scFv fragment 3-8.
XX Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
XX autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX Mus sp.
XX WO925818-A1.
XX 27-MAY-1999.
XX 16-NOV-1998; 98WO-EP007313.
XX 17-NOV-1997; 97EP-00120096.
XX (KUPE/) KUPER P.
XX Kufer P, Raum T, Borschert K, Zetcl F, Lutterbuese R;
XX WPI, 1999-338004/28.
XX N-PSDB; AAX77242.
XX Phase display system for identification of binding site domains retaining
XX capacity to bind an epitope.

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XX Claim 27, Fig 6.5; 152pp; English.
XX The invention relates to a method of identifying binding site domains
XX (BSD) that retain the capacity of binding to a predetermined epitope when
XX positioned C-terminal of at least one further domain in a recombinant bi-
XX or multivalent polypeptide. The method comprises (a) testing a panel of
XX BSD displayed on the surface of a biological display system as part of a
XX fusion protein for binding to a predetermined epitope, where the fusion
XX protein comprises an additional domain positioned N-terminal of the BSD
XX and an amino acid sequence that mediates anchoring of the fusion protein
XX to the surface of the display system; and (b) identifying a BSD that
XX binds to the predetermined epitope. The method is useful to identify bi-
XX or multivalent polypeptides that comprise antibody binding sites capable
XX of efficiently binding to the corresponding antigen. The polypeptides or
XX antibodies identified by the method are useful therapeutically and
XX diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
XX fragments that bind independently of their position within bifunctional
XX single-chain fusion proteins can be isolated from combinatorial antibody
XX libraries using the new in vitro method. Sequences AAY17957-965 represent
XX mouse scFv fragments
SQ Sequence 242 AA;

Query Match 100.0%; Score 32; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 185 SGGSTLOS 191

RESULT 27
AAB10863
ID AAB10863 standard; protein; 392 AA.
AC AAB10863;
AC AAB10863;
DE 02-FEB-2001 (first entry)
DE S11-VEGF2 construct protein in pSectagA SEQ ID NO: 38.
XX WVP; multivalent protein; treatment; dressing; skin; muscle; musculature;
XX nervous system; inner organ; hematopoietic system; immune system; joint;
XX support tissue; immunization.
XX Synthetic.
XX OS Homo sapiens.
XX WO200053790-A1.
XX 14-SEP-2000.
XX 26-FEB-2000; 2000WO-EP001612.
XX 10-MAR-1999; 99DE-01010419.
XX (AVER ) AVENTIS PHARMA DEUT GMBH.
XX Kontermann R, Nettelbeck D, Sedlacek H, Mueller R;
XX WPI; 2000-572272/53.
XX N-PSDB; AAA98173.
XX Cell specific multivalent proteins useful for targeting specific cells
XX for the treatment of disease.
XX Example 2; Page 66-67; 81pp; German.
XX This invention describes a method for the production of a novel cell
XX specific multivalent protein (WVP). The invention also describes (1) a
XX nucleic acid construct, which encodes an WVP; (2) a bacterium, yeast or

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CC mammalian cell, in which the nucleic acid construct of (1) is introduced;
CC (3) the MVP bound to a vector; (4) production of an MVP; (5) an MVP
CC comprising a scfv with a binding site for the adenoviral fibre protein or
CC CD3 molecule and two VEBF units, bound by a peptide linker; and (6) a
CC complex comprising at least two MVPs as above (in which each single
CC ligand can be 0=1). The MVP, optionally bound to a vector, is useful for
CC production of a remedy to treat cells outside tissue by dressings for
CC skin, mucus, nervous systems, inner organs, hematopoietic systems, immune
CC systems, musculature, support tissues or joints and to immunize to
CC prevent or treat diseases

CC SQ Sequence 392 AA;

Query Match 100.0%; Score 32; DB 3; Length 392;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7

Db 212 SGGSTLOS 218

RESULT 28

AD283409 standard; protein; 491 AA.

AD283409;

14-JUL-2005 (first entry)

C-terminal Epcam binder SEQ ID NO 31.

neoplasia; inflammation; immune disorder; infection; allergy;

graft versus host disease; cytostatic; Antiinflammatory;

immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;

Epcam.

Synthetic.

15-OCT-2004; 2004WO-EP011646.

16-OCT-2003; 2003EP-00023581.

(MICR-) MICROMET AG.

Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baenerle P;

Carr FJ, Hamilton AA, Williams S;

WPI; 2005-333494/34.

N-PSDB; AD283408.

New cytotoxically active CD3 specific binding construct comprises a first

domain specifically binding to human CD3 and an Ig-derived second binding

domain, useful for treating, preventing, or ameliorating, e.g.

proliferative disease.

Claim 20; SEQ ID NO 31; 639pp; English.

The invention relates to a cytotoxically active CD3 specific binding

construct comprising a first domain specifically binding to human CD3 and

an Ig-derived second binding domain. The CD3 specific binding construct

above or the construct produced by the process, nucleic acid molecule,

vector, or host is useful for the preparation of a pharmaceutical

composition for the prevention, treatment, or amelioration of a

proliferative disease, a tumor, an inflammatory disease, an immunological

disorder, an autoimmune disease, an infectious disease, viral disease,

allergic reactions, parasitic reactions, graft-versus-host diseases, or

host-versus-graft diseases. The cytotoxically active CD3 specific binding

construct is useful for treating, preventing, or ameliorating

CC proliferative disease, a tumor, an inflammatory disease, an immunological

CC disorder, an autoimmune disease, an infectious disease, viral disease,

CC allergic reactions, parasitic reactions, graft-versus-host diseases, or

CC host-versus-graft diseases. The present sequence represents the amino

CC acid sequence of an anti-Epcam binder.

CC SQ Sequence 491 AA;

Query Match 100.0%; Score 32; DB 9; Length 491;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7

Db 434 SGGSTLOS 440

RESULT 29

ADV66089 standard; protein; 494 AA.

ADV66089;

24-FEB-2005 (first entry)

Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 12.

bispecific single chain antibody; epithelial cell adhesion molecule;

Epcam; CD3; tumor; cancer; cytostatic.

Unidentified.

MO2004106383-A1.

09-DEC-2004.

26-MAY-2004; 2004WO-EP005687.

31-MAY-2003; 2003EP-00012133.

31-MAY-2003; 2003EP-00012134.

(MICR-) MICROMET AG.

Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;

Kohleisen B, Lenkeri-Schuetz U, Baenerle P;

WPI; 2005-021271/02.

N-PSDB; ADV66088.

New pharmaceutical composition having a bispecific single chain antibody

construct, useful for preventing, treating or ameliorating a tumorous

disease, such as an epithelial or minimal residual cancer.

Claim 12; SEQ ID NO 12; 227pp; English.

The invention comprises a composition that contains a bispecific single

chain antibody consisting of at least two domains, where one of domains

binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the

second domain binds to human CD3 antigen. The bispecific antibody

construct of the invention is useful for the prevention, treatment or

amelioration of a tumorous disease, such as an epithelial or minimal

residual cancer. The present amino acid sequence represents a bispecific

single chain antibody of the invention.

Sequence 494 AA;

Query Match 100.0%; Score 32; DB 9; Length 494;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7

Db 431 SGGSTLOS 437

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RESULT 30
ADV66123
ID ADV66123 standard; protein; 497 AA.
XX
AC ADV66123;
XX
DT 24-FEB-2005 (first entry)
XX
DE Anti-CD3-anti-BpCAM bispecific single chain antibody - SEQ ID 46.
XX
XX bispecific single chain antibody; epithelial cell adhesion molecule;
XX BpCAM; CD3; tumor; cancer; cytostatic.
XX
OS Unidentified.
XX
PN WO2004106383-A1.
XX
PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-EP005687.
XX
PR 31-MAY-2003; 2003EP-00012133.
XX 31-MAY-2003; 2003EP-00012134.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Berry M, Offner S, Brieschwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
PI WPI; 2005-021271/02.
DR N-PSDB; ADV66122.
XX
XX New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 12; SEQ ID NO 46; 227pp; English.
XX
CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (BpCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific
CC single chain antibody of the invention.
XX
SQ Sequence 497 AA;
Query Match 100.0%; Score 32; DB 9; Length 497;
Best Local Similarity 100.0%; Pred.No.1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTLOS 7
Db 434 SGGSTLOS 440

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OS Unidentified.
XX
XX WO2004106383-A1.
XX
XX 09-DEC-2004.
XX
XX 26-MAY-2004; 2004WO-EP005687.
XX
XX 31-MAY-2003; 2003EP-00012133.
XX 31-MAY-2003; 2003EP-00012134.
XX
XX (MICR-) MICROMET AG.
XX
XX Kufer P, Berry M, Offner S, Brieschwein K, Wolf A, Raum T;
XX PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
XX WPI; 2005-021271/02.
DR N-PSDB; ADV66124.
XX
XX New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 12; SEQ ID NO 48; 227pp; English.
XX
XX The invention comprises a composition that contains a bispecific single
XX chain antibody consisting of at least two domains, where one of domains
XX binds to human epithelial cell adhesion molecule (BpCAM) antigen, and the
XX second domain binds to human CD3 antigen. The bispecific antibody
XX construct of the invention is useful for the prevention, treatment or
XX amelioration of a tumorous disease, such as an epithelial or minimal
XX residual cancer. The present amino acid sequence represents a bispecific
XX single chain antibody of the invention.
XX
SQ Sequence 497 AA;
Query Match 100.0%; Score 32; DB 9; Length 497;
Best Local Similarity 100.0%; Pred.No.1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTLOS 7
Db 434 SGGSTLOS 440

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RESULT 32
ADZ83427
ID ADZ83427 standard; protein; 506 AA.
XX
AC ADZ83427;
XX
XX 14-JUL-2005 (first entry)
XX
XX Deimmunized construct 3-1xanti-CD3.
XX
XX neoplasm; inflammation; immune disorder; infection; allergy;
XX graft versus host disease; Cytostatic; Antiinflammatory;
XX Immunosuppressive; Virocid; Antibacterial; Antiallergic; Antiparasitic.
XX
XX Synthetic.
XX
XX WO2005040220-A1.
XX
XX 06-MAY-2005.
XX
XX 15-OCT-2004; 2004WO-EP011646.
XX
XX 16-OCT-2003; 2003EP-00023581.
XX
XX (MICR-) MICROMET AG.
XX
XX Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
XX PI Carr FJ, Hamilton AA, Williams S;

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XX MPI: 2005-333494/34.
DR N-PSDB; ADZ83426.
XX
PT New cytotoxically active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.
XX
PS Claim 20; SEQ ID NO 49; 639pp; English.
XX
CC The invention relates to a cytotoxically active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,
CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of deimmunized construct 3-ixanti-CD3.
XX
SQ Sequence 506 AA;

Query Match 100.0%; Score 32; DB 9; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTLQS 7
|||||
Db 69 SGGSTLQS 75

RESULT 33
AAB10864
ID AAB10864 standard; protein; 510 AA.
XX
AC AAB10864;
XX
DT 02-FEB-2001 (first entry)
XX
DE S11-scVEGF2 construct DNA in pSectaga SEQ ID NO: 40.
XX
KM MVP; multivalent protein; treatment; dressing; skin; mucus; musculature;
KM nervous system; inner organ; hematopoietic system; immune system; joint;
KM support tissue; immunization.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200053790-A1.
XX
PD 14-SEP-2000.
XX
PF 26-FEB-2000; 2000WO-BP001612.
XX
PR 10-MAR-1999; 99DE-01010419.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Kontermann R, Nettelbeck D, Sedlacek H, Mueller R;
XX MPI: 2000-572272/53.
DR N-PSDB; AAA98174.
XX
PT Cell specific multivalent proteins useful for targeting specific cells
PT for the treatment of disease.

XX Example 2; Page 67-69; 81pp; German.
XX

CC This invention describes a method for the production of a novel cell
CC specific multivalent protein (MVP). The invention also describes (1) a
CC nucleic acid construct, which encodes an MVP; (2) a bacterium, yeast or
CC mammalian cell, in which the nucleic acid construct of (1) is introduced;
CC (3) the MVP bound to a vector; (4) production of an MVP; (5) an MVP
CC comprising a scFv with a binding site for the adenoviral fibre protein or
CC CD3 molecule and two VEGF units, bound by a peptide linker; and (6) a
CC complex comprising at least two MVPs as above (in which each single
CC ligand can be 0=1). The MVP, optionally bound to a vector, is useful for
CC production of a remedy to treat cells outside tissue by dressings for
CC skin, mucus, nervous systems, inner organs, hematopoietic systems, immune
CC systems, musculature, support tissues or joints and to immunize to
CC prevent or treat diseases

SQ Sequence 510 AA;

Query Match 100.0%; Score 32; DB 3; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTLQS 7
|||||
Db 212 SGGSTLQS 218

RESULT 34
ADV66113
ID ADV66113 standard; protein; 515 AA.
XX
AC ADV66113;
XX
DT 24-FEB-2005 (first entry)
XX
DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 36.
XX
KM bispecific single chain antibody; epithelial cell adhesion molecule;
KM EpCAM; CD3; tumor; cancer; cytostatic.
XX
OS Unidentified.
OS
PN WO2004106383-A1.
XX
PD 09-DEC-2004.
XX
PF 26-MAY-2004; 2004WO-BP005687.
XX
PR 31-MAY-2003; 2003EP-00012133.
PR 31-MAY-2003; 2003EP-00012134.
XX
PA (MICR-) MICROMET AG.
XX
PI Kufer P, Berry M, Offner S, Birschwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkner-Schuetz U, Baerle P;
XX MPI: 2005-021271/02.
DR N-PSDB; ADV66112.
XX
PT New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.
XX
PS Claim 12; SEQ ID NO 36; 227pp; English.
XX
CC The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific

CC single chain antibody of the invention.
 XX Sequence 515 AA;
 SQ Query Match 100.0%; Score 32; DB 9; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
 :|||||
 Db 69 SGGTLOS 75

RESULT 35
 ADR03420 standard; peptide; 7 AA.
 XX ADR03420;
 AC ADR03420;
 XX 21-OCT-2004 (first entry)
 DT Humanised MEM24 CDR-L2 mutant peptide, SerLS0A1a.
 DE CD11a antibody; human immunodeficiency virus infection; HIV infection;
 XX rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MEM24; variable light chain;
 KW VL; murine; human; fusion protein; complementarity determining region;
 KW CDR; mutant; mutein.
 KW
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 OS
 XX
 PN US2004146507-A1.
 XX 29-JUL-2004.
 PD 03-DEC-2003; 2003US-00727737.
 PF 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX (GETH) GENENTECH INC.
 PA
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 57; 54pp; English.

CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary

CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD11a monoclonal antibody
 CC (MEM24) CDR-L2 mutant peptide. This sequence is used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 7 AA;
 QY Query Match 90.6%; Score 29; DB 8; Length 7;
 Best Local Similarity 85.7%; Pred. No. 2e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
 :|||||
 Db 1 AGSTLOS 7

RESULT 36
 ADR03421
 ID ADR03421 standard; peptide; 7 AA.
 XX ADR03421;
 AC ADR03421;
 XX 21-OCT-2004 (first entry)
 DT Humanised MEM24 CDR-L2 mutant peptide, SerLS2A1a.
 DE CD11a antibody; human immunodeficiency virus infection; HIV infection;
 XX rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MEM24; variable light chain;
 KW VL; murine; human; fusion protein; complementarity determining region;
 KW CDR; mutant; mutein.
 KW
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 OS
 XX
 PN US2004146507-A1.
 XX 29-JUL-2004.
 PD 03-DEC-2003; 2003US-00727737.
 PF 27-NOV-1996; 96US-0031945P.
 PR 20-NOV-1997; 97US-00975329.
 XX (GETH) GENENTECH INC.
 PA
 XX
 PI Jardieu PM, Presta LG;
 XX
 DR WPI; 2004-552640/53.
 PT New antibody mutant of a species-dependent antibody, useful for treating
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 58; 54pp; English.

CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin

CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC disease and ulcerative colitis, adult respiratory distress syndrome,
CC allergic diseases such as eczema and asthma, autoimmune diseases such as
CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC mellitus, Reynaud's syndrome, immunological diseases such as
CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC disorders such as poison ivy and poison oak, B-cell malignancies such as
CC chronic lymphocytic leukemia and hairy cell leukemia, graft versus host
CC disease and cancer. The invention is also useful in gene therapy. The
CC present sequence is humanised murine anti-human CD11a monoclonal antibody
CC (MHM24) CDR-L2 mutant peptide. This sequence is used in the
CC exemplification of the invention.

SQ Sequence 7 AA;

Query Match 90.6%; Score 29; DB 8; Length 7;
Best Local Similarity 85.7%; Pred. No. 2e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 1 SGAITLOS 7

RESULT 37

AAO22075 standard; protein; 82 AA.

AAO22075;

25-SEP-2002 (first entry)

Human protein tyrosine phosphatase 9-02.

Human protein tyrosine phosphatase 9.02; embryonic development deformity;

immunologic function disturbance disease; enzyme.

Homo sapiens.

CN1341739-A.

27-MAR-2002.

05-SEP-2000; 2000CN-00125013.

05-SEP-2000; 2000CN-00125013.

(SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.

Mao Y, Xie Y;

WPI; 2002-509466/55.

N-PSDB; AAL40703.

PT New polypeptide-human protein tyrosine phosphatase 9.02 for treating
PT embryonic development deformity and an immunologic function disturbance
PT disease.

Claim 1; Page 27 (Disclosure); 34p; Chinese.

CC The present invention relates to a novel human protein tyrosine
CC phosphatase 9.02 and a polynucleotide encoding the protein. The invention
CC also discloses curing several diseases, such as embryonic development
CC deformity and an immunologic function disturbance disease by using the
CC protein. The invention also discloses an antagonist for resisting the
CC protein and its therapeutic action, and the application of a
CC polynucleotide encoding the new human protein tyrosine phosphatase 9.02.
CC This sequence represents the human protein tyrosine phosphatase 9.02.

SQ Sequence 82 AA;

Query Match 90.6%; Score 29; DB 5; Length 82;

Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 61 SGSTLON 67

RESULT 38

ADFS9199 standard; protein; 90 AA.

ADFS9199;

12-FEB-2004 (first entry)

Human polypeptide sequence SEQ ID NO:1607.

biological activity; genetic engineering; hybridisation probe; oligomer;

primer; chromosome mapping; gene mapping; recombinant protein production;

Homo sapiens.

WO2003080795-A2.

02-OCT-2003.

09-AUG-2002; 2002WO-US025485.

09-AUG-2001; 2001US-0311261P.

(HYSE-) HYSEQ INC.

Tang YT, Yang Y, Wang Z, Weng G, Ma Y;

WPI; 2003-876918/81.

N-PSDB; ADFS8199.

PT New polynucleotides, useful as hybridization probes, oligomers or
PT primers, for chromosome or gene mapping, for the recombinant production
PT of proteins, and for generating antisense DNA or RNA.

Claim 20; SEQ ID NO 1607; 571p; English.

CC The present sequence represents a polypeptide (II) with biological
CC activity, which is encoded by an isolated polynucleotide sequence (I);
CC (2) an expression vector comprising (I); (3) a host cell genetically
CC engineered to comprise (I) which is operatively associated with a
CC regulatory sequence that modulates expression of (I) in the host cell;
CC (4) a polypeptide (II) encoded by (I); (5) a composition comprising the
CC polypeptide of (4) and a carrier; (6) an antibody directed against the
CC polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a
CC sample; (8) identifying a compound that binds to the polypeptide of (4);
CC (9) producing the polypeptide of (4); and (10) a collection of
CC polynucleotides comprising at least one of the polynucleotide sequences
CC (I). The polynucleotides (I) can be used as hybridisation probes,
CC oligomers or primers, for chromosome or gene mapping, for the recombinant
CC production of proteins, and for generating antisense DNA or RNA.

SQ Sequence 90 AA;

Query Match 90.6%; Score 29; DB 7; Length 90;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 65 SGSTLOA 71

RESULT 39

```

AA29449
ID  AA29449 standard; protein; 109 AA.
XX
AC  AA29449;
XX
DT  05-OCT-1999 (first entry)
XX
DE  Human light chain kappa-I consensus framework.
XX
KW  Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;
KW  diagnosis; inflammatory disorder; conjugate; immunoglobulin;
KW  fusion protein.
XX
OS  Homo sapiens.
XX
PN  WO937779-A1.
XX
PD  29-JUL-1999.
XX
PF  19-JAN-1999; 99WO-US001081.
XX
PR  22-JAN-1998; 98US-00012116.
XX  20-FEB-1998; 98WO-US003337.
XX  24-JUL-1998; 98US-00121952.
XX  24-JUL-1998; 98US-00122513.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Hsei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z, Zapata GA;
XX
DR  WPI; 1999-469134/39.
XX
PT  New conjugates of nonproteinaceous polymers with antibody fragments, used
PT  for treating inflammatory disorders.
XX
PS  Disclosure; Fig 29; 360pp; English.
XX
CC  The present invention describes a novel conjugate having one or more
CC  antibody fragments covalently attached to one or more nonproteinaceous
CC  polymer molecules, where the apparent size of the conjugate is at least
CC  about 500 kDa. Conjugates of antibody fragments which bind the human
CC  interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC  treating inflammatory disorders e.g. acute lung injury, ischaemic
CC  reperfusion disorder, and autoimmune diseases. They can also be used for
CC  treating e.g. inflammatory skin diseases including psoriasis and atopic
CC  dermatitis, systemic sclerosis and scleritis, and asthmatic diseases.
CC  The conjugates can also be used as reagents in an animal model system for
CC  in vivo study of the biological functions of the antigen recognised by
CC  the conjugate. The present sequence represents the human light chain
CC  kappa-I consensus framework from the present invention
CC
SQ  Sequence 109 AA;

Query Match          90.6%; Score 29; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 SGSTLOS 7
    |||||:|
DB  51 SGSTLS 57

RESULT 40
ID  AA77752 standard; protein; 109 AA.
XX
AC  AA77752;
XX
DT  06-JUN-2000 (first entry)
XX
DE  Human light chain k1 consensus framework.
XX
KW  Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4.2.SV1IN35A;
XX

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```

KW  inflammatory disorder; adult respiratory distress syndrome; chimeric;
KW  affinity purification; 6G4.2.5.
XX
OS  Homo sapiens.
XX
PN  US6025158-A.
XX
PD  15-FEB-2000.
XX
PF  20-FEB-1998; 98US-00027449.
XX
PR  21-FEB-1997; 97US-0038664P.
XX  22-JAN-1998; 98US-0074330P.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Presta LG, Leong SR, Gonzalez TN;
XX
DR  WPI; 2000-181809/16.
XX
PT  New nucleic acid molecule encodes a polypeptide which is an anti-
PT  interleukin-8 monoclonal antibody or antibody fragment useful for the
PT  production of anti-interleukin-8 monoclonal antibodies or fragments.
XX
PS  Example; Fig 29; 188pp; English.
XX
CC  The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
CC  (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs
CC  (complementarity determining regions) of the humanized anti-IL-8
CC  6G4.2.SV1IN35A light chain; and amino acids 24-253 of the humanized anti-
CC  IL-8 6G4.2.SV1IN35A heavy chain. The anti-IL-8 MAb and fragments can be
CC  used in diagnosis, for affinity purification of IL-8 from recombinant
CC  cell culture or natural sources and for the treatment of inflammatory
CC  disorders e.g. adult respiratory distress syndrome. Nucleic acids
CC  encoding the anti-IL-8 MAb can be associated in a vector with another
CC  gene encoding another protein or protein fragment to produce a fusion an
CC  protein which can make isolation and/or purification of the protein an
CC  easier process
CC
SQ  Sequence 109 AA;

Query Match          90.6%; Score 29; DB 3; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 SGSTLOS 7
    |||||:|
DB  51 SGSTLS 57

RESULT 41
ID  AAB30309 standard; protein; 109 AA.
XX
AC  AAB30309;
XX
DT  12-FEB-2001 (first entry)
XX
DE  Human light chain kappa1 consensus framework SEQ ID NO: 47.
XX
KW  Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
KW  adult respiratory distress syndrome; multiple organ failure;
KW  bacterial pneumonia; inflammatory bowel disease.
XX
OS  Homo sapiens.
XX
PN  US6133426-A.
XX
PD  17-OCT-2000.
XX
PF  20-FEB-1998; 98US-00026985.
XX  21-FEB-1997; 97US-0038664P.
XX

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PR 22-JAN-1998; 98US-0074330P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Presta LG, Leong SR, Gonzalez TN;
XX
XX WPI; 2000-686027/67.
XX
XX Humanized anti-interleukin 8 monoclonal antibody variant useful for
XX treating inflammatory disorders, such as adult respiratory distress
XX syndrome, hypovolemic shock and ulcerative colitis.
XX
XX Disclosure; Col 161-162; 240pp; English.
XX
XX The present invention provides a number of humanised monoclonal anti-IL-8
XX antibodies which can be used in the diagnosis and treatment of
XX inflammatory disorders, including adult respiratory distress syndrome,
XX septic shock, multiple organ failure, bacterial pneumonia and
XX inflammatory bowel disease. The present sequence comprises one of the
XX antibodies of the invention
XX
XX Sequence 109 AA;
SQ
Query Match 90.6%; Score 29; DB 3; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTLOS 7
DB 51 SGSTLES 57

RESULT 42
ID ABU13786
XX ABU13786 standard; protein; 109 AA.
XX
XX ABU13786;
AC
XX
XX 25-FEB-2003 (first entry)
DT
XX
XX Human light chain kappa consensus framework sequence.
DE
XX
XX Antibody; monoclonal antibody; 5.12.14; 6G4.2.5; interleukin-8; mAb;
XX anti-inflammatory; respiratory; acute lung injury; polyethylene glycol;
XX PEG; lung injury; adult respiratory distress syndrome; ARDS; asthma;
XX inflammatory disease; inflammatory bowel disease; psoriasis; sclerosis;
XX ischaemic reperfusion disorder; stroke; multiple sclerosis; meningitis;
XX osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis;
XX alcoholic hepatitis; cystic fibrosis; human.
XX
XX Homo sapiens.
OS
XX
XX US6468532-B1.
XX
XX 22-OCT-2002.
PD
XX
XX 20-JAN-1999; 99US-00234340.
PF
XX
XX 22-JAN-1998; 98US-0074330P.
XX
XX 20-FEB-1998; 98US-0075467P.
XX
XX 24-JUL-1998; 98US-0094003P.
XX
XX 24-JUL-1998; 98US-0094013P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
XX
XX WPI; 2003-138230/13.
XX
XX Treating acute lung injury in mammal by administering to mammal a 500 kD
XX conjugate comprising F(ab')2 antibody fragment that binds to human
XX interleukin-8, covalently attached to one or two polyethylene glycol
XX molecules.

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XX
XX Example G; Fig 29; 259pp; English.
PS
XX
XX The invention relates to treating acute lung injury in a mammal,
XX comprising administering to the mammal an effective amount of a conjugate
XX of a single antibody fragment covalently attached to 1 or 2 polyethylene
XX glycol (PEG) molecules, where the antibody fragment is a F(ab')2
XX comprising: (a) a first chain that is either a light chain or a heavy chain
XX ; (b) a first opposite chain that is either a heavy chain opposite the
XX first light chain or a light chain opposite the first heavy chain; (c) a
XX second chain that is either a light chain or a heavy chain; and (d) a
XX second opposite chain that is either a heavy chain opposite the second
XX light chain or a light chain opposite the second heavy chain; where every
XX PEG molecule is covalently attached to a first cysteine residue in the
XX first or second chain that would ordinarily form a disulphide bridge with
XX a second cysteine residue in the first or second opposite chain, where
XX the disulphide bridge is avoided by substitution of another amino acid
XX residue for the second cysteine residue in the first or second opposite
XX chain, where the F(ab')2 comprises an antigen binding site that binds to
XX human interleukin-8 (IL-8), and where the apparent size of the conjugate
XX is at least about 500 kD. The antigen binding sites may be derived from
XX murine monoclonal antibodies 5.12.14 or 6G4.2.5. The method is useful for
XX treating lung injury, including adult respiratory distress syndrome
XX (ARDS) in a mammal and inflammatory diseases (such as asthma,
XX inflammatory bowel disease, psoriasis and sclerosis), ischaemic
XX reperfusion disorders, stroke, multiple sclerosis, meningitis,
XX osteoarthritis, septic shock, autoimmune disease (e.g. rheumatoid
XX arthritis), alcoholic hepatitis, cystic fibrosis and many other diseases
XX and disorders listed in the specification. The present sequence
XX represents a human antibody sequence included for comparison with the
XX mouse humanised monoclonal antibody sequences
XX
XX Sequence 109 AA;
SQ
Query Match 90.6%; Score 29; DB 6; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTLOS 7
DB 51 SGSTLES 57

RESULT 43
ID ABUS9499
XX ABUS9499 standard; protein; 109 AA.
XX
XX ABUS9499;
AC
XX
XX 22-APR-2003 (first entry)
DT
XX
XX Human light chain kappa consensus framework.
DE
XX
XX Interleukin-8; IL-8; humanised antibody; antibody; 5.12.14; 6G4.2.5;
XX inflammatory disorder; psoriasis; atopic dermatitis; sclerosis;
XX systemic scleroderma; inflammatory bowel disease; Crohn's disease;
XX ulcerative colitis; ischaemia; reperfusion; myocardial infarction;
XX stroke; adult respiratory distress syndrome; rheumatoid arthritis;
XX alcoholic hepatitis; acute lung injury; asthma; cerebral oedema;
XX myocardial ischaemia; cranial trauma; asphyxia; Benec's disease;
XX dermatomyositis; polymyositis; multiple sclerosis; trauma;
XX encephalitis; uveitis; osteoarthritis; lupus nephritis; trauma;
XX autoimmune disease; Sjogren's syndrome; vasculitis; septicæmia;
XX central nervous system inflammatory disorder; sepsis; sarcoidosis;
XX multiple organ injury syndrome; bacterial pneumonia; glomerulonephritis;
XX inflammation of the lung; human.
XX
XX Homo sapiens.
OS
XX
XX US6458355-B1.
XX
XX 01-OCT-2002.
XX
XX

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PF 24-JUL-1998; 98US-00121952.
XX
XX 22-JAN-1998; 98US-0074330P.
PR 20-FEB-1998; 98US-0075467P.
XX
XX (GETH ) GENENTECH INC.
PI Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
DR WPI; 2003-208759/20.
XX
XX Treating inflammatory disorder in a mammal, involves administering a
PT conjugate of polyethylene glycol and a single antibody fragment
PT comprising antigen binding site that binds to human interleukin-8, to
PT mammal.
XX
XX Example 3G; Fig 29; 259pp; English.
XX
XX The invention relates to treating an inflammatory disorder in a mammal,
XX comprising administering to the mammal, an effective amount of a
XX conjugate of a single antibody fragment (e.g. the heavy or light chains
XX of the humanised mouse monoclonal antibodies 5.12.14 and 6G4.2.5, which
XX also have their intramolecular disulphide bridges ablated by substitution
XX mutations) covalently attached to one or two polyethylene glycol (PEG)
XX molecules. The antibodies comprise an antigen binding site that binds to
XX human interleukin-8 (IL-8), and the apparent size of the conjugate is at
XX least 500 kDa. The method is useful for treating an inflammatory disorder
XX e.g. ischaemic reperfusion disorder such as surgical tissue reperfusion
XX injury, myocardial ischaemia or myocardial infarction, or hypovolemic
XX shock, in a mammal e.g. human. The method is useful for treating
XX inflammatory disorders including psoriasis, atopic dermatitis, systemic
XX scleroderma and scleriosis, responses associated with inflammatory bowel
XX disease, ischaemic reperfusion disorders, myocardial ischemic
XX conditions, cerebral oedema secondary to stroke, cranial trauma,
XX asphyxia, adult respiratory distress syndrome, acute lung injury,
XX Behcet's disease, dermatomyositis, polymyositis, multiple sclerosis,
XX dermatitis, meningitis, encephalitis, uveitis, osteoarthritis, lupus
XX nephritis, autoimmune diseases such as rheumatoid arthritis, Sjogren's
XX syndrome, vasculitis, central nervous system inflammatory disorder,
XX multiple organ injury syndrome secondary to septicemia or trauma,
XX alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex,
XX mediated diseases including glomerulonephritis, sepsis, sarcoidosis,
XX immunopathologic responses to tissue/organ transplantation, inflammations
XX of the lung, inflammatory bowel disease such as ulcerative colitis and
XX asthma. The present sequence represents the light or heavy chain of human
XX IgG, used to design the humanising mutations in the two mouse antibodies
XX
SQ Sequence 109 AA;

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Query Match 90.6%; Score 29; DB 6; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 SGGSTLOS 7
   |||||:|
Db 51 SGGSTLES 57

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RESULT 44
AAE39082
ID AAE39082 standard; protein; 109 AA.
XX
XX AAE39082;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Human light chain kappa consensus framework protein.
DE
XX Interleukin-8 mediated disease; adult respiratory distress syndrome; IL;
XX bacterial pneumonia; inflammatory bowel disease; hypovolemic shock; ARDS;
XX ulcerative colitis; ischaemic reperfusion injury; myocardial infarction;
XX acute lung injury; inflammatory disease; asthma; antibody; human.
XX

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OS Homo sapiens.
XX
XX US2003021790-A1.
XX
XX 30-JAN-2003.
XX
XX 29-NOV-2000; 2000US-00726258.
XX
XX 22-JAN-1998; 98US-0074330P.
PR 20-FEB-1998; 98US-0075467P.
PR 24-JUL-1998; 98US-0094003P.
PR 24-JUL-1998; 98US-0094013P.
PR 20-JAN-1999; 99US-00234182.
XX
XX (GETH ) GENENTECH INC.
PA
XX Hsei V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
PI WPI; 2003-605694/57.
XX
XX Novel conjugates comprising antibody fragments covalently attached to
PT nonproteinaceous polymer molecules, useful for treating inflammatory
PT diseases, acute lung injury, ischemic reperfusion injury, pneumonia and
PT asthma.
XX
XX Example; Fig 29; 266pp; English.
XX
XX The invention relates to novel conjugates comprising antibody fragments
XX covalently attached to nonproteinaceous polymer molecules. The invention
XX is useful for treating interleukin (IL)-8 mediated diseases or disorders
XX such as inflammatory diseases, acute lung injury e.g. adult respiratory
XX distress syndrome (ARDS), ischaemic reperfusion injury e.g. myocardial
XX infarction, hypovolemic shock, inflammatory bowel disease e.g. ulcerative
XX colitis, bacterial pneumonia and asthma. The invention is also useful as
XX a reagent in an animal model system for in vivo study of the biological
XX functions of the antigen recognised by the conjugate. The present
XX sequence is human light chain kappa consensus framework protein. This
XX sequence is used in the exemplification of the invention
XX
SQ Sequence 109 AA;

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```

Query Match 90.6%; Score 29; DB 7; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 SGGSTLOS 7
   |||||:|
Db 51 SGGSTLES 57

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RESULT 45
ABU38629
ID ABU38629 standard; protein; 347 AA.
XX
XX ABU38629;
AC
XX
XX 19-JUN-2003 (first entry)
DT
XX
XX Protein encoded by Prokaryotic essential gene #24156.
DE
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Pseudomonas aeruginosa.
OS
XX
XX WO200277183-A2.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 21-MAR-2002; 2002WO-US009107.
PF
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.

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PR 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
PA
XX Venter JC, Adams M, Li PMD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
XX N-PSDB; ABL07435.
PT
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 16788; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB161676-AB130511), expressed DNA
CC sequences (AB161840-AB16175) and the encoded proteins (AB57737-
CC AB872072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 428 AA;
Query Match 90.6%; Score 29; DB 4; Length 428;
Best Local Similarity 85.7%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGTLOS 7
DB 420 SGGTLOS 426
RESULT 48
AAM58376
ID AAM58376 standard; protein; 665 AA.
XX
XX AAM58376;
AC
XX
XX 05-NOV-2001 (first entry)
DT
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 30481.
DE
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
OS Homo sapiens.
XX
XX WO200157275-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000667.
PR
XX
XX 04-FEB-2000; 2000US-0180312P.
PR
XX 26-MAY-2000; 2000US-0207456P.
PR
XX 30-JUN-2000; 2000US-00608408.
PR
XX 03-AUG-2000; 2000US-00632366.
PR
XX 21-SEP-2000; 2000US-0234687P.
PR
XX 27-SEP-2000; 2000US-0236359P.
PR
XX 04-OCT-2000; 2000GB-00024263.
XX
XX
XX (MOLEB-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483446/52.
DR
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT

PT brains.
XX
XX Example 4; SEQ ID NO 30481; 650bp + Sequence Listing; English.
PS
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 665 AA;
Query Match 90.6%; Score 29; DB 4; Length 665;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGTLOS 7
DB 533 NGSTLOS 539
RESULT 49
AAB41151
ID AAB41151 standard; protein; 1377 AA.
XX
XX AAB41151;
AC
XX
XX 08-FEB-2001 (first entry)
DT
XX
XX Human ORFX ORF915 polypeptide sequence SEQ ID NO:1830.
DE
XX
XX Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KM vulnerable; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
KM anticonvulsant; osteoplastic; antiarthritic; immunosuppressant; cardiant;
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
KM antiviral; antibacterial; antifungal; antineumatic; antihypoid;
KM antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KM neurodegenerative disorder; osteoarthritis; grapt vs host disease;
KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KM cholesterol ester storage; systemic lupus erythematosus; infection;
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KM allergy; aplastic anemia; nocturnal haemoglobinuria; burn; wound;
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
KM thrombosis; contraceptive.
XX
XX Homo sapiens.
XX
XX WO200058473-A2.
PN
XX
XX 05-OCT-2000.
PD
XX
XX 31-MAR-2000; 2000WO-US008621.
PR
XX
XX 31-MAR-1999; 99US-0127607P.
PR
XX 02-APR-1999; 99US-0127636P.
PR
XX 05-APR-1999; 99US-0127728P.
PR
XX 30-MAR-2000; 2000US-00540763.
XX
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
PI
XX WPI; 2000-602362/57.
DR
XX N-PSDB; AAC75360.
DR
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
XX Claim 11; Page 1419-1422; 5507pp; English.
PS

XX AAC74446 to AAC7606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antiparasitic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antidiabetic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antineumatic; antithyroid; and antianemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive

XX SQ Sequence 1377 AA;

Query Match 90.6%; Score 29; DB 3; Length 1377;
Best Local Similarity 85.7%; Pred. No. 2.7e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQS 7
:|||||
Db 486 NGSTLQS 492

RESULT 50

ABR41958
ID ABR41958 standard; protein; 1377 AA.

AC ABR41958;

DT 11-AUG-2003 (first entry)

DE Human HMGI/2, implicated in pain.

KW Human: HMGI/2; nociceptive; analgesic; signal transduction;
transgenic animal.

OS Homo sapiens.

PN EP1281775-A2.

PD 05-FEB-2003.

PF 26-JUL-2002; 2002BP-00255231.

PR 27-JUL-2001; 2001GB-00018354.

PR 07-FEB-2002; 2002GB-00002892.

PA (WARN) WARNER LAMBERT CO.

PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

DR WPI; 2003-335009/32.

XX Use of isolated gene or nucleic acid sequence, recombinant vector, host
PT cell, non-human animal, polypeptide encoded by the nucleic acid sequence,
PT or antibody, for screening of compounds for the treatment of pain, or for
PT diagnosing pain.

PS Disclosure; Page 63-73; 87pp; English.

XX The present sequence is the protein sequence of human HMGI/2. This
CC protein is encoded by a gene that has been identified as being up-
CC regulated in 2 models of chronic pain, i.e. streptozocin-induced diabetes

CC and chronic constrictive injury to a nerve leading to the spine. The
CC expression products of such genes can be used to screen libraries for
CC compounds and peptide agonists and antagonists of gene product activity
CC that may be useful in the treatment or prevention of chronic pain, and in
CC the development of diagnostic tools for the identification and
CC characterisation of pain

XX SQ Sequence 1377 AA;

Query Match 90.6%; Score 29; DB 6; Length 1377;
Best Local Similarity 85.7%; Pred. No. 2.7e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQS 7
:|||||
Db 486 NGSTLQS 492

Search completed: January 17, 2006, 11:59:18
Job time : 72.803 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:48:18 ; Search time 6.57576 Seconds
(without alignments)
102.424 Million cell updates/sec

Title: US-10-665-658-14

Perfect score: 32

Sequence: 1 SGSTLOS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

PIR 80: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	32	100.0	98	2 PH1083	Ig light chain V r
2	32	100.0	103	2 H30502	Ig kappa chain V r
3	32	100.0	106	2 S26345	Ig light chain V r
4	32	100.0	109	1 KVR121	Ig kappa chain V r
5	32	100.0	127	2 S04574	Ig kappa chain pre
6	29	90.6	147	2 AE3475	hypothetical sigma5 m
7	29	90.6	347	2 GB3171	hypothetical prote
8	29	90.6	609	2 S65208	probable membrane
9	29	90.6	613	2 T27528	hypothetical prote
10	29	90.6	672	2 S46086	RNA-binding protei
11	29	90.6	1254	2 T47141	hypothetical prote
12	28	87.5	171	2 B86719	hypothetical prote
13	28	87.5	419	2 S56073	opaque-2, protein -
14	28	87.5	435	2 T19733	hypothetical prote
15	28	87.5	524	2 AE2214	serine/threonine k
16	28	87.5	530	2 B75080	hypothetical prote
17	28	87.5	574	2 JB0339	Fizzled-7 protein
18	28	87.5	624	2 T41341	probable serine-th
19	28	87.5	873	2 P96615	probable Myb-famil
20	28	87.5	923	1 B35905	endopeptidase C1p
21	28	87.5	952	2 AC0447	probable insectici
22	28	87.5	1011	2 AD0447	ATP-dependent dadN
23	28	87.5	1046	2 AB6790	hypothetical prote
24	28	87.5	1398	2 T13741	Rab3 GDP/GTP excha
25	28	87.5	1602	2 T11671	bone morphogenetic
26	27	84.4	69	2 B61387	probable priplami
27	27	84.4	280	2 AC0411	nodulin-26-like pr
28	27	84.4	294	2 T05028	hypothetical prote
29	27	84.4	315	2 B82229	hypothetical prote

30	27	84.4	426	2 S58304	hypothetical prote
31	27	84.4	484	2 T34251	hypothetical prote
32	27	84.4	581	2 A05204	hypothetical prote
33	27	84.4	594	2 AH1786	autolysin, N-acety
34	27	84.4	653	2 T37772	telomere length re
35	27	84.4	862	2 S30911	SMP2 protein - yea
36	27	84.4	934	2 A22798	paraaporal crystal
37	27	84.4	1155	2 A26513	paraaporal crystal
38	27	84.4	1155	2 S02134	paraaporal crystal
39	27	84.4	1155	2 I39838	paraaporal crystal
40	27	84.4	1155	2 JD0002	paraaporal crystal
41	27	84.4	1156	2 A29125	paraaporal crystal
42	27	84.4	1156	2 A29638	paraaporal crystal
43	27	84.4	1176	2 A22617	paraaporal crystal
44	27	84.4	1176	2 JC2219	paraaporal crystal
45	27	84.4	1176	2 JT0341	paraaporal crystal
46	27	84.4	1176	2 S02215	paraaporal crystal
47	26	81.2	89	2 B84312	hypothetical prote
48	26	81.2	153	2 S51119	MalDI proteain - ap
49	26	81.2	172	2 F83696	hypothetical prote
50	26	81.2	192	2 E86679	prophage pil prote
51	26	81.2	195	2 D81030	transcription regu
52	26	81.2	223	2 H82895	conserved hypotet
53	26	81.2	226	2 D90026	hypothetical prote
54	26	81.2	299	2 C81255	ATP phosphoribosyl
55	26	81.2	310	2 S04358	lacc proteain - Sta
56	26	81.2	310	2 D90015	tagatose-6-phospha
57	26	81.2	318	2 G81976	probable arac-fami
58	26	81.2	320	2 AC1958	hypothetical prote
59	26	81.2	342	2 AE2490	WD-repeat protein
60	26	81.2	374	2 AB3183	conserved hypotet
61	26	81.2	384	2 T49084	hypothetical prote
62	26	81.2	409	2 T45797	hypothetical prote
63	26	81.2	411	2 T46681	probable glycosylt
64	26	81.2	436	2 B86469	protein P12K21.16
65	26	81.2	455	2 T27415	hypothetical prote
66	26	81.2	480	2 S66057	lysine decarboxyla
67	26	81.2	487	2 T45923	hypothetical prote
68	26	81.2	504	2 H87422	methy1-accepting c
69	26	81.2	521	2 T05684	hypothetical prote
70	26	81.2	549	2 F82415	conserved hypotet
71	26	81.2	552	2 S71811	probable transcrip
72	26	81.2	590	2 AB1411	autolysin, N-acety
73	26	81.2	592	2 C42594	L-amino acid hydraz
74	26	81.2	601	2 T49745	hypothetical prote
75	26	81.2	611	2 B85077	probable reverse t
76	26	81.2	612	2 A49403	tetratricopeptide-
77	26	81.2	713	2 D87617	sensory box histid
78	26	81.2	748	2 D84595	transducer protein
79	26	81.2	805	2 T48840	protein kinase (EC
80	26	81.2	819	2 A53714	hypothetical prote
81	26	81.2	855	2 G86189	hypothetical prote
82	26	81.2	891	2 B97759	hypothetical prote
83	26	81.2	975	2 T22788	hypothetical prote
84	26	81.2	1092	2 S42798	fibronectin-bindin
85	26	81.2	1117	2 S33851	genome polyprotein
86	26	81.2	2095	2 S29529	hypothetical prote
87	26	81.2	2216	2 S78398	hypothetical prote
88	26	81.2	2271	2 F90073	hypothetical prote
89	26	81.2	2535	2 AC0304	probable hemolysin
90	26	81.2	3079	1 RGBY12	probable Grpase-ac
91	26	81.2	3079	1 RGBY12	BIR repeat contain
92	26	81.2	4845	2 T31067	plasmid maintenanc
93	25	78.1	71	2 T08482	hypothetical prote
94	25	78.1	82	2 A43943	orf 5'of lenc - L
95	25	78.1	85	2 C82269	ribosomal protein,
96	25	78.1	109	2 S31950	penicillin-binding
97	25	78.1	129	2 C72678	hypothetical prote
98	25	78.1	144	2 H41700	C6 protein - rabbi
99	25	78.1	146	2 AB0001	probable flavoprot
100	25	78.1	157	2 A46735	photosystem I comp
101	25	78.1	158	2 S15484	hypothetical prote
102	25	78.1	173	2 T17385	vif protein - Dic

103	25	78.1	177	2	C95922	hypothetical prote
104	25	78.1	178	2	S31955	penicillin-binding
105	25	78.1	179	2	B84587	probable glutaredo
106	25	78.1	186	2	Q01987	hypothetical 21.0K
107	25	78.1	196	2	D85645	probable enzyme Z1
108	25	78.1	196	2	F64842	hypothetical prote
109	25	78.1	196	2	F90785	probable enzyme [1
110	25	78.1	203	2	AC0151	probable class II
111	25	78.1	204	2	AC0525	probable fibrinial
112	25	78.1	214	2	S47098	hypothetical prote
113	25	78.1	254	2	C70032	N-hydroxyarylamine
114	25	78.1	265	2	AF2007	hypothetical prote
115	25	78.1	265	2	AS9141	silaffin sllip pre
116	25	78.1	271	2	G90016	conserved hypotet
117	25	78.1	278	2	D86841	conserved hypotet
118	25	78.1	281	2	AC0661	probable lipoprote
119	25	78.1	286	2	T21545	hypothetical prote
120	25	78.1	291	2	T51668	myb-related transc
121	25	78.1	293	2	A71946	hypothetical prote
122	25	78.1	298	2	C64563	conserved hypotet
123	25	78.1	299	2	S61248	hypothetical prote
124	25	78.1	308	1	H65050	probable ATP-bind
125	25	78.1	308	1	C85919	hypothetical prote
126	25	78.1	308	2	D91074	probable ATP-bind
127	25	78.1	313	2	AG2099	phosphoribulokinas
128	25	78.1	322	1	W20919	E2 protein - human
129	25	78.1	322	2	T50919	hypothetical prote
130	25	78.1	336	2	AH0201	probable zinc-bind
131	25	78.1	343	2	G71979	probable type II D
132	25	78.1	349	2	T42965	glycoprotein - ate
133	25	78.1	350	1	RGBOT1	GMP-binding regula
134	25	78.1	350	1	RGHUT1	GMP-binding regula
135	25	78.1	350	1	RCMST1	GMP-binding regula
136	25	78.1	350	2	B84634	hypothetical prote
137	25	78.1	351	2	F81959	site-specific DNA-
138	25	78.1	355	2	D56271	long polar fibrinria
139	25	78.1	359	1	ADBY2	fructose-biophosph
140	25	78.1	373	2	S54545	hypothetical prote
141	25	78.1	378	2	C87425	aldose 1-epimerase
142	25	78.1	384	2	F72223	iron-sulfur cofact
143	25	78.1	400	2	C85899	hypothetical prote
144	25	78.1	400	2	H91054	hypothetical prote
145	25	78.1	400	2	E65031	hypothetical prote
146	25	78.1	407	2	S56660	aminomethyltransfe
147	25	78.1	414	2	A86229	hypothetical prote
148	25	78.1	425	2	E97172	flagellin [impor
149	25	78.1	431	2	G82235	sensor histidine K
150	25	78.1	437	2	F75344	penicillin-binding
151	25	78.1	438	2	AE3231	conjugal transfer
152	25	78.1	446	2	T19902	hypothetical prote
153	25	78.1	448	2	G88639	protein C34H4.2 [1
154	25	78.1	456	2	T38821	hypothetical serin
155	25	78.1	459	2	G84752	En/Spm-like transp
156	25	78.1	470	2	T33478	hypothetical prote
157	25	78.1	474	2	E69481	4-hydroxybutyrate
158	25	78.1	491	2	AB1117	hypothetical prote
159	25	78.1	495	2	E70992	probable amidase -
160	25	78.1	495	2	B89614	protein C43C3.3 [1
161	25	78.1	497	1	RNPSSN	transcription init
162	25	78.1	510	2	A10490	sugar transport AT
163	25	78.1	529	2	T42584	tegument protein 4
164	25	78.1	530	1	WZBED4	gene 40 protein -
165	25	78.1	534	2	S31300	regulatory protein
166	25	78.1	547	2	E70630	thiamin biosynthes
167	25	78.1	558	2	T10672	aspartate-activat
168	25	78.1	559	2	A46459	macrophage-activat
169	25	78.1	591	2	G96592	probable beta-fruc
170	25	78.1	591	2	S43506	hypothetical prote
171	25	78.1	592	2	A41258	guanine nucleotide
172	25	78.1	602	2	E97351	single-stranded-DN
173	25	78.1	602	2	AF2771	single-stranded-DN
174	25	78.1	615	2	S61390	dipla protein - leg
175	25	78.1	623	2	I49684	guanylate binding
176	25	78.1	652	2	T02001	hypothetical prote
177	25	78.1	666	2	S54399	penicillin-binding
178	25	78.1	675	2	S16629	penicillin-binding
179	25	78.1	675	2	S16624	penicillin-binding
180	25	78.1	675	2	S16627	penicillin-binding
181	25	78.1	675	2	S16628	penicillin-binding
182	25	78.1	694	2	F71786	wingless receptor
183	25	78.1	695	2	F64135	carboxy-terminal p
184	25	78.1	710	2	S62575	hypothetical prote
185	25	78.1	726	2	A87334	ABC transporter, H
186	25	78.1	735	2	S76425	hypothetical prote
187	25	78.1	740	1	T02567	probable ATP-bind
188	25	78.1	750	2	S06726	penicillin-binding
189	25	78.1	750	2	F95039	penicillin-binding
190	25	78.1	750	2	H97909	penicillin-binding p
191	25	78.1	806	2	H70647	probable NADH2 deh
192	25	78.1	836	2	B96716	probable serine/th
193	25	78.1	859	2	S49046	luxX protein - Vib
194	25	78.1	875	2	T17382	vrlC protein - Dic
195	25	78.1	910	2	T38539	probable importin
196	25	78.1	930	2	A25923	progesterone recep
197	25	78.1	933	1	ORHUP	hypothetical prote
198	25	78.1	997	2	T32814	hypothetical prote
199	25	78.1	1004	2	T38074	hypothetical prote
200	25	78.1	1024	2	T34517	zinc finger/leucin
201	25	78.1	1027	2	I38759	hypothetical prote
202	25	78.1	1072	2	A86827	hypothetical prote
203	25	78.1	1097	2	AD2572	hypothetical prote
204	25	78.1	1111	1	FKMUC	phytochrome C - Ar
205	25	78.1	1113	2	JB0315	low-density lipopr
206	25	78.1	1132	2	S37206	phytochrome - moss
207	25	78.1	1133	2	T13384	hypothetical prote
208	25	78.1	1153	2	T31080	nitric-oxide synth
209	25	78.1	1367	2	A41228	protein-tyrosine k
210	25	78.1	1274	2	T30258	adenomatous polypo
211	25	78.1	1405	2	S28600	hypothetical prote
212	25	78.1	55	2	AF2035	hypothetical prote
213	25	75.0	81	2	A43537	heat-stable antige
214	25	75.0	81	2	AH2564	hypothetical prote
215	25	75.0	105	4	S59325	hypothetical prote
216	25	75.0	108	2	B40085	ubiquitin carboxyl
217	25	75.0	113	2	T48774	ubiquitin carboxyl
218	25	75.0	114	2	S47998	kinesin light chal
219	25	75.0	114	2	A72489	hypothetical prote
220	25	75.0	135	2	H86794	hypothetical prote
221	25	75.0	141	2	S15785	heat-stable antige
222	25	75.0	154	2	D82795	phage-related endo
223	25	75.0	154	2	S48026	ribosomal protein
224	25	75.0	156	2	F84356	hypothetical prote
225	25	75.0	163	2	T27368	hypothetical prote
226	25	75.0	177	2	T22603	hypothetical prote
227	25	75.0	189	2	S46927	phytochrome - Nym
228	25	75.0	191	2	F96957	spore maturation p
229	25	75.0	192	2	E75541	MutR/nudix family
230	25	75.0	193	2	C75374	xanthine phosphori
231	25	75.0	207	2	T51296	phosphoribosylglyc
232	25	75.0	211	2	D64505	hypothetical prote
233	25	75.0	214	1	A8BYD	ABE8 protein - yea
234	25	75.0	222	2	H83528	phosphoribosylamin
235	25	75.0	222	2	F81124	conserved hypotet
236	25	75.0	223	2	A35917	NK-cell receptor p
237	25	75.0	224	2	S42982	hypothetical prote
238	25	75.0	227	2	A46467	natural killer cel
239	25	75.0	230	2	A40085	ubiquitin thiolest
240	25	75.0	230	2	JC7688	ubiquitin carboxyl
241	25	75.0	231	2	E90887	cryptic nitrate re
242	25	75.0	231	2	D85730	cryptic nitrate re
243	25	75.0	232	2	S50292	ribosomal protein
244	25	75.0	233	2	JC7689	ubiquitin carboxyl
245	25	75.0	233	2	T01233	hypothetical prote
246	25	75.0	243	2	F90197	hypothetical prote
247	25	75.0	263	2	T21619	hypothetical prote
248	25	75.0	269	2	F97327	nitroreductase fam

249	24	75.0	278	2	A56570	homeobox protein D	322	24	75.0	463	1	GRECNK	nitrite extrusion
250	24	75.0	285	2	I51412	hypothetical trans	323	24	75.0	463	1	H90844	nitrite extrusion
251	24	75.0	287	2	A10782	probable transcript	324	24	75.0	464	1	TVHUM2	transferring prote
252	24	75.0	288	2	E71428	hypothetical prote	325	24	75.0	465	2	AG0648	nitrite extrusion
253	24	75.0	290	2	AG0159	probable LysR-fam	326	24	75.0	480	2	H70854	hypothetical prote
254	24	75.0	293	2	D64984	hypothetical trans	327	24	75.0	482	2	H69392	4-hydroxybutyrate
255	24	75.0	293	2	C85854	probable transcript	328	24	75.0	485	2	S64945	probable membrane
256	24	75.0	293	2	A98010	probable transcript	329	24	75.0	485	2	PC4427	Nck, Ash and phosph
257	24	75.0	296	2	A44011	adrenocortical est	330	24	75.0	487	2	T49424	hypothetical prote
258	24	75.0	296	2	G70613	probable transcript	331	24	75.0	491	2	S58153	hypothetical prote
259	24	75.0	301	2	T04374	jakalin homolog -	332	24	75.0	500	2	AD1625	transporter homolo
260	24	75.0	304	2	T04375	jacalin homolog -	333	24	75.0	501	2	T01981	sucrose-phosphate
261	24	75.0	306	2	T04376	jacalin homolog -	334	24	75.0	501	2	AB1263	transporter homolo
262	24	75.0	309	2	AC1249	hypothetical prote	335	24	75.0	502	2	A46679	differentiated ker
263	24	75.0	312	2	H70107	methionyl-tRNA for	336	24	75.0	503	2	C86717	glycine hydroxymet
264	24	75.0	317	2	B87666	homoserine kinase	337	24	75.0	504	1	VCPV3A	kinesin light chai
265	24	75.0	318	2	AC2296	L-asparaginase [im	338	24	75.0	505	1	S77034	hypothetical prote
266	24	75.0	318	2	A43746	nisin resistance p	339	24	75.0	509	2	T06300	hypothetical prote
267	24	75.0	321	2	B69649	L-lactate dehydrog	340	24	75.0	513	2	C81736	60 kDa chaperonin,
268	24	75.0	327	2	S47965	polygalacturonase	341	24	75.0	515	2	H70663	hypothetical glyci
269	24	75.0	328	2	B83504	probable oxidoredu	342	24	75.0	517	2	T05620	hypothetical prote
270	24	75.0	328	2	F64187	p-aminobenzoate sy	343	24	75.0	522	2	T15619	transporter homolo
271	24	75.0	329	2	S76221	hypothetical prote	344	24	75.0	532	2	T15619	sucrose-phosphate
272	24	75.0	334	2	C70673	probable gp42 pro	345	24	75.0	542	2	A82965	transferring prote
273	24	75.0	341	2	H86476	protein F1504.35 l	346	24	75.0	542	2	A82356	differentiated ker
274	24	75.0	347	2	A95849	probable ABC trans	347	24	75.0	551	2	S58238	glycine hydroxymet
275	24	75.0	348	2	AE0590	probable membrane	348	24	75.0	552	1	A53621	hypothetical prote
276	24	75.0	351	2	A69808	H+/Ca2+ exchanger	349	24	75.0	552	1	S51025	hypothetical prote
277	24	75.0	354	2	S59521	mucln 5ac - mouse	350	24	75.0	554	2	B85015	hypothetical prote
278	24	75.0	363	2	E96546	probable electron	351	24	75.0	559	2	T01724	protein F10A5.7 [l
279	24	75.0	363	2	AH2616	heat-inducible tra	352	24	75.0	567	2	H96786	hemolysin secretio
280	24	75.0	363	2	H97398	heat-inducible tra	353	24	75.0	583	2	S75805	cellulose biosynth
281	24	75.0	365	2	F85671	flagellar basal bo	354	24	75.0	584	1	I39710	collagen two-compo
282	24	75.0	365	2	B90811	flagellar basal bo	355	24	75.0	585	2	T37034	hypothetical prote
283	24	75.0	365	2	E64851	flagellar basal bo	356	24	75.0	598	2	A84616	hypothetical prote
284	24	75.0	365	2	B30930	flagellar P-ring p	357	24	75.0	600	2	T06292	hypothetical prote
285	24	75.0	367	2	AF0640	flagellar P-ring p	358	24	75.0	609	2	S30910	Na+/H+-exchanging
286	24	75.0	369	1	A23559	dihydroorotate oxi	359	24	75.0	616	2	T08708	hypothetical prote
287	24	75.0	369	1	B87171	Pets component of	360	24	75.0	632	2	T37810	RNA-binding post-c
288	24	75.0	370	2	H70583	phosphate-binding	361	24	75.0	634	2	S32349	probable ethylene-
289	24	75.0	370	2	E96929	transaldolase - My	362	24	75.0	636	2	T03439	hypothetical prote
290	24	75.0	375	2	T11020	transaldolase - My	363	24	75.0	660	2	T28016	hypothetical prote
291	24	75.0	387	2	T15462	glucose-6-phosphat	364	24	75.0	663	2	D83545	probable helicase
292	24	75.0	387	2	T01210	conserved hypotet	365	24	75.0	678	2	H82379	methy1-accepting c
293	24	75.0	388	2	A83120	hypothetical prote	366	24	75.0	690	2	T41296	probable alcohol d
294	24	75.0	389	2	F86212	hypothetical prote	367	24	75.0	693	2	S49228	sodium-dependent p
295	24	75.0	395	2	E75155	hypothetical prote	368	24	75.0	698	2	S25409	transcription fact
296	24	75.0	401	2	C96614	polynucleotide ade	369	24	75.0	713	2	UC2534	RVlg protein - rat
297	24	75.0	402	2	E71912	polynucleotide ade	370	24	75.0	722	2	D89701	protein P28H6.4 [l
298	24	75.0	402	2	S31196	hypothetical prote	371	24	75.0	731	2	T16524	sideophore recept
299	24	75.0	403	2	A84592	(1-4)-beta-mannan	372	24	75.0	746	2	T46821	RhA Rhizobactin r
300	24	75.0	407	2	D87010	probable membrane	373	24	75.0	746	2	A95420	DNA-directed DNA p
301	24	75.0	407	2	E70595	hypothetical prote	374	24	75.0	750	1	JDU1VH	hypothetical prote
302	24	75.0	409	2	C82072	D-3-phosphoglycera	375	24	75.0	752	2	T16508	fibroblast activat
303	24	75.0	410	1	C64070	phosphoglycerate d	376	24	75.0	759	2	I38593	NADH dehydrogenase
304	24	75.0	410	2	T25575	hypothetical prote	377	24	75.0	774	2	A70010	general secretory
305	24	75.0	416	1	OKBYRC	protein kinase (EC	378	24	75.0	775	2	B82671	hypothetical prote
306	24	75.0	418	2	A39567	thioxine-binding	379	24	75.0	794	2	T46073	protein T27G7.8 [l
307	24	75.0	430	2	T46420	hypothetical prote	380	24	75.0	817	2	D86217	verpoxin - yeast
308	24	75.0	431	2	T09048	probable mannan en	381	24	75.0	817	2	S51342	hypothetical prote
309	24	75.0	440	2	C69545	conserved hypotet	382	24	75.0	831	2	S76235	DNA-directed DNA p
310	24	75.0	441	2	A97000	pectate lyase rela	383	24	75.0	832	1	JDU1VA	DNA-directed DNA p
311	24	75.0	449	2	I39358	heterogeneous nucl	384	24	75.0	832	1	JDU1VB	DNA-directed DNA p
312	24	75.0	450	2	T08701	hypothetical prote	385	24	75.0	832	1	JDU1VB	DNA-directed DNA p
313	24	75.0	450	2	S07886	site-specific DNA-	386	24	75.0	832	1	S20752	DNA-directed DNA p
314	24	75.0	452	2	T01337	hypothetical prote	387	24	75.0	832	1	S20757	DNA-directed DNA p
315	24	75.0	456	1	TVHUMC	transferring prote	388	24	75.0	832	1	S47406	DNA-directed DNA p
316	24	75.0	457	2	T44871	probable aldehyde	389	24	75.0	832	2	S17185	heat shock atp-dep
317	24	75.0	459	2	T45559	NADH dehydrogenas	390	24	75.0	842	2	G90576	neurofilament trip
318	24	75.0	462	2	AC0672	nitrite extrusion	391	24	75.0	858	2	S15762	hypothetical prote
319	24	75.0	462	2	S11431	nitrite extrusion	392	24	75.0	868	2	T22281	probable fibritial
320	24	75.0	462	2	A85730	nitrite extrusion	393	24	75.0	883	2	B85725	transferrin-blidin
321	24	75.0	462	2	H90887	nitrite extrusion	394	24	75.0	908	2	JN0819	transferrin-blidin

395	24	75.0	925	2	T18747	probable potassium
396	24	75.0	988	2	T03307	hypothetical 109.6
397	24	75.0	992	2	T08772	hypothetical prote
398	24	75.0	1000	2	T21522	hypothetical prote
399	24	75.0	1014	2	T04721	Ca2+-transporting
400	24	75.0	1022	2	T16599	hypothetical prote
401	24	75.0	1032	2	T34433	hypothetical prote
402	24	75.0	1033	2	A96714	hypothetical prote
403	24	75.0	1041	2	T33699	conserved hypothet
404	24	75.0	1052	2	AP2959	hypothetical prote
405	24	75.0	1066	2	G84746	suppressor protein
406	24	75.0	1082	2	S37837	sucrose-phosphate
407	24	75.0	1083	2	T04062	Similar to disease
408	24	75.0	1112	2	D96753	phycocrome B - ri
409	24	75.0	1171	2	S14065	metabolicropic gluta
410	24	75.0	1180	2	JC2132	outer membrane pro
411	24	75.0	1230	2	B64664	probable exported
412	24	75.0	1238	2	AH0038	multidrug resistan
413	24	75.0	1279	1	DVH03	hypothetical prote
414	24	75.0	1298	2	A64157	probable Athila re
415	24	75.0	1303	2	B84493	TCOP1 protein - mo
416	24	75.0	1320	2	JC5630	embryonic receptor
417	24	75.0	1330	2	S49010	receptor tyrosine
418	24	75.0	1333	2	I78875	hypothetical prote
419	24	75.0	1341	2	H98323	protein-tyrosine k
420	24	75.0	1378	2	I48751	glutamate synthase
421	24	75.0	1399	2	A89813	conserved hypothet
422	24	75.0	1516	2	P83085	peptidoglycan boun
423	24	75.0	1582	2	AD1512	adhesin homolog 1m
424	24	75.0	1582	2	AC1153	long chain fatty a
425	24	75.0	1607	2	T02837	verican precursor
426	24	75.0	1633	2	T14274	Clathrin heavy cha
427	24	75.0	1681	2	S42369	DNA-directed RNA p
428	24	75.0	1765	2	A31494	DNA-directed RNA p
429	24	75.0	1765	2	B31494	DNA-directed RNA p
430	24	75.0	1766	2	B31875	DNA-directed RNA p
431	24	75.0	1766	2	A31875	genome polyprotein
432	24	75.0	2151	1	S16449	Munc13-3 protein -
433	24	75.0	2207	2	T42759	hypothetical prote
434	24	75.0	2232	2	T34434	verican precursor
435	24	75.0	2409	1	A60979	kinesin-related pr
436	24	75.0	2354	2	T14156	hypothetical prote
437	24	75.0	3262	2	AH2137	verican precursor
438	24	75.0	3381	2	T42389	probable spectrin
439	24	75.0	4063	2	T42993	hypothetical prote
440	24	75.0	4101	2	T23530	syrimyomycin synth
441	24	75.0	9376	2	T14593	hypothetical prote
442	23	71.9	60	2	T00005	pept protein - Acti
443	23	71.9	62	2	T21205	Ig kappa chain V r
444	23	71.9	71	2	S21526	hypothetical prote
445	23	71.9	72	2	T25597	metallohionein -
446	23	71.9	74	1	SMER1	ATP synthase regul
447	23	71.9	84	1	S12201	Ig kappa chain V r
448	23	71.9	86	2	S16827	Ig kappa chain V r
449	23	71.9	87	2	S21523	Ig kappa chain V r
450	23	71.9	88	2	S21525	Ig kappa chain V r
451	23	71.9	88	2	S21520	Ig kappa chain V r
452	23	71.9	88	2	S34104	Ig kappa chain V r
453	23	71.9	88	2	S21524	Ig kappa chain V r
454	23	71.9	93	1	A27086	small acid-soluble
455	23	71.9	93	1	I47624	Ig heavy chain V-V
456	23	71.9	95	2	S68998	Ig kappa chain V r
457	23	71.9	95	2	PH0863	Ig kappa chain V r
458	23	71.9	96	2	T04060	probable molybdopt
459	23	71.9	97	2	H96743	probable DnaU prot
460	23	71.9	100	2	AF1490	hypothetical prote
461	23	71.9	101	2	S44117	Ig kappa chain V-J
462	23	71.9	107	2	S36275	Ig lambda chain V
463	23	71.9	107	2	S40366	Ig kappa chain V-J
464	23	71.9	108	2	S19574	Ig kappa chain V r
465	23	71.9	108	2	S36279	Ig lambda chain V
466	23	71.9	109	2	JN0296	Ig kappa chain V-J
467	23	71.9	109	2	A86505	I31 ribosomal prot
468	23	71.9	109	2	H72118	ribosomal protein
469	23	71.9	114	2	S22559	Ig heavy chain V r
470	23	71.9	117	2	S41812	Ig kappa chain V r
471	23	71.9	119	2	P95327	hypothetical prote
472	23	71.9	122	1	A1HUTR	Ig heavy chain V-I
473	23	71.9	123	2	F71178	hypothetical prote
474	23	71.9	124	2	S40318	Ig kappa chain V r
475	23	71.9	124	2	S40336	Ig kappa chain V-J
476	23	71.9	128	1	NROW2	pancreatic ribonuc
477	23	71.9	128	2	S46372	Ig light chain var
478	23	71.9	131	2	S43552	Ig kappa chain V-J
479	23	71.9	132	2	S38646	Ig kappa chain V r
480	23	71.9	139	2	F84701	hypothetical prote
481	23	71.9	146	1	C64085	hypothetical prote
482	23	71.9	147	1	QOEC16	mioc protein - Esc
483	23	71.9	147	2	AD0953	mioc protein limpo
484	23	71.9	147	2	B86060	initiation of chro
485	23	71.9	147	2	D91214	Mioc protein limpo
486	23	71.9	149	2	B72555	hypothetical prote
487	23	71.9	157	2	B87037	major allergen Mal
488	23	71.9	159	2	JC4276	hypothetical prote
489	23	71.9	159	2	AB1220	hypothetical prote
490	23	71.9	159	2	AB1573	allophycocyanin be
491	23	71.9	161	1	AFKKB	rod shape-determin
492	23	71.9	162	2	D85989	rod shape-determin
493	23	71.9	162	2	JV0060	rod shape-determin
494	23	71.9	162	2	A91144	rod shape-determin
495	23	71.9	163	2	A10911	Ig light chain - r
496	23	71.9	167	2	S28579	alpha-crystallin c
497	23	71.9	173	1	CYNQA	hypothetical prote
498	23	71.9	174	2	T13538	R-phycocerythrin be
499	23	71.9	177	2	S30932	hypothetical prote
500	23	71.9	180	2	AG0049	probable adenine p
501	23	71.9	180	2	D75464	hypothetical prote
502	23	71.9	181	2	AH3614	probable moab2 pro
503	23	71.9	181	2	D70821	probable molydenu
504	23	71.9	181	2	T45449	T-cell receptor al
505	23	71.9	185	2	S37479	embryonal lethal (
506	23	71.9	187	2	S42032	dTMP kinase (BC 2.
507	23	71.9	188	2	F64336	lcmo protein - Leg
508	23	71.9	192	2	D97327	transcription regu
509	23	71.9	192	2	F85519	hypothetical prote
510	23	71.9	195	2	C90669	hypothetical prote
511	23	71.9	195	2	E64755	YagG protein - Esc
512	23	71.9	204	2	AB0299	probable luxR-fam1
513	23	71.9	209	2	S65767	hypothetical prote
514	23	71.9	209	2	S65768	hypothetical prote
515	23	71.9	212	2	T06015	hypothetical prote
516	23	71.9	213	2	C70555	bcl-x transmembran
517	23	71.9	214	2	I49057	hypothetical prote
518	23	71.9	221	2	H97021	hypothetical prote
519	23	71.9	222	2	D72361	probable oxidoredu
520	23	71.9	222	2	T37108	proteasome endopep
521	23	71.9	223	2	T47893	hypothetical prote
522	23	71.9	227	2	A12401	hypothetical prote
523	23	71.9	227	2	T06204	hemagglutinin asbo
524	23	71.9	229	2	S18997	respiratory nitrat
525	23	71.9	230	2	AH0671	toxic shock syndro
526	23	71.9	231	2	KCSAS1	toxic shock syndro
527	23	71.9	234	1	B89992	hypothetical prote
528	23	71.9	234	2	D71199	hypothetical prote
529	23	71.9	237	2	T25643	enoyl CoA hydratase
530	23	71.9	249	2	H90212	hydroxyacylglutath
531	23	71.9	252	2	H81017	hypothetical prote
532	23	71.9	252	2	T27535	hypothetical prote
533	23	71.9	252	2	T25177	probable membrane
534	23	71.9	253	2	S48547	actin-binding prot
535	23	71.9	256	2	S07105	sodium-translocati
536	23	71.9	256	2	S65528	oxioreductase hom
537	23	71.9	257	2	B82094	hypothetical prote
538	23	71.9	257	2	AB1533	
539	23	71.9	259	2	T24147	
540	23	71.9				

541	23	71.9	260	1	B26325	deoxyribonuclease	614	23	71.9	360	2	T36763	probable secreted
542	23	71.9	260	2	C71478	probable nifu-rela	615	23	71.9	360	2	S75350	hypothetical prote
543	23	71.9	260	2	B81741	Nifu-related prote	616	23	71.9	363	2	A37009	CD44 homolog membr
544	23	71.9	264	1	A32044	acid phosphatase (617	23	71.9	363	2	D49889	HrpI 3'-region hyp
545	23	71.9	265	2	H84867	probable endochiti	618	23	71.9	365	2	A34424	CD44 membrane glyc
546	23	71.9	266	2	AE0393	Na+-translocating	619	23	71.9	369	2	AE2326	periplasmic amino
547	23	71.9	266	2	C86598	Nifu-related prote	620	23	71.9	370	2	D70584	phosphate uptake s
548	23	71.9	266	2	F81512	nifu protein, prob	621	23	71.9	373	2	A84699	hypothetical prote
549	23	71.9	266	2	E72025	nifu-related prote	622	23	71.9	375	2	D70388	acetoin utilization
550	23	71.9	267	2	E70837	hypothetical prote	623	23	71.9	375	2	E71479	riboflavin bifunct
551	23	71.9	270	2	T52403	hypothetical prote	624	23	71.9	377	2	AG1416	conserved hypotet
552	23	71.9	274	2	D82784	phosphomethyllyrim	625	23	71.9	384	2	G85948	fructose-bisphosph
553	23	71.9	274	2	F72689	hypothetical prote	626	23	71.9	385	2	T18180	protein-rich prote
554	23	71.9	275	1	D43664	cryptophan synthas	627	23	71.9	385	2	G84051	hypothetical prote
555	23	71.9	277	2	C70017	4-hydroxybenzoyl-C	628	23	71.9	389	2	A84680	hypothetical prote
556	23	71.9	278	2	B69663	formamidopyrimidin	629	23	71.9	392	2	A56123	streptogristin D (B
557	23	71.9	280	2	AD0410	conserved hypotet	630	23	71.9	394	2	G86190	hypothetical prote
558	23	71.9	282	1	NDB0A	deoxyribonuclease	631	23	71.9	394	2	F86190	hypothetical prote
559	23	71.9	283	1	JC5579	chymotrypsin-like	632	23	71.9	397	2	JW0075	cysteine-dependent
560	23	71.9	285	2	C64750	probable transcrip	633	23	71.9	397	2	T06183	serpin - barley
561	23	71.9	287	2	P96738	hypothetical prote	634	23	71.9	398	2	T41600	probable pre-mRNA
562	23	71.9	288	2	T02327	nodulin-26 homolog	635	23	71.9	401	2	D64500	glucose-6-phosphat
563	23	71.9	289	2	A81738	AMP nucleosidase-r	636	23	71.9	401	2	T17515	hypothetical prote
564	23	71.9	294	2	AE2457	hypothetical prote	637	23	71.9	402	2	B82491	Nupc family protei
565	23	71.9	296	2	D97052	homoserine kinase	638	23	71.9	403	2	JN0611	probable transcrip
566	23	71.9	300	2	AE3328	hfc protein (BC 3	639	23	71.9	404	2	T44488	protein C09G12.9 (
567	23	71.9	303	1	D64070	ATP phosphoribosyl	640	23	71.9	405	2	H88650	multidrug transloc
568	23	71.9	303	2	B83122	conserved hypotet	641	23	71.9	409	2	AD0492	probable integrase
569	23	71.9	303	2	T00479	probable phosphat	642	23	71.9	409	2	B95372	probable integrase
570	23	71.9	304	2	A97768	hypothetical protease	643	23	71.9	409	2	F95409	probable integrase
571	23	71.9	304	2	B99374	hypothetical prote	644	23	71.9	411	2	B70215	hypothetical prote
572	23	71.9	305	2	AD0260	hypothetical phage	645	23	71.9	411	2	E71873	hypothetical prote
573	23	71.9	306	1	B48947	orf106 - Lactobaci	646	23	71.9	412	2	S57387	hypothetical prote
574	23	71.9	308	2	E71597	probable proteinas	647	23	71.9	414	2	G70360	hypothetical prote
575	23	71.9	309	2	AB0757	probable exported	648	23	71.9	418	2	T34660	probable sorbitol
576	23	71.9	310	1	HNWZRA	hemagglutinin prec	649	23	71.9	420	2	C84201	multidrug resistan
577	23	71.9	312	2	A31846	130K paracrystall	650	23	71.9	420	2	A71327	probable protein-e
578	23	71.9	316	2	T21044	hypothetical prote	651	23	71.9	420	2	E86162	hypothetical prote
579	23	71.9	318	2	T37548	probable lacyl-car	652	23	71.9	423	2	C81266	probable efflux pr
580	23	71.9	318	2	AG0829	sigma-E factor reg	653	23	71.9	425	2	AH1041	Vi polysaccharide
581	23	71.9	318	2	T06010	hypothetical prote	654	23	71.9	425	2	B36892	A-kinase anchor pr
582	23	71.9	323	2	T42683	hypothetical prote	655	23	71.9	427	2	A43453	PTS system, TTC co
583	23	71.9	324	2	A98316	chuF protein (AF17	656	23	71.9	431	2	F95236	hypothetical prote
584	23	71.9	324	2	AB2967	hypothetical prote	657	23	71.9	431	2	H98100	periplasmic sugar-
585	23	71.9	324	2	T37834	hypothetical prote	658	23	71.9	432	2	AH1934	hypothetical prote
586	23	71.9	326	2	S76360	hypothetical prote	659	23	71.9	437	2	T33331	high affinity gluc
587	23	71.9	329	2	T22497	hypothetical prote	660	23	71.9	438	2	E97342	hypothetical prote
588	23	71.9	330	2	S74205	asparaginase (EC 3	661	23	71.9	442	2	T16773	hypothetical prote
589	23	71.9	330	2	AD0305	probable sugar tra	662	23	71.9	443	2	T48708	mrsa protein (impo
590	23	71.9	330	2	F82338	unknown protein [i	663	23	71.9	444	2	D84974	lysel1 endopeptid
591	23	71.9	331	2	UC6194	Atii methylase (E	664	23	71.9	445	2	C69233	probable disease r
592	23	71.9	331	2	E82389	probable outer mem	665	23	71.9	447	2	G84687	hypothetical prote
593	23	71.9	332	2	T44437	aminodeoxychrotri	666	23	71.9	449	2	G84091	hypothetical prote
594	23	71.9	335	2	B72668	hypothetical prote	667	23	71.9	452	2	G90654	hypothetical prote
595	23	71.9	336	1	MMVZPI	F1 protein - fowlp	668	23	71.9	452	2	G85505	regulatory protei
596	23	71.9	342	2	A96511	unknown protein [i	669	23	71.9	452	2	E64745	cytochrome P450 [i
597	23	71.9	343	2	G90680	probable periplasm	670	23	71.9	455	2	A12409	hypothetical prote
598	23	71.9	343	2	C85531	periplasmic ferric	671	23	71.9	457	2	D83867	probable glutamine
599	23	71.9	344	2	B70136	flagellar motor sw	672	23	71.9	458	2	A83391	probable glutamine
600	23	71.9	344	2	G82428	iron(III) ABC tran	673	23	71.9	458	2	B83609	menquinone-specif
601	23	71.9	345	2	T14211	NADH2 dehydrogenas	674	23	71.9	462	2	AG1655	gastric inhibitory
602	23	71.9	345	2	T37576	probable mitochond	675	23	71.9	462	2	JC2462	pre-B cell enhanci
603	23	71.9	345	2	S21094	alpha-2-HS-glycopr	676	23	71.9	462	2	S77002	cellulase (EC 3.2.
604	23	71.9	345	2	T06098	hypothetical prote	677	23	71.9	463	2	A48375	probable membrane
605	23	71.9	349	2	C95866	probable fructose-	678	23	71.9	464	2	T36256	hypothetical prote
606	23	71.9	349	2	T49791	hypothetical prote	679	23	71.9	467	2	T47773	hypothetical prote
607	23	71.9	350	2	A10837	conserved hypotet	680	23	71.9	468	2	A83359	protein-tyrosine-P
608	23	71.9	352	2	T33433	hypothetical prote	681	23	71.9	474	1	A33386	3-isopropylmalate
609	23	71.9	356	2	B70724	hypothetical prote	682	23	71.9	474	2	H82564	probable integral
610	23	71.9	356	2	F89934	hypothetical prote	683	23	71.9	475	2	G95379	hypothetical prote
611	23	71.9	359	1	ADEC2A	fructose-bisphosph	684	23	71.9	481	2	T00863	6-phosphogluconate
612	23	71.9	359	1	AC0875	fructose 1,6-bisph	685	23	71.9	483	2	D87167	salicylaldehyde de
613	23	71.9	359	2	D91103	fructose-bisphosph	686	23	71.9	483	2	E49343	

667	23	71.9	486	2	T44750	probable phosphogl	760	23	71.9	615	2	T20839	hypothetical prote
668	23	71.9	491	2	C96585	hypothetical prote	761	23	71.9	617	2	B85044	hypothetical prote
669	23	71.9	491	2	T19635	hypothetical prote	762	23	71.9	618	2	T48193	hypothetical prote
690	23	71.9	493	2	AD2070	hypothetical prote	763	23	71.9	620	2	T15273	hypothetical prote
691	23	71.9	495	2	A57053	germ cell nuclear	764	23	71.9	622	2	T52439	prtm homolog (lipo
692	23	71.9	497	2	AG3134	N-methylammine ch	765	23	71.9	627	2	G96537	hypothetical prote
693	23	71.9	498	2	B98153	N-methylammine ch	766	23	71.9	630	2	C98851	oligopeptide-bindi
694	23	71.9	498	2	D70978	hypothetical prote	767	23	71.9	639	2	T23424	hypothetical prote
695	23	71.9	503	2	B38745	cell adhesion mole	768	23	71.9	640	1	Z1BPT5	tail protein pbs -
696	23	71.9	504	2	T22269	hypothetical prote	769	23	71.9	640	1	F81191	hypothetical prote
697	23	71.9	505	2	S68518	tub protein, brain	770	23	71.9	641	2	A45054	probable intercell
698	23	71.9	506	2	AC3255	1-isobornone dehydr	771	23	71.9	642	2	S52730	probable membrane
699	23	71.9	506	2	AF2192	bifunctional purin	772	23	71.9	643	2	D70697	hypothetical prote
700	23	71.9	508	2	AC1119	fatty-acid-CoA lig	773	23	71.9	644	2	C70585	hypothetical prote
701	23	71.9	508	2	AF1479	fatty-acid-CoA lig	774	23	71.9	646	2	C96729	hypothetical prote
702	23	71.9	509	2	T48168	hypothetical prote	775	23	71.9	647	2	JE0337	frizzled-1 prote
703	23	71.9	512	2	D32302	probable aspartate	776	23	71.9	652	2	T38704	glycyl tRNA synthet
704	23	71.9	512	2	B71474	probable hept6 cha	777	23	71.9	659	2	E84852	hypothetical prote
705	23	71.9	513	2	S11439	cellulose 1,4-beta	778	23	71.9	670	2	T65967	disintegrin-like m
706	23	71.9	513	2	B36094	diphosphate-fructo	779	23	71.9	673	2	C70204	exonuclease ABC c
707	23	71.9	519	2	C86372	hypothetical prote	780	23	71.9	673	2	AH2964	hypothetical prote
708	23	71.9	522	2	B86453	CDS protein F911.	781	23	71.9	673	2	F87636	TPR domain protein
709	23	71.9	524	2	S38539	disintegrin-like m	782	23	71.9	673	2	H69828	ABC transporter (A
710	23	71.9	525	2	B96786	protein F10A5.13 (783	23	71.9	674	2	D82118	conserved hypothet
711	23	71.9	525	2	T48824	hypothetical prote	784	23	71.9	674	2	B83794	ABC transporter (A
712	23	71.9	527	2	C64139	translation releas	785	23	71.9	680	2	E98318	hypothetical prote
713	23	71.9	528	2	B88989	protein F02C9.2 [l	786	23	71.9	680	2	E96551	hypothetical prote
714	23	71.9	530	2	T32812	glucose-6-phosphat	787	23	71.9	694	2	I40866	exo-alpha-sialidas
715	23	71.9	532	2	A70191	glucose-6-phosphat	788	23	71.9	707	2	T00665	hypothetical prote
716	23	71.9	533	2	A71812	probable phosphate	789	23	71.9	713	2	D85503	lysine decarboxyla
717	23	71.9	535	2	A71319	probable glucose-6	790	23	71.9	713	2	D90652	lysine decarboxyla
718	23	71.9	536	2	H71563	hypothetical prote	791	23	71.9	713	2	B64743	lysine decarboxyla
719	23	71.9	537	2	D70960	probable fad4 pro	792	23	71.9	718	2	G71688	flagellar hook pro
720	23	71.9	538	2	A41533	reticuline oxidase	793	23	71.9	718	2	F64628	deoxyxylulose synt
721	23	7											

833	23	71.9	864	1	VCLG4	env polypeptide -
834	23	71.9	865	2	H7147	trehalose-6-phosph
835	23	71.9	868	2	AF3204	autotransporter pr
836	23	71.9	872	2	T25186	hypothetical prote
837	23	71.9	907	2	E96692	probable wall-asso
838	23	71.9	923	2	S50482	hypothetical prote
839	23	71.9	926	1	A35905	endopeptidase Clp
840	23	71.9	941	2	T51135	ligand-gated chan
841	23	71.9	955	2	A45441	chromopondrin 4 -
842	23	71.9	955	2	G64866	probable membrane
843	23	71.9	957	2	T15976	hypothetical prote
844	23	71.9	962	2	D86186	hypothetical prote
845	23	71.9	972	2	T49773	related to actin-1
846	23	71.9	973	2	T21069	hypothetical prote
847	23	71.9	976	2	T51137	ionotropic glutama
848	23	71.9	981	2	B88794	protein K07F5_12a
849	23	71.9	982	2	T13653	hypothetical prote
850	23	71.9	1000	2	D87244	conserved hypotet
851	23	71.9	1003	1	PVZAM	spheroidin precurs
852	23	71.9	1008	2	T12532	hypothetical prote
853	23	71.9	1016	2	H71460	probable outer mem
854	23	71.9	1025	2	S50293	probable membrane
855	23	71.9	1026	2	A48895	paracrystalline su
856	23	71.9	1033	2	T37715	actin-interacting
857	23	71.9	1035	2	C87373	TonB-dependent rec
858	23	71.9	1036	2	D84741	probable cellulose
859	23	71.9	1037	2	AF0101	probable exported
860	23	71.9	1042	2	S41705	EVII protein - hum
861	23	71.9	1042	2	A31591	transcription regul
862	23	71.9	1051	2	A60191	oncogene Evi-1 - h
863	23	71.9	1054	2	S54473	TPS3 protein - yea
864	23	71.9	1058	2	T19282	hypothetical prote
865	23	71.9	1069	2	C87374	hypothetical prote
866	23	71.9	1073	2	C87373	S-layer protein R8
867	23	71.9	1099	2	T16283	hypothetical prote
868	23	71.9	1115	2	A47058	Fe-regulated RTX c
869	23	71.9	1123	2	T51517	telomerase reverse
870	23	71.9	1132	2	S37932	hypothetical prote
871	23	71.9	1146	2	H96796	hypothetical prote
872	23	71.9	1148	2	F86403	probable transposo
873	23	71.9	1166	2	T13958	synap-B1 protein
874	23	71.9	1171	2	A42916	metabotropic gluta
875	23	71.9	1181	2	A41052	paraaporal crystal
876	23	71.9	1186	2	S61647	probable membrane
877	23	71.9	1187	2	C84568	hypothetical prote
878	23	71.9	1214	2	T00356	hypothetical prote
879	23	71.9	1214	2	AG2897	conserved hypotet
880	23	71.9	1217	2	C86159	hypothetical prote
881	23	71.9	1219	2	T14578	nucleoporin Nup153
882	23	71.9	1239	2	G02750	DNA-directed DNA p
883	23	71.9	1249	2	P86405	probable P-glycopr
884	23	71.9	1249	2	H71404	hypothetical prote
885	23	71.9	1249	2	F86909	probable DNA gyras
886	23	71.9	1249	2	T14270	Ras-GTPase activat
887	23	71.9	1252	2	T31119	mem protein - Vib
888	23	71.9	1252	2	C82328	hypothetical prote
889	23	71.9	1260	2	S60896	agglutinin-like pr
890	23	71.9	1273	2	T10006	DNA topoisomerase
891	23	71.9	1275	2	T33369	hypothetical prote
892	23	71.9	1287	2	T42658	hypothetical prote
893	23	71.9	1293	2	T14259	ras GTPase-activat
894	23	71.9	1321	2	T29308	hypothetical prote
895	23	71.9	1323	2	T30253	hypothetical prote
896	23	71.9	1332	2	T29309	spalt protein - mo
897	23	71.9	1387	2	A97673	hypothetical prote
898	23	71.9	1438	2	B71610	probable periplasm
899	23	71.9	1449	2	A12017	WD40 WEB-1 homolo
900	23	71.9	1480	2	S48440	poly(A)-specific r
901	23	71.9	1493	2	A38218	GAP-associated pro
902	23	71.9	1501	2	T45623	hypothetical prote
903	23	71.9	1695	2	T19823	hypothetical prote
904	23	71.9	1696	2	T00057	hypothetical prote
905	23	71.9	1743	2	T15893	hypothetical prote
906	23	71.9	1821	2	AG2335	hypothetical prote
907	23	71.9	1829	2	S35027	cytotoxin RTX homo
908	23	71.9	1829	2	E81086	iron-regulated pro
909	23	71.9	1846	2	T10670	hypothetical prote
910	23	71.9	2021	2	A97859	190-kDa cell surf
911	23	71.9	2067	2	A42854	probable spindle p
912	23	71.9	2116	2	A26655	myosin heavy chain
913	23	71.9	2249	2	A41477	190k surface anti
914	23	71.9	2276	2	T00076	hypothetical prote
915	23	71.9	2321	2	S78549	notch3 protein - h
916	23	71.9	2415	1	A39086	aggrexin precursor
917	23	71.9	2496	2	A71616	secreted protein P
918	23	71.9	2700	2	D88450	protein F21H11.2 l
919	23	71.9	2824	2	T22759	hypothetical prote
920	23	71.9	3175	1	RRWV	genome polypeptide
921	23	71.9	3216	2	C90538	hypothetical prote
922	23	71.9	3429	2	T13853	hypothetical prote
923	23	71.9	3436	2	S55659	tegument protein 6
924	23	71.9	3512	2	T17121	CpV protein - midg
925	23	71.9	4196	2	T43274	dynein heavy chain
926	23	68.8	24	2	I73583	alpha 1-proteinase
927	22	68.8	45	2	T26203	hypothetical prote
928	22	68.8	46	1	LOPDA	ligand toxin A - Arge
929	22	68.8	53	2	D82632	hypothetical prote
930	22	68.8	57	2	B49570	plasma membrane ca
931	22	68.8	60	1	PMBOE	H+-transporting tw
932	22	68.8	71	2	B83791	conserved hypotet
933	22	68.8	72	2	T18044	hypothetical prote
934	22	68.8	72	2	F88992	hypothetical prote
935	22	68.8	73	2	B70068	hypothetical prote
936	22	68.8	80	2	B95151	ribosomal protein
937	22	68.8	80	2	H98018	50S ribosomal prot
938	22	68.8	82	2	S34090	Ig kappa chain V r
939	22	68.8	85	2	S78707	Ig kappa chain V r
940	22	68.8	86	2	S16839	Ig kappa chain V r
941	22	68.8	86	2	S16832	Ig kappa chain V r
942	22	68.8	86	2	S16828	Ig kappa chain V r
943	22	68.8	86	2	S16835	Ig kappa chain V r
944	22	68.8	86	2	S27893	Ig kappa chain V r
945	22	68.8	95	2	PH0865	Ig kappa chain V r
946	22	68.8	95	2	D95201	Ig kappa chain V r
947	22	68.8	95	2	B98068	Ig kappa chain V r
948	22	68.8	99	2	T45440	Ig kappa chain V r
949	22	68.8	99	2	D84010	Ig kappa chain V r
950	22	68.8	100	2	S67141	Ig kappa chain V r
951	22	68.8	101	1	B69598	Ig kappa chain V r
952	22	68.8	103	2	T28354	Ig kappa chain V r
953	22	68.8	103	2	A64847	Ig kappa chain V r
954	22	68.8	104	2	G71174	Ig kappa chain V r
955	22	68.8	106	2	C83730	Ig kappa chain V r
956	22	68.8	106	1	K1HUBN	Ig kappa chain V-I
957	22	68.8	108	2	S40330	Ig kappa chain V-J
958	22	68.8	108	2	S34007	Ig kappa chain V r
959	22	68.8	108	2	S44122	Ig kappa chain V r
960	22	68.8	108	2	S30521	Ig kappa chain V r
961	22	68.8	108	2	S31977	Ig kappa chain V r
962	22	68.8	109	2	S31998	Ig kappa chain - h
963	22	68.8	109	2	S32001	Ig kappa chain - h
964	22	68.8	109	2	S31983	Ig kappa chain - h
965	22	68.8	109	2	S31980	Ig kappa chain - h
966	22	68.8	109	2	S31979	Ig kappa chain - h
967	22	68.8	110	2	G72574	hypothetical prote
968	22	68.8	110	2	T47180	hypothetical prote
969	22	68.8	110	2	UC5445	glutaredoxin - ric
970	22	68.8	112	2	D72465	hypothetical prote
971	22	68.8	114	2	A35984	phosphoprotein pho
972	22	68.8	120	2	A44201	Ca2+-transporting
973	22	68.8	120	2	G02493	KR-ZNPF1 - human
974	22	68.8	121	2	S17718	anthr-specific pr
975	22	68.8	121	2	S12245	anthr-specific pr
976	22	68.8	127	2	B72732	hypothetical prote
977	22	68.8	131	2	A83350	hypothetical prote
978	22	68.8	131	2	S62360	squamosa-promoter

979 22 68.8 131 2 A11540
 980 22 68.8 132 2 S40334
 981 22 68.8 133 2 S40334
 982 22 68.8 134 2 B95216
 983 22 68.8 136 2 D70650
 984 22 68.8 137 2 B72786
 985 22 68.8 138 2 C64743
 986 22 68.8 138 2 E90652
 987 22 68.8 138 2 B85503
 988 22 68.8 139 2 T28243
 989 22 68.8 141 2 H98079
 990 22 68.8 148 2 JC7261
 991 22 68.8 150 2 C96647
 992 22 68.8 151 2 T38090
 993 22 68.8 153 2 A29472
 994 22 68.8 155 1 W6W56
 995 22 68.8 155 2 A44890
 996 22 68.8 157 2 H69849
 997 22 68.8 158 2 S65132
 998 22 68.8 158 2 S30091
 999 22 68.8 158 2 T09506
 1000 22 68.8 158 2 S33916

ALIGNMENTS

RESULT 1
 PH1083
 Ig light chain V region (clone 111.67) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: PH1083
 R:Fillman, D.M.; Jov, N.T.; Hill, R.J.; Matton, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1083
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-98 <TTL>
 A:Cross-references: UNIPARC:UPI0000176ABF
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
 DB 50 SGSTLOS 56

RESULT 2
 H30502
 Ig kappa chain V region (D42) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 03-Nov-1988 #sequence_revision 03-Aug-1992 #text_change 21-Jan-2000
 C:Accession: H30502
 R:Elia, D.; Webster, D.M.; Rees, A.R.
 J. Immunol. 141, 1745-1753, 1988
 A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
 A:Reference number: A30502; MUID:88315787; PMID:2457627
 A:Accession: H30502
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-103 <TTL>
 A:Cross-references: UNIPARC:UPI0000114DD4; GB:M21912; NID:g197077; PIDN:AAA38910.1; PID:
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
 DB 47 SGSTLOS 53

RESULT 3

S26345
 Ig light chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
 C:Accession: S26345; S78447
 R:Stark, S.E.; Caton, A.U.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421; PMID:1908510
 A:Accession: S26345
 A:Molecule type: mRNA
 A:Residues: 1-106 <STA>
 A:Cross-references: UNIPARC:UPI00001769B1; EMBL:X59177
 R:Caton, A.U.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S78447
 A:Accession: S78447
 A:Molecule type: mRNA
 A:Residues: 1-96, 'S', '98-106 <CAT>
 A:Cross-references: UNIPARC:UPI0000115F72; EMBL:X59177; NID:G52307; PIDN:CAA41887.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
 DB 50 SGSTLOS 56

RESULT 4

KVRT21
 Ig kappa chain V region (S211) - rat (tentative sequence)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 C:Accession: A01944
 R:Starace, V.; Querleu, P.
 J. Immunol. 115, 59-62, 1975
 A:Title: The primary structure of a rat kappa Bence Jones protein: phylogenetic relation
 A:Reference number: A92807; MUID:75212238; PMID:807630
 A:Accession: A01944
 A:Molecule type: protein
 A:Residues: 1-109 <STA>
 A:Cross-references: UNIPROT:P01681; UNIPARC:UPI000012E12C
 A:Experimental source: strain LOU
 A:Note: the sequence of the C region is also given
 C:Comment: This is a Bence Jones protein.
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kay
 bain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-91/Domain: immunoglobulin homology <IMM>
 F:23-89/Disulfide bonds: #status predicted

Query Match 100.0%; Score 32; DB 1; Length 109;

Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
|||||
Db 51 SGGSTLOS 57

RESULT 5
S04574

IG kappa chain precursor V region (MRL-RF24L) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000

C/Accession: S04574

R/Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th

Bur, J.; Immunol. 17, 91-95, 1987

A/Title: Molecular analysis of the murine lupus-associated anti-self response: involvement

A/Reference number: S04573; PMID:87133856; PMID:3102255

A/Accession: S04574

A/Molecule type: mRNA

A/Residues: 1-127 <KOF>

A/Cross-references: UNIPARC:UPI0000115DF; EMBL:X14621; NID:G52404; PIDN:CAA32774.1; PID

A/Note: the authors translated the codon TAT for residue 30 as Thr

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/1-20/Domain: signal sequence #status predicted <SIG>

F/21-127/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

F/36-110/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 32; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
|||||
Db 70 SGGSTLOS 76

RESULT 6
AE3475

probable sigma54 modulation protein / SSU ribosomal protein S30P [imported] - Brucella m

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C/Accession: AE3475

R/Delvecchio, V.G.; Kaputral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A/Reference number: AD3252; PMID:11756688

A/Accession: AE3475

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-197 <KUR>

A/Cross-references: UNIPROT:Q8YEU0; UNIPARC:UPI00000581DF; GB:AE008917; PIDN:ALU52968.1;

A/Experimental source: strain 16M

A/Genetics: BME11787

A/Map position: 1

Query Match 90.6%; Score 29; DB 2; Length 197;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
|||||
Db 59 SGGSTLOS 65

RESULT 7
G83171

hypothetical protein PA3804 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: G83171

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A/Reference number: AB2950; PMID:20437337; PMID:10984043

A/Accession: G83171

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-347 <STO>

A/Cross-references: UNIPROT:Q9HXJ3; UNIPARC:UPI00000C5B1E; GB:AE004798; GB:AE004091; NIT

C/Genetics: PA3804

Query Match 90.6%; Score 29; DB 2; Length 347;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
|||||
Db 95 SGGSTLOS 101

RESULT 8
S65208

probable membrane protein YPL189w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein P2201

C/Species: Saccharomyces cerevisiae

C/Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 09-Jul-2004

C/Accession: S65208; S65201

R/Reger, M.; Mueller-Auer, S.; Schaefer, M.

A/Reference number: S65202

A/Accession: S65208

A/Molecule type: DNA

A/Residues: 1-609 <RIE>

A/Cross-references: UNIPROT:Q08929; UNIPARC:UPI000006BF3D; EMBL:Z73545; NID:G1370394; P

A/Experimental source: strain S288C (AB972)

R/Bene, V.; Rechmann, S.; Nentwich, U.; Voss, H.; Ansoyge, W.

submitted to the Protein Sequence Database, May 1996

A/Reference number: S65183

A/Accession: S65201

A/Molecule type: DNA

A/Residues: 177-609 <BEN>

A/Cross-references: UNIPARC:UPI0000168FA2; EMBL:Z73545; MIPS:YPL189W

A/Experimental source: strain S288C (AB972)

C/Genetics:

A/Gene: SGD:GUP2

A/Cross-references: SGD:S0006110

A/Map position: 16L

C/Keywords: transmembrane protein

F/79-95/Domain: transmembrane #status predicted <TM1>

F/136-152/Domain: transmembrane #status predicted <TM2>

F/164-180/Domain: transmembrane #status predicted <TM3>

F/201-217/Domain: transmembrane #status predicted <TM4>

F/328-344/Domain: transmembrane #status predicted <TM5>

F/376-392/Domain: transmembrane #status predicted <TM6>

F/406-422/Domain: transmembrane #status predicted <TM7>

F/498-514/Domain: transmembrane #status predicted <TM8>

F/534-550/Domain: transmembrane #status predicted <TM9>

F/578-594/Domain: transmembrane #status predicted <TM10>

Query Match 90.6%; Score 29; DB 2; Length 609;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
|||||
Db 293 SGGSTLOS 299

RESULT 9
T27528

hypothetical protein ZC374.2 - Caenorhabditis elegans

C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27528
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20383
A:Accession: T27528
A:Status: preliminary; translated from GB/EMBL/DDBT
A:Molecule type: DNA
A:Residues: 1-613 <MIL>
A:Cross-references: UNIPROT:Q23266; UNIPARC:UPI000007879B; EMBL:Z72518; PIDD:CAA96700.1;
A:Experimental source: clone ZC374
C:Genetics:
A:Gene: CESP:ZC374.2
A:Map position: X
A:Introns: 48/1; 90/3; 114/3; 219/1; 241/3; 287/1; 326/1; 359/2; 389/1; 434/3; 490/1; 52

Query Match 90.6%; Score 29; DB 2; Length 613;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||:
Db 233 SGSTLOS 239

RESULT 10
S46086
RNA-binding protein RBP1 - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein YBR1459; protein YBR212w
C:Species: *Saccharomyces cerevisiae*
C:Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C:Accession: S46086; A47108; S30033
R:Rieger, M.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45734
A:Accession: S46086
A:Molecule type: DNA
A:Residues: 1-672 <RIE>
A:Cross-references: UNIPROT:P32831; UNIPARC:UPI0000130006; EMBL:Z36081; NID:G536595; PIDD:
A:Experimental source: strain S288C
R:Lee, F.J.S.; Moss, J.
J. Biol. Chem. 268, 15080-15087, 1993
A:Title: An RNA-binding protein gene (RBP1) of *Saccharomyces cerevisiae* encodes a putative
A:Reference number: A47108; MUID:93315487; PMID:8325883
A:Accession: A47108
A:Molecule type: DNA
A:Residues: 1-321, 'S', 323-567, 'N', 569-584, 'S', 586-672 <LEE>
A:Cross-references: UNIPARC:UPI0000168D20; GB:Z14097; NID:G4030; PIDD:CAA78478.1; PIDD:G4
C:Genetics:
A:Gene: SGD:NGR1, RBP1
A:Cross-references: SGD:S0000416; MIPS:YBR212w
A:Map position: 2R
F:193-261/Domain: ribonucleoprotein repeat homology <RRM1>
F:361-422/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 90.6%; Score 29; DB 2; Length 672;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||:
Db 178 SGSTLOS 184

RESULT 11
T47141
hypothetical protein DKFZp761N1024.1 - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47141; T08736
R:Boecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Well, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000

A:Reference number: Z24376
A:Accession: T47141
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1254 <AAA>
A:Cross-references: UNIPROT:Q9NSL4; UNIPARC:UPI000007101B; EMBL:AL162056
A:Experimental source: adult amygdala; clone DKFZp761N1024
R:Ottewald, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16474
A:Accession: T08736
A:Molecule type: mRNA
A:Residues: 794-1254 <OTT>
A:Cross-references: UNIPARC:UPI00000729DF; EMBL:AL050080
A:Experimental source: fetal kidney; clone DKFZp56610746
C:Genetics:
A:Note: DKFZp761N1024.1; DKFZp56610746.1

Query Match 90.6%; Score 29; DB 2; Length 1254;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||:
Db 363 SGSTLOS 369

RESULT 12
B86719
hypothetical protein yhgB [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)
C:Species: *Lactococcus lactis* subsp. *lactis*
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: B86719
R:Boletín, A.; Winker, P.; Manger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* 88
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: B86719
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <STO>
A:Cross-references: UNIPROT:Q9CHH7; UNIPARC:UPI00000689DB; GB:AE005176; PIDD:G12723671; PIDD:
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yhgB

Query Match 87.5%; Score 28; DB 2; Length 171;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||:
Db 85 SGSTLOS 91

RESULT 13
S56073
opaque-2 protein - sorghum
C:Species: *Sorghum bicolor* (sorghum)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 31-Dec-2004
C:Accession: S56073
R:Hartings, H.
submitted to the EMBL Data Library, April 1993
A:Reference number: S56073
A:Accession: S56073
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-419 <HAR>
A:Cross-references: UNIPROT:Q07795; UNIPARC:UPI00000450DA; EMBL:X71636; NID:G297481; PIDD:
C:Genetics:
A:Introns: 133/3; 151/1; 217/2; 242/3; 284/3
C:Superfamily: B2IP protein; fos/jun DNA-binding domain homology
F:206-246/Domain: fos/jun DNA-binding domain homology <FOD>

Query Match 87.5%; Score 28; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||||
Db 398 SGGSTLQ 403

RESULT 14

T19733
hypothetical protein C34F6.8 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C:Accession: T19733
R:White, S.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19171
A:Accession: T19733
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-435 <MIL>
A:Cross-references: UNIPROT:Q17643; UNIPARC:UPI0000083512; EMBL:Z81479; PIDN:CAE03943.1;
A:Experimental source: clone C34F6
C:Genetics:
A:Gene: CRSP:C34F6.8
A:Map position: X
A:Introns: 52/3; 78/3; 255/2; 306/1; 376/2
C:Superfamily: isocitrate dehydrogenase (NADP)

Query Match 87.5%; Score 28; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||||
Db 171 SGGSTLQ 176

RESULT 15

AE2214
serine/threonine kinase [imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: *Nostoc* sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2214
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuriitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807; M01D:21595285; PMID:11759640
A:Accession: AE2214
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-524 <NUR>
A:Cross-references: UNIPROT:Q8YS23; UNIPARC:UPI00000CEB71C; GB:BA000019; PIDN:BAB74967.1;
C:Genetics:
A:Gene: alr3268
C:Superfamily: Synechocystis sp. protein kinase pKna, 63k; protein kinase homology

Query Match 87.5%; Score 28; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||||
Db 121 SGGSTLQ 126

RESULT 16

B75080

hypothetical protein PAB0690 - *Pyrococcus abyssi* (strain Orsay)
C:Species: *Pyrococcus abyssi*
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: B75080
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: B75080
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <KAW>
A:Cross-references: UNIPROT:Q9UZW3; UNIPARC:UPI000006339B; GB:AJ248286; GB:AL096836; NIT
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0690
C:Superfamily: *Pyrococcus abyssi* hypothetical protein PAB0690

Query Match 87.5%; Score 28; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||||
Db 319 SGGSTLQ 324

RESULT 17

JB0339
frizzled-7 protein - human
C:Species: *Homo sapiens* (man)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C:Accession: JB0339
R:Saggar, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A:Title: Molecular cloning, differential expression, and chromosomal localization of hu
A:Reference number: JB0339; M01D:99032814; PMID:9613155
A:Accession: JB0339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-574 <SAG>
A:Cross-references: UNIPROT:Q96B74; UNIPARC:UPI0000051051; DDBJ:AB017365; NID:g3927886;
C:Superfamily: fruit fly frizzled protein

Query Match 87.5%; Score 28; DB 2; Length 574;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTLQ 7
|||||
Db 550 SGGSTLQ 556

RESULT 18

T41341
probable serine-threonine-protein kinase - fission yeast (*Schizosaccharomyces pombe*)
C:Species: *Schizosaccharomyces pombe*
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41341
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21970
A:Accession: T41341
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-624 <LYN>
A:Cross-references: UNIPROT:Q94487; UNIPARC:UPI000006BAA9; EMBL:AL035076; PIDN:CAA22652
A:Experimental source: strain 972h-; cosmid c417
C:Genetics:
A:Gene: SPDB:SPCC417.06c
A:Map position: 1
A:Introns: 203/3; 353/3

Query Match	87.5%	Score 28	DB 2	Length 624
Best Local Similarity	100.0%	Pred. No.	13e+02	
Matches	6	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
QY	1	SGSTLQ	6	
db	398	SGSTLQ	403	

RESULT 19
F96615
probable Myb-family transcription factor F16M22.4 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F96615
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maltl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: F96615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-873 <STD>
A:Cross-references: UNIPROT:Q9C548; UNIPARC:UPI0000A1EF8; GB:AE005173; NID:g11055843; E
C:Genetics:
A:Gene: F16M22.4
A:Map position: 1

Query Match	87.5%;	Score 28;	DB 2;	Length 873;
Best Local Similarity	100.0%;	Pred. No. 1.9e+02;		
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

```

QY      1  S G S T L Q  6
          |||||
Db      345 S G S T L Q  350

```

RESULT 20

B35905

endopeptidase Clp (EC 3.4.21.-) ATP-binding chain cd4B, chloroplast [similarity] - tomato

N:Alternate names: ATP-dependent Clp proteinase regulatory chain B; CD4B protein

N:Contains: adenosinetriphosphatase (EC 3.6.1.3)

C:Species: Lycopersicon esculentum (tomato)

C:Date: 30-Jun-1993 #sequence #revision 30-Jun-1993 #text_change 09-Jul-2004

C:Accession: B35905

R:Gottesman, S.; Squires, C.; Pichersky, E.; Carrington, M.; Hobbe, M.; Mattick, J.S.; D

Proc. Natl. Acad. Sci. U.S.A. 87, 3513-3517, 1990

A:Title: Conservation of the regulatory subunit for the Clp ATP-dependent protease in pro

A:Reference number: A35905; MUID:90239044; PMID:2185473

A:Accession: B35905

A:Molecule type: DNA

A:Residues: 1-923 <GOT>

A:Cross-references: UNIPROT:P31542; UNIPARC:UPI0000127286; GB:M32604; NID:gl70434; PIDN

C:Genetics:

A:Gene: cd4B

A:Map position: 12

C:Function:

A:Description: allows clp to hydrolyze polypeptides and proteins, probably by a chaperon

e activity; ATP hydrolysis is required for Clp hydrolysis of proteins but not of smaller

C:Superfamily: endopeptidase Clp ATP-binding chain

C:Keywords: ATP; chloroplast; hydrolase; molecular chaperone; nucleotide binding; P-loop

P:300-307/Region: nucleotide-binding motif A (P-loop)

F:367-371/Region: nucleotide-binding motif B

F:643-650/Region: nucleotide-binding motif A (P-loop)

F:711-715/Region: nucleotide-binding motif B

F:306/Binding site: ATP (Lys) #status predicted

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F:649/Binding site: ATP (Lys) #status predicted
Query Match      87.5%; Score 28; DB 1; Length 923;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 SGGTLQS 7
        |||||
Db      64 SGGTLQS 70

```

RESULT 21
 AC0447
 probable insecticidal toxin YPO3673 [imported] - *Yersinia pestis* (strain CO92)
 C:Species: *Yersinia pestis*
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AC0447
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deleno-Tarrasa, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 Ikin, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586560
 A:Accession: AC0447
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-952 <KUR>
 A:Cross-references: UNIPROT:Q8ZAV9; UNIPARC:UPI000000DCTE2; GB:AL590842; PIDN:CAC93143.1,
 C:Gene: YPO3673

```

Query Match      87.5%; Score 28; DB 2; Length 952;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;
QY 1 GCGTTC 6
    |||||
Db 86 GCGTTC 91

```

QY	1	SGSTLQ	6
Db	86	SGSTLQ	91

RESULT 22
 AD0447
 probable insecticidal toxin YPO3674 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AD0447
 R:Parkhill, J., Wren, B.W.; Thomson, N.R.; Tlthball, R.W.; Holden, M.T.G.; Prentice, M.B
 deno-Tarragoe, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 I., M., Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586350
 A:Accession: AD0447
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1011 <R>
 A:Cross-references: UNIPROT:Q8ZAV8; UNIPARC:UPI00000CDA64; GB:AL590842; PIDD:CA93144.1
 C:Genetics:
 A:Gene: YPO3674

Query Match	87.5%	Score 28:	DB 2:	Length 1011:
Best Local Similarity	100.0%	Pred. No.	2.2e+02:	
Matches	6	Conservative	0	Mismatches 0; Gaps 0

```
QY      1 SGSTLQ 6
Db      154 SGSTLQ 155
```

RESULT 23
A66790
ATP-dependent dsDNA exonuclease [imported] - *Lactococcus lactis* subsp. *lactis* (strain I
C1:Species: *Lactococcus lactis* subsp. *lactis*

C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C/Accession: A86790
 R/Bolotin, A.; Wincker, P.; Manger, S.; Jallou, O.; Malarne, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A/Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s8
 A/Reference number: A86625; MUID:21235186; PMID:11337471
 A/Accession: A86790
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1046 <STO>
 A/Cross-references: UNIPROT:Q9CFZ0; UNIPARC:UPI0000135595; GB:AE005176; PID:q12724301; F
 A/Experimental source: strain IL1403
 C/Genetics:
 A/Gene: sbcc

Query Match 87.5%; Score 28; DB 2; Length 1046;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGGTLO 6
 |||||
 Db 104 SGGTLO 109

RESULT 24
 T13741
 hypothetical protein 22E5.8 - fruit fly (*Drosophila melanogaster*)
 C/Species: *Drosophila melanogaster*
 C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C/Accession: T13741
 R/Murphy, L.; Harris, D.; Barrell, B.
 submitted to the EMBL Data Library, April 1999
 A/Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.
 A/Reference number: 217668
 A/Accession: T13741
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1398 <MUR>
 A/Cross-references: UNIPROT:O77268; UNIPARC:UPI0000820A3; EMBL:AL031765; NID:e1371523;
 C/Genetics:
 A/Cross-references: FlyBase:FBgn0000667
 A/Intons: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3
 A/Note: EG:22E5.8

Query Match 87.5%; Score 28; DB 2; Length 1398;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SGGTLO 7
 |||||
 Db 340 SGGTLO 345

RESULT 25
 T31671
 Rab3 GDP/GNP exchange protein - rat
 C/Species: *Rattus norvegicus* (Norway rat)
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T31671
 R/Wada, M.; Nakanishi, H.; Satoh, A.; Hirano, H.; Obaishi, H.; Matsuura, Y.; Takai, Y.
 J. Biol. Chem. 272, 3875-3878, 1997
 A/Title: Isolation and characterization of a GDP/GNP exchange protein specific for the R
 A/Reference number: 221055; MUID:91172442; PMID:9020086
 A/Accession: T31671
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1602 <MAD>
 A/Cross-references: UNIPROT:O08873; UNIPARC:UPI0000E725C; EMBL:U72995; NID:g1947049; P1
 A/Experimental source: brain

Query Match 87.5%; Score 28; DB 2; Length 1602;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGGTLO 6
 |||||
 Db 137 SGGTLO 142

RESULT 26
 B61387
 bone morphogenetic protein 3 - bovine (fragments)
 C/Species: *Bos primigenius taurus* (cattle)
 C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
 C/Accession: B61387
 R/Bentz, H.; Thompson, A.Y.; Armstrong, R.; Chang, R.J.; Piez, K.A.; Rosen, D.M.
 Matrix 11, 269-275, 1991
 A/Title: Transforming growth factor-beta2 enhances the osteo-inductive activity of a bo
 A/Reference number: A61387; MUID:92017396; PMID:1921853
 A/Accession: B61387
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-69 <BEN>
 A/Cross-references: UNIPROT:Q7M229; UNIPARC:UPI000017656A
 C/Superfamily: inhibin

Query Match 84.4%; Score 27; DB 2; Length 69;
 Best Local Similarity 71.4%; Pred. No. 23;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGGTLO 7
 |||||
 Db 20 SGGTLO 26

RESULT 27
 AC0411
 probable priplasmic metal binding protein YPO3385 [imported] - *Yersinia pestis* (strain
 C/Species: *Yersinia pestis*
 C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C/Accession: AC0411
 R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibbail, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A/Reference number: AB0001; MUID:21470413; PMID:11586360
 A/Accession: AC0411
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-280 <KUR>
 A/Cross-references: UNIPROT:Q8ZBM3; UNIPARC:UPI0000126B28; GB:AL590842; PIDN:CA092615.1
 C/Genetics:
 A/Gene: YPO3385

Query Match 84.4%; Score 27; DB 2; Length 280;
 Best Local Similarity 85.7%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGGTLO 7
 |||||
 Db 178 SGGTLO 184

RESULT 28
 T05028
 nodulin-26-like protein F13C5.80 - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
 C/Accession: T05028
 R/Beyan, M.; Pohl, T.; Weisenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schue
 submitted to the Protein Sequence Database, February 1998
 A/Reference number: 215395
 A/Accession: T05028
 A/Molecule type: DNA
 A/Residues: 1-294 <BEV>

Query Match 87.5%; Score 28; DB 2; Length 1602;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Cross-references: UNIPARC:UPI000000AC495; EMBL:AL021711
A;Experimental source: cultivar Columbia; BAC clone F13C5
C;Genetics:
A;Map position: 4
A;Introns: 53/3; 128/3; 201/3; 222/2
A;Note: F13C5.80
C;Superfamily: aquaporin

Query Match 84.4%; Score 27; DB 2; Length 294;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 171 SGGNLOS 177

RESULT 29
B82229
hypothetical protein VC1207 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82229
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardon, D.; Ermlaeva, M.D.; Vamathevan, J.; Basu, S.; Qin, H.; Dragol, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82229
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <HIT>
A;Cross-references: UNIPROT:Q9KSP9; UNIPARC:UPI000000C2BEC; GB:AE004200; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1207
A;Map position: 1

Query Match 84.4%; Score 27; DB 2; Length 315;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 152 SGGTLOS 158

RESULT 30
S58304
hypothetical protein SPAC18B11.05 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: T37909; S58304
R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Raftery, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z21753
A;Accession: T37909
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-426 <DS2>
A;Cross-references: UNIPROT:Q09712; UNIPARC:UPI0000139F3A; EMBL:Z50728; NID:G929886; PID
A;Experimental source: strain 972h-; cosmid c18B11
C;Genetics:
A;Gene: SPAC18B11.05
A;Map position: 1L

Query Match 84.4%; Score 27; DB 2; Length 426;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 171 SGGNLOS 177

DB 338 SGGTLOS 344

RESULT 31
T34251
hypothetical protein F31D5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34251
R;Milcox, L.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F31D5.
A;Reference number: Z21494
A;Accession: T34251
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-484 <HIT>
A;Cross-references: UNIPROT:Q19932; UNIPARC:UPI000017B958; EMBL:U28941; PIDN:AACT1105.1,
A;Experimental source: strain Bristol N2; clone F31D5
C;Genetics:
A;Gene: CRSP:F31D5.2
A;Map position: 2
A;Introns: 54/2; 131/1; 163/2; 188/3; 230/1; 260/1; 350/2; 395/3; 446/1

Query Match 84.4%; Score 27; DB 2; Length 484;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 466 SGGTLOS 472

RESULT 32
A05204
hypothetical protein 581 - common tobacco chloroplast
C;Species: chloroplast Nicotiana tabacum (common tobacco)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05204
R;Sugiura, M.
submitted to the EMBL Data Library, August 1986
A;Reference number: A00149
A;Accession: A05204
A;Molecule type: DNA
A;Residues: 1-581 <SUG>
A;Cross-references: UNIPROT:P09776; UNIPARC:UPI000017B086
A;Experimental source: cv. Bright Yellow 4
R;Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakaue, T.; Hayashida, N.; Matsubayashi, T.; S.
Deno, H.; Kamogashira, T.; Yamada, K.; Kusuda, D.; Takaiwa, F.; Kato, A.; Tondou, N.; Si
EMBO J. 5, 2043-2049, 1986
A;Title: The complete nucleotide sequence of the tobacco chloroplast genome: its gene o
A;Reference number: A38013
A;Contents: annotation; gene organization, sites, features
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast

Query Match 84.4%; Score 27; DB 2; Length 581;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 288 SGGTLOS 294

RESULT 33
AH1786
autolysin, N-acetylmuramidase homolog 1ln2838 [imported] - Listeria innocua (strain Cl
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1786
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgelet, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefte, U.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Me
ok, C.; Schlueter, T.; Smoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of *Listeria species*.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1077
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-594 <GLA>
A:Cross-references: UNIPROT:Q927F1; UNIPARC:UPI000000CC9BC; GB:AL592022; PIDN:CA098064.1;
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: lin2838

Query Match 84.4%; Score 27; DB 2; Length 594;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 149 SGTATOS 155

RESULT 34

737772 telomere length regulator taz1 - fission yeast (*Schizosaccharomyces pombe*)

N:Alternate names: Myb-domain protein

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004

C:Accession: T37772; T34324

R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1997

A:Reference number: Z21738

A:Accession: T37772

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-663 <MUR>

A:Cross-references: UNIPROT:P79005; UNIPARC:UPI0000136961; EMBL:Z57165; PIDN:CAB10000.1;

A:Experimental source: strain 972h-; cosmid c16A10

R:Cooper, J.P.; Nimmo, E.R.; Allshire, R.C.; Cech, T.R.

Nature 385, 744-747, 1997

A:Title: Regulation of telomere length and function by a Myb-domain protein in fission Y

A:Reference number: Z08606; MUID:97186558; PMID:9034194

A:Accession: T43424

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-663 <COO>

A:Cross-references: UNIPARC:UPI0000136961; EMBL:Y09406; NID:G1872134; PIDN:CAAT0568.1; F

A:Experimental source: strain 972

C:Genetics:

A:Gene: taz1; myb; SPAC16A10.07C

C:Function:

A:Description: taz1 is involved in the regulation of telomere length and required for th

C:Superfamily: telomere length regulator Taz1

Query Match 84.4%; Score 27; DB 2; Length 663;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 388 SGGTLOS 394

RESULT 35

S30911

SM2 protein - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: protein YMR520.14c; protein YMR165c

C:Species: *Saccharomyces cerevisiae*

C:Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 09-Jul-2004

C:Accession: S30911; JQ1117; S54523; S54610

R:Rie, K.; Takase, M.; Araki, H.; Oshima, Y.
Mol. Gen. Genet. 236, 283-288, 1993
A:Title: A gene, *SM2*, involved in plasmid maintenance and respiration in *Saccharomyces*

A:Reference number: S30911; MUID:93173103; PMID:8437575

A:Accession: S30911

A:Molecule type: DNA

A:Residues: 1-862 <IR1>

A:Cross-references: UNIPROT:P32567; UNIPARC:UPI0000135ABD; EMBL:D01095; NID:G218487; PID

R:Rie, K.; Araki, H.; Oshima, Y.

submitted to JRPID, July 1991

A:Reference number: JQ1117

A:Accession: JQ1117

A:Molecule type: DNA

A:Residues: 1-862 <IR12>

A:Cross-references: UNIPARC:UPI0000135ABD

R:Hunt, S.; Bowman, S.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54510

A:Accession: S54523

A:Molecule type: DNA

A:Residues: 1-862 <HUN>

A:Cross-references: UNIPARC:UPI0000135ABD; GB:Z49705; EMBL:Z49700; NID:G825556; PID:G825

A:Experimental source: strain AB972

C:Genetics:

A:Gene: SGD:SM2

A:Cross-references: SGD:S0004775; MIPS:YMR165c

A:Map position: 13R

Query Match 84.4%; Score 27; DB 2; Length 862;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 299 SGGTLOS 305

RESULT 36

A22798

paraportal crystal protein - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*

C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 05-Oct-2004

C:Accession: A22798

R:Shibano, Y.; Yamagata, A.; Nakamura, N.; Iizuka, T.; Sugisaki, H.; Takemai, M.

Gene 34, 243-251, 1985

A:Title: Nucleotide sequence coding for the insecticidal fragment of the *Bacillus thurin*

A:Reference number: A22798; MUID:8532070; PMID:2989108

A:Accession: A22798

A:Molecule type: DNA

A:Residues: 1-934 <SH1>

A:Cross-references: UNIPROT:Q9S5V8; UNIPARC:UPI000014439A; GB:M10917; NID:G143100; PIDN

C:Comment: The authors translated the codon ACA for residue 264 as Ser.

C:Superfamily: Paraportal crystal protein

C:Keywords: delta-endotoxin

Query Match 84.4%; Score 27; DB 2; Length 934;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 556 SGGTLOS 562

RESULT 37

A26513

paraportal crystal protein - *Bacillus thuringiensis* (strain aizawai)

C:Species: *Bacillus thuringiensis*

C:Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 05-Oct-2004

C:Accession: A26513

R:Oeda, K.; Oshie, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H

Gene 53, 113-119, 1987

A:Title: Nucleotide sequence of the insecticidal protein gene of *Bacillus thuringiensis*

A:Reference number: A26513; MUID:87248103; PMID:3297927
 A:Accession: A26513
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1155 <OED>
 A:Cross-references: UNIPROT:P06578; UNIPARC:UPI0000156D0A; GB:M16463; NID:g143098; PIDN:
 C:Superfamily: Parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 84.4%; Score 27; DB 2; Length 1155;
 Best Local Similarity 85.7%; Pred. No. 4.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
 ||| |||
 Db 557 SGSNLOS 563

RESULT 38
 S02134
 parasporal crystal protein cryIC1 - *Bacillus thuringiensis* (strain aizawai ICI)
 N:Alternate names: delta-endotoxin ICI; entomocidal crystal protein
 C:Species: *Bacillus thuringiensis*
 A:Variety: strain aizawai ICI
 C:Date: 21-Nov-1993 #sequence__revision 10-Nov-1995 #text_change 05-Oct-2004
 R:Haider, M.Z.; Ellar, D.J.
 C:Accession: S02134; S04994
 A:Reference number: S02134; MUID:89083518; PMID:3205732
 A>Title: Nucleotide sequence of a *Bacillus thuringiensis* aizawai ICI entomocidal crystal
 A:Reference number: S02134; MUID:89083518; PMID:3205732
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1155 <HAI>
 A:Cross-references: UNIPROT:P06578; UNIPARC:UPI000016EA35; EMBL:X13233; NID:g40277; PIDN:
 A:Experimental source: strain aizawai ICI
 R:Haider, M.Z.; Ellar, D.J.
 J. Mol. Biol. 208, 183-194, 1989
 A>Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid changes
 A:Reference number: S04994; MUID:89362455; PMID:2769751
 A:Accession: S04994
 A:Molecule type: DNA
 A:Residues: 429-449, 'A', 451-724 <HAN>
 A:Cross-references: UNIPARC:UPI000017819E; EMBL:X16315
 A:Experimental source: strain aizawai ICI
 C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
 C:Superfamily: Parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 84.4%; Score 27; DB 2; Length 1155;
 Best Local Similarity 85.7%; Pred. No. 4.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
 ||| |||
 Db 557 SGSNLOS 563

RESULT 39
 I39838
 parasporal crystal protein - *Bacillus thuringiensis*
 C:Species: *Bacillus thuringiensis*
 C:Date: 19-Jul-1996 #sequence__revision 19-Jul-1996 #text_change 05-Oct-2004
 R:Haider, M.Z.; Ellar, D.J.
 C:Accession: I39838
 A:Reference number: I39838
 A>Title: Sequence of a lepidopteran toxin gene of *Bacillus thuringiensis* subsp. kurstaki
 A:Reference number: I39838
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1155 <RES>
 A:Cross-references: UNIPROT:P06578; UNIPARC:UPI000016EA38; GB:M37263; NID:g142885; PIDN:

C:Superfamily: Parasporal crystal protein
 C:Keywords: delta-endotoxin

Query Match 84.4%; Score 27; DB 2; Length 1155;
 Best Local Similarity 85.7%; Pred. No. 4.4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
 ||| |||
 Db 557 SGSNLOS 563

RESULT 40
 JD0002
 parasporal crystal protein cryIAB3 - *Bacillus thuringiensis*
 N:Alternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal pro
 C:Species: *Bacillus thuringiensis*
 C:Date: 28-Dec-1987 #sequence__revision 28-Dec-1987 #text_change 05-Oct-2004
 C:Accession: A90025; A91560; A90955; S14555; A26461; A24172; A29043; JD0002
 R:Kondo, S.; Tamura, N.; Kunitake, A.; Hattori, M.; Akashi, A.; Ohmori, I.
 Agric. Biol. Chem. 51, 455-463, 1987
 A>Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes fro
 A:Reference number: A90025
 A:Accession: A90025
 A:Molecule type: mRNA
 A:Residues: 1-1155 <KON>
 A:Cross-references: UNIPROT:P06578; UNIPARC:UPI000002F08
 A:Experimental source: subsp. kurstaki
 R:Gaiser, M.; Schweitzer, S.; Grimm, C.
 Gene 48, 109-118, 1986
 A>Title: The hypervariable region in the genes coding for entomopathogenic crystal prote
 A:Reference number: A91560; MUID:87163505; PMID:3557124
 A:Accession: A91560
 A:Molecule type: DNA
 A:Residues: 1-1155 <GRI>
 A:Cross-references: UNIPARC:UPI000002F08; GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:
 A:Experimental source: subsp. kurstaki
 R:Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
 DNA 5, 305-314, 1986
 A>Title: *Bacillus thuringiensis* entomocidal protoxin gene sequence and gene product anal
 A:Reference number: A90955; MUID:86300092; PMID:3743328
 A:Accession: A90955
 A:Molecule type: DNA
 A:Residues: 1-1155 <WAB>
 A:Cross-references: UNIPARC:UPI000002F08; GB:M13898; NID:g142719; PIDN:AAA22330.1; PID:
 A:Experimental source: subsp. berliner
 R:Chak, K.F.; Jen, J.C.
 Submitted to the EMBL Data Library, October 1990
 A:Description: Complete nucleotide sequence and expression in *Escherichia coli* of a cry
 A:Reference number: S14555
 A:Accession: S14555
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1155 <CHA>
 A:Cross-references: UNIPARC:UPI000002F08; EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:
 R:Hoite, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandeckerck
 Eur. J. Biochem. 161, 273-280, 1986
 A>Title: Structural and functional analysis of a cloned delta endotoxin of *Bacillus thur*
 A:Reference number: A26461; MUID:87054026; PMID:3023091
 A:Accession: A26461
 A:Molecule type: DNA
 A:Residues: 1-730, 'L', 732-784, 'R', 786-1155 <HOF>
 A:Cross-references: UNIPARC:UPI0000144396; GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g
 A:Experimental source: strain berliner 1715
 C:Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
 C:Genetics:
 A:Gene: cry-1-2; bt2
 C:Superfamily: Parasporal crystal protein
 C:Keywords: delta-endotoxin
 F:82-300/Product: toxic peptide #status predicted <TRP>
 F:82-300/Region: toxic #status predicted
 F:300-586/Region: insecticidal #status predicted

Query Match 84.4%; Score 27; DB 2; Length 1155;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
||| |||
Db 557 SGSNLOS 563

RESULT 41

A29125
paraasporal crystal protein Bc2 - *Bacillus thuringiensis* subsp. *kurstaki* (strain HD-1)

C:Species: *Bacillus thuringiensis* subsp. *kurstaki*
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 05-Oct-2004

C:Accession: A29125
R:Rischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederme

Bio/Technology 5, 807-813, 1987
A:Title: Insect tolerant transgenic tomato plants.

A:Reference number: A29125
A:Accession: A29125

A:Status: not compared with conceptual translation
A:Molecule type: DNA

A:Residues: 1-1156 <FIS>
A:Cross-references: UNIPROT:Q9F296; UNIPARC:UPI000014260B

C:Superfamily: Paraasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 84.4%; Score 27; DB 2; Length 1156;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
||| |||
Db 557 SGSNLOS 563

RESULT 42

A29838
paraasporal crystal protein - *Bacillus thuringiensis* subsp. *kurstaki*

C:Species: *Bacillus thuringiensis* subsp. *kurstaki*
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004

C:Accession: A29838
R:Thorne, L.; Garduno, F.; Thompson, T.; Decker, D.; Zouner, M.; Wild, M.; Walfield, A.M

J. Bacteriol. 166, 801-811, 1986

A:Title: Structural similarity between the Lepidoptera- and Diptera-specific insecticidal
A:Reference number: A94672; MUID:86223796; PMID:3011746

A:Accession: A29838
A:Molecule type: DNA

A:Residues: 1-1156 <THO>
A:Cross-references: UNIPROT:P06578; UNIPARC:UPI000016EA3D; GB:M12661; NID:gt143226; PIDN:

C:Superfamily: Paraasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 84.4%; Score 27; DB 2; Length 1156;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
||| |||
Db 558 SGSNLOS 564

RESULT 43

A22617
paraasporal crystal protein cryIAa1 - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*
C:Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 05-Oct-2004

C:Accession: A22617
R:Schnepf, H.B.; Wong, H.C.; Whiteley, H.R.

J. Biol. Chem. 260, 6264-6272, 1985

A:Title: The amino acid sequence of a crystal protein from *Bacillus thuringiensis* deduce
A:Reference number: A22617; MUID:85207613; PMID:2581950

A:Accession: A22617

A:Molecule type: DNA
A:Residues: 1-1176 <SCH>
A:Cross-references: UNIPROT:P02965; UNIPARC:UPI000016EA37; GB:M11250; NID:gt142764; PIDN:
C:Superfamily: Paraasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 84.4%; Score 27; DB 2; Length 1176;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
||| |||
Db 556 SGSNLOS 562

RESULT 44

JC2219
paraasporal crystal protein cryIAa - *Bacillus thuringiensis*

C:Species: *Bacillus thuringiensis*
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Oct-2004

C:Accession: JC2219
R:Udayasuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.

Biosci. Biotechnol. Biochem. 58, 830-835, 1994

A:Title: Cloning of a new cryIA(a) gene from *Bacillus thuringiensis* strain FU-2-7 and an
A:Reference number: JC2219; MUID:94289859; PMID:7764972

A:Accession: JC2219
A:Molecule type: DNA

A:Residues: 1-1176 <UDA>
A:Cross-references: UNIPROT:Q45736; UNIPARC:UPI00000B742F; DDBJ:D17518; NID:gs06190; PID

C:Genetics:
A:Gene: cryIA(a)

C:Superfamily: Paraasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 84.4%; Score 27; DB 2; Length 1176;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
||| |||
Db 556 SGSNLOS 562

RESULT 45

JT0241
paraasporal crystal protein - *Bacillus thuringiensis* (strain aizawai IPL7)

N:Alternate names: 135K insecticidal protein
C:Species: *Bacillus thuringiensis*

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004
C:Accession: JT0241

R:Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.

Agric. Biol. Chem. 52, 1565-1573, 1988

A:Title: Cloning and expression in *Escherichia coli* of the 135-kDa insecticidal protein
A:Reference number: JT0241

A:Accession: JT0241
A:Molecule type: DNA

A:Residues: 1-1176 <SHI>
A:Cross-references: UNIPROT:P02965; UNIPARC:UPI0000156D9D

A:Note: b. *thuringiensis* aizawai IPL7 produces similar 130K and 135K insecticidal protei
C:Comment: The 135K protein has insecticidal activity against *Plutella xylostella* larvae

C:Superfamily: Paraasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 84.4%; Score 27; DB 2; Length 1176;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
||| |||
Db 556 SGSNLOS 562

RESULT 46

S02215

paraportal crystal protein cryA - *Bacillus thuringiensis* (strain entomocidus)C:Species: *Bacillus thuringiensis*

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 05-Oct-2004

C:Accession: S02215

C:Masson, L.; Marcotte, P.; Prefontaine, G.; Brousseau, R.

Nucleic Acids Res. 17, 446, 1989

A:Title: Nucleotide sequence of a gene cloned from *Bacillus thuringiensis* subspecies ent

A:Reference number: S02215; MUID:89098405; PMID:2911478

A:Accession: S02215

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-1176 <MAS>

A:Cross-references: UNIPROT:P02965; UNIPARC:UPI0000126BD0; EMBL:X15335; NID:g40266; PIDN

C:Superfamily: Paraportal crystal protein

C:Keywords: delta-endotoxin

Query Match

Best Local Similarity 84.4%; Score 27; DB 2; Length 1176;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7

Db 556 SGSNLOS 562

RESULT 47

B84312

hypothetical protein Vng1590h [imported] - *Halobacterium* sp. NRC-1C:Species: *Halobacterium* sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: B84312

R:Ng, W.V.; Kennedy, S.P.; Mahatras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S

; Letthauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jdlic

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of *Halobacterium* species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: B84312

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-89 <STO>

A:Cross-references: UNIPROT:Q9HPK5; UNIPARC:UPI000006391C; GB:AE004437; NID:g10581072; F

C:Genetics:

A:Gene: VNG1590H

Query Match

Best Local Similarity 81.2%; Score 26; DB 2; Length 89;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTLOS 7

Db 77 SGSTIRS 83

RESULT 48

S51119

MALDI protein - apple tree (fragment)

C:Species: *Malus domestica* (apple tree)

C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C:Accession: S51119

R:Schoening, B.; Ziegler, W.H.; Viehs, S.; Baltes, W.

submitted to the EMBL Data Library, December 1994

A:Reference number: S51119

A:Accession: S51119

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-153 <SCS>

A:Cross-references: UNIPROT:Q941P6; UNIPARC:UPI0000177F53; EMBL:X83672

C:Superfamily: pathogenesis-related protein

Query Match

81.2%; Score 26; DB 2; Length 153;

Best Local Similarity 71.4%; Pred. No. 93;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTLOS 7

Db 104 SGSTIRS 110

RESULT 49

F83696

hypothetical protein BH0374 [imported] - *Bacillus halodurans* (strain C-125)C:Species: *Bacillus halodurans*

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: F83696

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeki, R.; Masui, N.; Fuji, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and c

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83696

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-172 <STO>

A:Cross-references: UNIPROT:Q9KEU7; UNIPARC:UPI00000C3866; GB:AF001508; GB:BA000004; NID

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH0374

Query Match

Best Local Similarity 81.2%; Score 26; DB 2; Length 172;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 GSTLOS 7

Db 49 GSTLOS 54

RESULT 50

B86679

prophage p11 protein 02 [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL1403)C:Species: *Lactococcus lactis* subsp. *lactis*

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: B86679

R:Boletín, A.; Winkler, P.; Mauger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: B86679

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-192 <STO>

A:Cross-references: UNIPROT:Q9CIC7; UNIPARC:UPI0000098702; GB:AE005176; PID:g12723315; PJ

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: p1102

Query Match

Best Local Similarity 81.2%; Score 26; DB 2; Length 192;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTLOS 7

Db 79 SGSNLOS 85

Search completed: January 17, 2006, 12:06:16
Job time : 16.5758 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:47:28 ; Search time 39.4545 Seconds
(without alignments)

125.174 Million cell updates/sec

Title: US-10-665-658-14

Perfect score: 32

Sequence: 1 SGSTLQIS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	ID	Description
1	32	100.0	109	1 KVO1_RAT	P01681 rattus norv
2	32	100.0	294	2 Q4HCC8_9DEIO	Q4hcc8 delnoccus
3	32	100.0	690	2 Q757S8_ASHGO	Q757s8 ashya goss
4	30	93.8	361	2 Q6DRCS_XENIA	Q6drcs xenopus lae
5	30	93.8	371	2 Q5BK12_XENTR	Q5bk12 xenopus tro
6	29	90.6	144	2 Q7XC80_ORYSA	Q7xc80 oryza sativ
7	29	90.6	144	2 Q8SB90_ORYSA	Q8sb90 oryza sativ
8	29	90.6	197	2 Q57FL6_BRUBA	Q57fl6 bruceella ab
9	29	90.6	197	2 Q8G2Z7_BRUBA	Q8g2z7 bruceella ab
10	29	90.6	197	2 Q8YEU0_BRUBA	Q8yeu0 bruceella me
11	29	90.6	219	2 Q9L0H5_STRCO	Q9l0h5 streptomyce
12	29	90.6	292	2 Q739H5_BACCI	Q739h5 bacillus ce
13	29	90.6	347	2 Q9HXJ3_PSEAE	Q9hxj3 pseudomonas
14	29	90.6	355	2 Q7PZD1_ANOGA	Q7pzd1 anopheles g
15	29	90.6	372	2 Q6ACF0_LEIXX	Q6acf0 leishmania x
16	29	90.6	378	2 Q4P349_USTMA	Q4p349 ustilago ma
17	29	90.6	406	2 Q51CUE_ENTHI	Q51cue entamoeba h
18	29	90.6	419	1 INXS_DROME	Q9vw15 drosophila
19	29	90.6	438	2 Q6BCG8_EDMIC	Q6bcg8 edwardsiella
20	29	90.6	448	2 Q4KYN6_PECPC	Q4kyn6 peccinatus
21	29	90.6	481	2 Q7SEK3_ASHGO	Q7sek3 ashya goss
22	29	90.6	530	2 Q4SIO6_TETNG	Q4sio6 tetraodon n
23	29	90.6	609	1 GUP2_YEAST	Q08929 saccharomyc
24	29	90.6	613	2 Q23266_CAEEL	Q23266 caenorhabdi
25	29	90.6	672	1 NGRI_YEAST	P32831 saccharomyc
26	29	90.6	680	2 Q623A3_CABER	Q623a3 caenorhabdi
27	29	90.6	757	2 Q4WAD5_ASPRU	Q4wad5 aspergillus
28	29	90.6	802	2 Q6FMW2_CANCA	Q6fmw2 candida gla
29	29	90.6	879	2 Q4J6T1_SULAC	Q4j6t1 sulfolobus
30	29	90.6	927	2 Q4HYT6_GIBZE	Q4hyt6 gibberella
31	29	90.6	1117	2 Q9H5J5_HUMAN	Q9h5j5 homo sapien

32	29	90.6	1221	2 Q4RL32_TETNG	Q4rl32 tetraodon n
33	29	90.6	1254	2 Q9NSU4_HUMAN	Q9nsl4 homo sapien
34	29	90.6	1558	2 Q9UPN5_HUMAN	Q9upn5 homo sapien
35	29	90.6	1568	2 Q5MZM5_SYNP6	Q5mzm5 synchococc
36	29	90.6	2369	2 Q5TA12_HUMAN	Q5tal2 homo sapien
37	29	90.6	6735	2 Q4QHGS_LEIMA	Q4qhg5 leishmania
38	28	87.5	37	2 Q9CUZ6_MOUSE	Q9cu26 mus musculu
39	28	87.5	92	2 Q5DMT8_9ROSI	Q5dm8 petalodiscu
40	28	87.5	114	2 Q39765_GINBI	Q39765 ginkgo blio
41	28	87.5	168	2 Q6ZP90_HUMAN	Q6z90 homo sapien
42	28	87.5	171	2 Q9CHH7_LACLA	Q9chh7 lactococcu
43	28	87.5	182	2 Q9PD01_ERWST	Q9pd01 erwinia ste
44	28	87.5	186	2 Q9WZ21_DROME	Q9wz21 drosophila
45	28	87.5	193	2 Q5DMX1_9ROSI	Q5dmx1 nemecetia p
46	28	87.5	200	2 Q4VMK1_9ROSI	Q4vmk1 reverchonla
47	28	87.5	206	2 Q5DMZ7_9ROSI	Q5dmz7 gonatogyne
48	28	87.5	221	2 Q5DMY7_9ROSI	Q5dm7 petalodiscu
49	28	87.5	223	2 Q5DN10_9ROSI	Q5dn10 baccaurea j
50	28	87.5	224	2 Q5DMY6_9ROSI	Q5dm6 petalodiscu
51	28	87.5	224	2 Q5DMY9_9ROSI	Q5dm9 petalodiscu
52	28	87.5	232	2 Q991H6_MOUSE	Q991h6 mus musculu
53	28	87.5	235	2 Q609S4_METCA	Q609s4 methylococc
54	28	87.5	275	1 BTUF_PHOIL	Q7842 photorhabdu
55	28	87.5	275	1 Q7S5B1_NEUCR	Q7s5b1 neurospora
56	28	87.5	283	2 Q6EPA2_ORYSA	Q6epa2 oryza sativ
57	28	87.5	302	2 Q4S64_TETNG	Q4s64 tetraodon n
58	28	87.5	318	2 Q8VFT1_MOUSE	Q8vft1 mus musculu
59	28	87.5	352	2 Q6AG46_LEIXX	Q6ag46 leifsonia x
60	28	87.5	362	2 Q6CY06_KLUYA	Q6cy06 kluyveromyc
61	28	87.5	366	2 Q4RYP5_TETNG	Q4ryf5 tetraodon n
62	28	87.5	368	2 Q6KCD3_PARUM	Q6mcd3 parachlamy
63	28	87.5	378	2 Q4ANA73_9M1CC	Q4ana73 artirobacte
64	28	87.5	391	2 Q6TBC1_9ROSI	Q6tbc1 micranthem
65	28	87.5	391	2 Q6TBD5_9ROSI	Q6tbd5 elatine tri
66	28	87.5	397	2 Q6TBD6_9ROSI	Q6tbd6 elatine tri
67	28	87.5	397	2 Q5SRC9_CRYNE	Q5src9 cryptococcu
68	28	87.5	397	2 Q5KEU2_CRYNE	Q5keu2 cryptococcu
69	28	87.5	411	2 Q6WJ00_CHICK	Q6wj00 gallus gall
70	28	87.5	419	2 Q07795_SORBI	Q07795 sorghum bic
71	28	87.5	425	2 Q83C11_COXBI	Q83c11 coxella bu
72	28	87.5	435	2 Q17643_CAEEL	Q17643 caenorhabdi
73	28	87.5	444	2 Q84M63_ORYSA	Q84m63 oryza sativ
74	28	87.5	454	2 Q5NKR9_CANAL	Q5nkr9 candida alb
75	28	87.5	461	2 Q5BJ21_BRARE	Q5bj21 brachydanio
76	28	87.5	462	2 Q4RZP1_TETNG	Q4rzp1 tetraodon n
77	28	87.5	468	2 Q6P941_BRARE	Q6p941 brachydanio
78	28	87.5	488	2 Q9GP14_IXORI	Q9gp14 ixodes ricci
79	28	87.5	518	2 Q6P121_BRARE	Q6p121 brachydanio
80	28	87.5	524	2 Q8YS23_ANASP	Q8y23 anabaena ep
81	28	87.5	530	2 Q9UZW3_PYPAB	Q9uzw3 pyrococcu
82	28	87.5	534	2 Q6A051_DESPS	Q6a51 desulfotale
83	28	87.5	542	2 Q754S5_ASHGO	Q754s5 ashya goss
84	28	87.5	548	2 Q8AVJ3_XENIA	Q8avj3 xenopus lae
85	28	87.5	548	2 Q5BL72_XENTR	Q5bl72 xenopus tro
86	28	87.5	549	1 FZD7_XENIA	Q9upk8 xenopus lae
87	28	87.5	550	2 Q9K3U9_STRCO	Q9k3u9 streptomyce
88	28	87.5	553	2 Q4T738_TETNG	Q4t738 tetraodon n
89	28	87.5	556	2 Q7ZU08_BRARE	Q7zu08 brachydanio
90	28	87.5	557	2 Q8QFM3_BRARE	Q8qfm3 brachydanio
91	28	87.5	559	2 Q90T73_BRARE	Q90t73 brachydanio
92	28	87.5	559	2 Q98S12_BRARE	Q98s12 brachydanio
93	28	87.5	559	2 Q6NV44_BRARE	Q6nv44 brachydanio
94	28	87.5	559	2 Q7SZR7_BRARE	Q7szr7 gallus gall
95	28	87.5	567	1 FZD7_CHICK	Q57329 gallus gall
96	28	87.5	572	1 FZD7_MOUSE	Q6190 mus musculu
97	28	87.5	572	2 Q6P551_MOUSE	Q6p551 mus musculu
98	28	87.5	574	1 FZD7_HUMAN	Q6584 homo sapien
99	28	87.5	574	2 Q53S59_HUMAN	Q73589 homo sapien
100	28	87.5	612	2 Q51NY4_MAGGR	Q51ny4 magnaporthe
101	28	87.5	618	2 Q4RLB9_MAGGR	Q4rlb9 magnaporthe
102	28	87.5	624	2 Q94487_SCHPO	Q94487 schizosacch
103	28	87.5	639	2 Q5LNU8_SILPO	Q5lnu8 silicibacte
104	28	87.5	642	2 Q4WG54_ASPFU	Q4wg54 aspergillus

105	28	87.5	713	2	Q8T008_DROME	Q8T008_drosophila	178	27	84.4	182	2	003033_9CARY	003033_silene scha
106	28	87.5	722	2	Q551v5_DICTDI	Q551v5_dictyosteli	179	27	84.4	182	2	003036_9CARY	003036_sarcobatus
107	28	87.5	722	2	Q7KMS7_DICTDI	Q7KMS7_dictyosteli	180	27	84.4	182	2	003039_TETRT	003039_tetragona
108	28	87.5	725	2	Q4IRU0_GIBZE	Q4IRU0_gibberella	181	27	84.4	182	2	003011_MIRNY	003011_mirabilis n
109	28	87.5	732	2	Q9V5N4_DROME	Q9V5N4_drosophila	182	27	84.4	182	2	003013_MOLVE	003013_mollugo ver
110	28	87.5	750	2	Q810L8_MOUSE	Q810L8_mus musculus	183	27	84.4	184	2	003016_PRYAM	003016_pyrolaccas
111	28	87.5	762	2	Q9E293_ZYMMO	Q9E293_zymomonas m	184	27	84.4	187	2	Q4ZWJ3_PESTY	Q4ZWJ3_pseudomonas
112	28	87.5	763	2	Q5NM05_ZYMMO	Q5NM05_zymomonas m	185	27	84.4	189	2	Q4SM03_TETNG	Q4SM03_tetradodon n
113	28	87.5	798	2	Q8BXJ4_MOUSE	Q8BXJ4_m mus muscu	186	27	84.4	204	2	Q8XMK3_CLOPE	Q8XMK3_clostridium
114	28	87.5	798	2	Q8BFX2_MOUSE	Q8BFX2_m mus muscu	187	27	84.4	219	2	Q8NCK5_HUMAN	Q8NCK5_homo sapien
115	28	87.5	834	2	Q8GZ96_ARATH	Q8GZ96_arabidopsis	188	27	84.4	239	2	Q8BAD9_PESSE	Q8BAD9_pseudomonas
116	28	87.5	869	2	Q8PQ99_XANAC	Q8PQ99_xanthomonas	189	27	84.4	242	2	Q4Q8N5_LEIMA	Q4Q8N5_leishmania
117	28	87.5	873	2	Q9C548_ARATH	Q9C548_arabidopsis	190	27	84.4	244	2	Q4WAT3_ASPFU	Q4WAT3_aspergillus
118	28	87.5	884	2	Q5A9W9_CANAL	Q5A9W9_candida alb	191	27	84.4	280	1	BRUP_YERPE	Q8abm1_yersinia ps
119	28	87.5	888	2	Q552L1_DICTDI	Q552L1_dictyosteli	192	27	84.4	280	1	BRUP_YERPE	Q66ee1_yersinia ps
120	28	87.5	923	1	CLAB_LYCES	P31542_lycopersico	193	27	84.4	285	2	Q66J3_XENTR	Q66fj7_xenopus tro
121	28	87.5	930	2	Q7R5C2_GIALA	Q7R5C2_giardia lam	194	27	84.4	294	1	NIRP12_ARATH	Q81fp7_arabidopsis
122	28	87.5	943	2	Q8D1P5_YERPE	Q8D1P5_yersinia pe	195	27	84.4	297	2	Q4V5R0_DROME	Q4V5R0_drosophila
123	28	87.5	952	2	Q665G1_YERPE	Q665G1_yersinia ps	196	27	84.4	299	2	Q4V5X8_DROME	Q4V5X8_drosophila
124	28	87.5	952	2	Q8ZAV9_YERPE	Q8ZAV9_yersinia pe	197	27	84.4	315	2	Q9KSP9_VIBCH	Q9KSP9_vibrio chol
125	28	87.5	963	2	Q8H935_VICFA	Q8H935_vicia faba	198	27	84.4	318	2	Q5FK77_NEIGO	Q5FK77_neisseria g
126	28	87.5	1011	2	Q8ZAV8_YERPE	Q8ZAV8_yersinia pe	199	27	84.4	318	2	Q5FAK9_NEIGL	Q5FAK9_neisseria g
127	28	87.5	1046	1	SBCCL_LACLA	Q9C4Z0_lactococcus	200	27	84.4	330	2	Q5N8G0_PRAAT	Q5n8go_franciella
128	28	87.5	1115	2	Q8CBC1_MOUSE	Q8CBC1_mus musculus	201	27	84.4	343	2	Q4XBP5_SORBI	Q4XBP5_sorghum bic
129	28	87.5	1128	2	Q80WL3_MOUSE	Q80WL3_mus musculus	202	27	84.4	357	2	Q56948_YERPE	Q56948_yersinia pe
130	28	87.5	1273	2	Q41102_GIBZE	Q41102_gibberella	203	27	84.4	357	2	Q7BTY0_YERPE	Q7BTY0_yersinia pe
131	28	87.5	1346	2	Q9V477_DROME	Q9V477_drosophila	204	27	84.4	357	2	Q57159_YERPE	Q57159_yersinia pe
132	28	87.5	1377	2	Q6RT27_DREBA	Q6RT27_debaryomye	205	27	84.4	390	2	Q821A3_STRAW	Q821A3_streptomyces
133	28	87.5	1397	2	Q9M532_DROME	Q9M532_drosophila	206	27	84.4	424	2	Q91MG9_ARATH	Q91mg9_arabidopsis
134	28	87.5	1398	2	Q77268_DROME	Q77268_drosophila	207	27	84.4	426	1	YA35_SCHPO	Q09712_schizosacch
135	28	87.5	1489	2	Q80GL4_MOUSE	Q80GL4_mus musculus	208	27	84.4	438	2	Q9VSQ4_DROME	Q9Vsq4_drosophila
136	28	87.5	1489	2	Q8QGD4_RANCA	Q8QGD4_rana catesb	209	27	84.4	462	2	Q9BAD4_BRANA	Q9bad4_brassica na
137	28	87.5	1497	2	Q80WL4_MOUSE	Q80WL4_mus musculus	210	27	84.4	470	2	Q19932_CAEEL	Q19932_cenozoabadi
138	28	87.5	1506	2	Q80WL5_MOUSE	Q80WL5_mus musculus	211	27	84.4	512	2	Q745K3_MYCPA	Q745k3_mycobacteri
139	28	87.5	1508	2	Q80M00_MOUSE	Q80M00_mus musculus	212	27	84.4	573	2	Q4QAO6_LEIMA	Q4QAO6_leishmania
140	28	87.5	1509	2	Q80WL6_MOUSE	Q80WL6_mus musculus	213	27	84.4	582	2	Q41LR8_DICTDI	Q41LR8_dictyosteli
141	28	87.5	1521	2	Q80WL7_MOUSE	Q80WL7_mus musculus	214	27	84.4	594	2	Q927F1_LISTIN	Q927F1_listeria in
142	28	87.5	1525	2	Q80WL7_MOUSE	Q80WL7_mus musculus	215	27	84.4	607	2	Q5FSD6_GIUXO	Q5FSD6_gluconobac
143	28	87.5	1528	2	Q80MML_MOUSE	Q80MML_mus musculus	216	27	84.4	612	2	Q6FOM4_CANGA	Q6fom4_candida gla
144	28	87.5	1558	2	Q6P416_MOUSE	Q6P416_mus musculus	217	27	84.4	619	2	Q8SZNO_DROME	Q8szno_drosophila
145	28	87.5	1567	2	Q80M02_MOUSE	Q80M02_mus musculus	218	27	84.4	620	2	Q9VZK3_DROME	Q9Vzk3_drosophila
146	28	87.5	1581	2	Q80U28_MOUSE	Q80U28_mus musculus	219	27	84.4	620	2	Q45720_BACTU	Q45720_bacillus th
147	28	87.5	1602	2	Q08873_RAT	Q08873_rattus norv	220	27	84.4	649	2	Q4WMG2_ASPFU	Q4Wmg2_aspergillus
148	28	87.5	1617	2	Q4MWC5_ASPFU	Q4MWC5_aspergillus	221	27	84.4	658	2	Q68FO3_RAT	Q68fO3_rattus norv
149	28	87.5	1983	2	Q57982_BRUAB	Q57982_brucella ab	222	27	84.4	663	1	TAZ1_SCHPO	P79005_schizosacch
150	28	87.5	2021	2	Q4RP83_TETNG	Q4RP83_tetradodon n	223	27	84.4	663	2	Q52D72_MAGGR	Q52d72_magnaporthe
151	28	87.5	2110	2	Q916B1_PASMU	Q916B1_pasteurella	224	27	84.4	753	2	Q52AK1_MAGGR	Q52ak1_magnaporthe
152	28	87.5	2833	2	Q8VPL1_PASMU	Q8VPL1_pasteurella	225	27	84.4	768	2	Q51ST9_MAGGR	Q51st9_magnaporthe
153	28	87.5	3392	2	Q7ZA38_ASHGO	Q7ZA38_ashbya gos	226	27	84.4	774	2	Q51Q22_MAGGR	Q51q22_magnaporthe
154	28	87.5	3392	2	Q75AD9_ASHGO	Q75AD9_ashbya gos	227	27	84.4	789	2	Q41H81_GIBZE	Q41h81_gibberella
155	28	87.5	3919	2	Q9CPH9_PASMU	Q9CPH9_pasteurella	228	27	84.4	793	2	Q6PYW7_BACTX	Q6PYW7_bacillus th
156	28	87.5	4533	2	Q9B1X3_TERTH	Q9B1X3_tetrachymena	229	27	84.4	822	2	Q9BMM6_APLCA	Q9Bmm6_apylysia cal
157	27	84.4	69	2	Q7M2Z9_BOVIN	Q7M2Z9_bos taurus	230	27	84.4	846	2	Q7MA33_MOLSU	Q7ma33_molynella s
158	27	84.4	144	2	Q4UXU4_XANCP	Q4UXU4_xanthomonas	231	27	84.4	847	2	Q4UBT8_THIBAN	Q4ubt8_theileria a
159	27	84.4	144	2	Q8P672_XANCP	Q8P672_xanthomonas	232	27	84.4	860	2	Q5RDU1_PONPY	Q5rdU1_pongo pygma
160	27	84.4	167	2	Q5OVN0_ENTHI	Q5OVN0_entomoeba h	233	27	84.4	862	1	Q5MP2_YEAST	P33567_saccharomyc
161	27	84.4	167	2	Q6POK4_BACTU	Q6POK4_bacillus th	234	27	84.4	867	2	Q5S1E1_CRYNE	Q5S1E1_cryptococcu
162	27	84.4	179	2	Q03019_PBERG	Q03019_perekskia gr	235	27	84.4	867	2	Q5K7Y0_CRYNE	Q5K7Y0_cryptococcu
163	27	84.4	179	2	Q03031_STILA	Q03031_silene laci	236	27	84.4	934	1	CR1AA_BACTS	P03369_bacillus th
164	27	84.4	182	2	Q02975_CELAR	Q02975_celosia arg	237	27	84.4	942	1	WDR22_HUMAN	Q96Jk5_homo sapien
165	27	84.4	182	2	Q02978_ANRCO	Q02978_anredera co	238	27	84.4	946	1	WDR22_MOUSE	Q80t8s_mus musculu
166	27	84.4	182	2	Q02982_9CARY	Q02982_alluandua m	239	27	84.4	1118	2	Q9AM81_BACTU	Q9am81_bacillus th
167	27	84.4	182	2	Q02986_9CARY	Q02986_bougainvill	240	27	84.4	1118	2	Q9AM82_BACTU	Q9am82_bacillus th
168	27	84.4	182	2	Q02892_9CARY	Q02892_calandrinia	241	27	84.4	1150	2	Q9AM83_BACTU	Q9am83_bacillus th
169	27	84.4	182	2	Q02893_CORLT	Q02893_cortigiosa	242	27	84.4	1150	1	CR3EA_BACTA	Q9zn19_bacillus th
170	27	84.4	182	2	Q02996_9CARY	Q02996_claytonia p	243	27	84.4	1150	1	Q71RP4_BACTU	Q71RP4_bacillus th
171	27	84.4	182	2	Q02999_9CARY	Q02999_didierea ma	244	27	84.4	1155	1	CR1AB_BACTB	P03372_bacillus th
172	27	84.4	182	2	Q03002_FROPL	Q03002_froelichia	245	27	84.4	1155	1	CR1AB_BACTB	P03370_bacillus th
173	27	84.4	182	2	Q03014_NEPAL	Q03014_nepenthes a	246	27	84.4	1155	1	CR1AB_BACTX	P03373_bacillus th
174	27	84.4	182	2	Q03017_9CARY	Q03017_peltiveria a	247	27	84.4	1155	2	Q517E3_BACTU	Q517E3_bacillus th
175	27	84.4	182	2	Q03021_POROL	Q03021_pertulica o	248	27	84.4	1155	2	Q7BE98_BACTU	Q7BE98_bacillus th
176	27	84.4	182	2	Q03024_THIHO	Q03024_thium thiho	249	27	84.4	1155	2	Q93T21_BACTU	Q93T21_bacillus th
177	27	84.4	182	2	Q03029_STEHA	Q03029_stegnoeperm	250	27	84.4	1155	2	Q9AM80_BACTU	Q9am80_bacillus th

251	27	84.4	1155	2	Q9P296_BACTU	Q9P296 bacillus th	324	25	81.2	233	2	Q64HL8_VIRU	Q64HL8 bacterioph
252	27	84.4	1156	2	Q6GUW7_BACTU	Q6GUW7 bacillus th	325	26	81.2	233	2	Q64HL7_VIRU	Q64HL7 bacterioph
253	27	84.4	1163	2	Q4PNY7_BACTU	Q4PNY7 bacillus th	326	26	81.2	233	2	Q64HL6_VIRU	Q64HL6 bacterioph
254	27	84.4	1176	1	CR1AA_BACTA	P0367 bacillus th	327	26	81.2	233	2	Q64HL5_VIRU	Q64HL5 bacterioph
255	27	84.4	1176	1	CR1AA_BACTE	P0368 bacillus th	328	26	81.2	233	2	Q9HTY5_PSEAE	Q9HTY5 pseudomonas
256	27	84.4	1176	1	CR1AA_BACTK	P0366 bacillus th	329	26	81.2	234	2	Q64HL4_VIRU	Q64HL4 bacterioph
257	27	84.4	1176	1	CR1AG_BACTK	P0365 bacillus th	330	26	81.2	235	2	Q5XBT3_STRP6	Q5XBT3 streptococ
258	27	84.4	1176	1	CR1AG_BACTU	Q95515 bacillus th	331	26	81.2	247	2	Q8PIN9_STRP8	Q8PIN9 streptococ
259	27	84.4	1176	2	Q45736_BACTU	Q7WZ27 bacillus th	332	26	81.2	253	2	Q9D1H0_MOUSE	Q9D1H0 mus musculi
260	27	84.4	1176	2	Q7WZ79_BACTU	Q7WZ27 bacillus th	333	26	81.2	256	2	Q6G741_STAAS	Q6G741 staphylococ
261	27	84.4	1176	2	Q9RC30_BACTK	Q9RC30 bacillus th	334	26	81.2	256	2	Q6GEF3_STAAR	Q6GEF3 staphylococ
262	27	84.4	1176	2	Q9S514_BACTU	Q9S514 bacillus th	335	26	81.2	256	2	Q5HDS6_STAAC	Q5HDS6 staphylococ
263	27	84.4	1180	2	Q5K629_BACTS	Q5K629 bacillus th	336	26	81.2	256	2	Q7A436_STAAN	Q7A436 staphylococ
264	27	84.4	1180	2	Q9S5V8_BACTU	Q9S5V8 bacillus th	337	26	81.2	256	2	Q8NV94_STAAN	Q8NV94 staphylococ
265	27	84.4	1183	2	Q5QXM8_BACTU	Q5QXM8 bacillus th	338	26	81.2	256	2	Q99R21_STAAM	Q99R21 staphylococ
266	27	84.4	1222	2	Q4Q115_LEIMA	Q4Q115 leishmania	339	26	81.2	259	2	Q5BBF7_EMENT	Q5BBF7 aspergillus
267	27	84.4	1294	2	Q6WLB1_9DIP1	Q6WLB1 epulonis sig	340	26	81.2	260	1	NORC_PAMNU	NORC magnaporthe
268	27	84.4	1428	2	Q4PHB5_USTMA	Q4PHB5 ustilago ma	341	26	81.2	263	2	Q5ZEF8_MAGGR	Q5ZEF8 schizosacch
269	27	84.4	1453	2	Q4P4W1_USTMA	Q4P4W1 ustilago ma	342	26	81.2	269	2	Q8HMZ1_SCHUP	Q8HMZ1 shigella fl
270	27	84.4	1691	2	Q4QAH8_LEIMA	Q4QAH8 leishmania	343	26	81.2	285	2	Q83R44_SHIFL	Q83R44 pseudomonas
271	27	84.4	2020	2	Q8ST27_DICDI	Q8ST27 dictyosteli	344	26	81.2	285	2	Q8BAH0_PSEBM	Q8BAH0 mus musculi
272	27	84.4	2185	2	Q8W6J4_9CAUD	Q8W6J4 sinorhizobi	345	26	81.2	291	2	Q7TPZ5_MOUSE	Q7TPZ5 staphylococ
273	27	84.4	2223	1	YCF2_STILA	Q589A6 silene lari	346	26	81.2	292	2	Q63C87_BACGZ	Q63C87 bacillus th
274	27	84.4	2275	1	Q8TSE8_METAC	Q8TSE8 mechanosarc	347	26	81.2	292	2	Q6HJP8_BACHK	Q6HJP8 bacillus th
275	27	84.4	2280	1	YCF2_OENHO	Q9MEF2 oenothera h	348	26	81.2	296	2	Q81R05_BACAN	Q81R05 bacillus an
276	27	84.4	2280	1	YCF2_TOBAC	P09976 nicotiana t	349	26	81.2	297	2	Q7NL96_GLOVI	Q7NL96 gloeobacter
277	27	84.4	2291	1	YCF2A_ATRBE	Q088V2 atropa bell	350	26	81.2	307	2	Q4HR22_CAMUP	Q4HR22 campylobact
278	27	84.4	2291	1	YCF2B_ATRBE	Q888U1 atropa bell	351	26	81.2	299	1	HIS1_CAMUR	HIS1 campylobact
279	27	84.4	2291	1	YCF2_ARATH	P56786 arabidopsis	352	26	81.2	299	1	Q4HDJ9_CAMCO	Q4HDJ9 campylobact
280	27	84.4	2298	1	YCF2_LOTUA	Q9D1K6 locus japon	353	26	81.2	301	2	Q9PT05_ARATH	Q9PT05 arabidopsis
281	27	84.4	3071	2	Q54CF8_DICDI	Q54CF8 dictyosteli	354	26	81.2	307	2	Q4S236_TETNG	Q4S236 tetradodon n
282	27	84.4	4654	2	Q8D418_VIBUV	Q8D418 vibrio vuln	355	26	81.2	308	2	Q5TQ66_ANOGA	Q5TQ66 anopheles g
283	27	84.4	4656	2	Q7WFI9_VIEBV	Q7WFI9 vibrio vuln	356	26	81.2	310	1	LACC_STAAM	LACC_STAAM staphylococ
284	27	84.4	4936	2	Q6D5C2_ERMCK	Q6D5C2 erwinia car	357	26	81.2	310	1	LACC_STAAM	LACC_STAAM staphylococ
285	27	84.4	7317	2	Q4PMA4_9RICK	Q4PMA4 candidatus	358	26	81.2	310	1	LACC_STAAR	LACC_STAAR staphylococ
286	26	81.2	39	2	Q7JGX4_WOLPM	Q7JGX4 wolbachia p	359	26	81.2	310	1	LACC_STAAS	LACC_STAAS staphylococ
287	26	81.2	88	2	Q71XZ4_LISMF	Q71XZ4 listeria mo	360	26	81.2	310	1	LACC_STAUV	LACC_STAUV staphylococ
288	26	81.2	89	2	Q9HPK5_HALSA	Q9HPK5 halobacteri	361	26	81.2	310	1	IACC_STAAM	IACC_STAAM staphylococ
289	26	81.2	105	2	Q8KUM4_SYMP7	Q8KUM4 synecchococ	362	26	81.2	310	1	Q5HE12_STPAC	Q5HE12 staphylococ
290	26	81.2	107	2	Q6YV07_ORYSA	Q6YV07 oryza activ	363	26	81.2	310	2	Q7R7R0_PLAYO	Q7R7R0 plasmodium
291	26	81.2	110	2	Q7UGH2_RHOBA	Q7UGH2 rhodospirell	364	26	81.2	311	2	Q9JW23_PLAYO	Q9JW23 neisseria m
292	26	81.2	145	2	Q59X69_CANAL	Q59X69 candida alb	365	26	81.2	318	2	Q5JW23_NEIMA	Q5JW23 neisseria m
293	26	81.2	145	2	Q59XB7_CANAL	P43211 candida alb	366	26	81.2	319	1	C0U06_HUMAN	C0U06 homo sapien
294	26	81.2	158	1	MAL11_MALDO	Q65200 pyrus commu	367	26	81.2	320	1	Q53FD2_HUMAN	Q53FD2 homo sapien
295	26	81.2	159	1	PYRC1_PYRGO	Q941P6 malus domes	368	26	81.2	327	2	UPPP_ANASP	UPPP ANASP yarrowia li
296	26	81.2	159	2	Q941P6_MALDO	Q941P6 malus domes	369	26	81.2	327	2	Q6CCG5_YARLI	Q6CCG5 yarrowia li
297	26	81.2	159	2	Q9S1V2_MALDO	Q9S1V2 malus domes	370	26	81.2	329	2	Q7RK10_PLAYO	Q7RK10 plasmodium
298	26	81.2	159	2	Q9S1V5_MALDO	Q9S1V5 malus domes	371	26	81.2	332	2	Q6FRS3_CORER	Q6FRS3 coxynabacte
299	26	81.2	159	2	Q9S1V6_MALDO	Q9S1V6 malus domes	372	26	81.2	335	2	Q6VH06_MOUSE	Q6VH06 mus musculi
300	26	81.2	159	2	Q9S1V7_MALDO	Q9S1V7 malus domes	373	26	81.2	335	2	Q6JZN9_MOUSE	Q6JZN9 mus musculi
301	26	81.2	159	2	Q9S1V8_MALDO	Q9S1V8 malus domes	374	26	81.2	338	2	Q6FDJ5_ACTIAD	Q6FDJ5 actinobact
302	26	81.2	159	2	Q9S1V3_MALDO	Q9S1V3 malus domes	375	26	81.2	342	2	Q8L999_ARATH	Q8L999 arabidopsis
303	26	81.2	162	2	Q5WDM3_BACHD	Q5WDM3 bacillus ci	376	26	81.2	342	2	Q8YL34_ANASP	Q8YL34 anabaena sp
304	26	81.2	172	2	Q9KRU7_BACHD	Q9KRU7 bacillus ha	377	26	81.2	346	2	Q7Q2K5_ANOGA	Q7Q2K5 anopheles g
305	26	81.2	176	2	Q5OYU8_ENTHI	Q5OYU8 entamoeba h	378	26	81.2	350	2	Q6DUF0_XENTH1	Q6DUF0 xenopus lae
306	26	81.2	191	2	Q5OYU4_ENTHI	Q5OYU4 entamoeba h	379	26	81.2	352	1	Q4TR71_SEPHN	Q4TR71 erythrobact
307	26	81.2	191	2	Q6VDU2_9HBP	Q6VDU2 hepatitis c	380	26	81.2	351	2	Q8PIY4_ECOL6	Q8PIY4 escherichia
308	26	81.2	192	2	Q7JUL4_9CAUD	Q7JUL4 bacterioph	381	26	81.2	358	2	Q8EAK6_SHEON	Q8EAK6 shewanella
309	26	81.2	192	2	Q9AZQ9_VIRU	Q9AZQ9 lactococcus	382	26	81.2	369	2	Q8L7M2_ARATH	Q8L7M2 arabidopsis
310	26	81.2	192	2	Q9CIC7_LACTA	Q9CIC7 lactococcus	383	26	81.2	372	2	Q8TWC1_METKA	Q8TWC1 methanopyru
311	26	81.2	195	2	Q9JXU7_NEIMB	Q9JXU7 neisseria m	384	26	81.2	374	2	Q8UKD2_AGRTS	Q8UKD2 agrobacteri
312	26	81.2	199	1	SCPB_LACPE	Q88YU8 lactobacill	385	26	81.2	381	2	Q4JMP2_9PACT	Q4JMP2 uncultured
313	26	81.2	202	2	Q73ME9_TREDE	Q73ME9 triponema d	386	26	81.2	384	2	Q9SUZ9_ARATH	Q9SUZ9 arabidopsis
314	26	81.2	203	2	Q5O1T9_BRABE	Q5O1T9 brachydanio	387	26	81.2	409	2	Q9M2M8_ARATH	Q9M2M8 arabidopsis
315	26	81.2	204	2	Q864T3_SHEEP	Q864T3 ovis aries	388	26	81.2	411	2	Q9R1P9_STRNO	Q9R1P9 streptomyce
316	26	81.2	205	2	Q8MKC4_SHEEP	Q8MKC4 ovis aries	389	26	81.2	412	2	Q7U894_SYNFX	Q7U894 synecchococ
317	26	81.2	205	2	Q5GTD5_WOLTR	Q5GTD5 wolbachia s	390	26	81.2	423	2	Q89NY7_BRABA	Q89NY7 bradyrhizob
318	26	81.2	206	2	Q8TJH1_METAC	Q8TJH1 mechanosarc	391	26	81.2	426	2	Q55082_MOUSE	Q55082 mus musculi
319	26	81.2	207	2	Q8MTM3_BRABE	Q8MTM3 brachydanio	392	26	81.2	436	2	Q9BYG6_HUMAN	Q9BYG6 homo sapien
320	26	81.2	214	2	Q5XJ71_BRABE	Q5XJ71 brachydanio	393	26	81.2	436	2	Q9JN12_ARATH	Q9JN12 arabidopsis
321	26	81.2	218	2	Q8TKA3_METAC	Q8TKA3 mechanosarc	394	26	81.2	438	2	Q9V319_DROME	Q9V319 drosophila
322	26	81.2	218	2	Q4KL20_MOUSE	Q4KL20 mus musculi	395	26	81.2	441	2	Q7D3P6_AGRTS	Q7D3P6 agrobacteri
323	26	81.2	233	2	Q64HL9_VIRU	Q64HL9 bacterioph	396	26	81.2	441	2		

397	26	81.2	442	2	Q4HW3_GIBZE	470	26	81.2	663	2	Q4IIJ3_GIBZE	Q4IIJ3_gibberella
398	26	81.2	443	2	Q5NFJ6_FRATY	471	26	81.2	666	2	Q6XM06_9PHYC	Q6xm06_feldmannia
399	26	81.2	454	2	Q67IUI_ORYSA	472	26	81.2	671	2	Q7ODI6_ANOGA	Q7od16_anopheles
400	26	81.2	465	2	Q9UIJ3_CABEU	473	26	81.2	673	2	Q4MPR8_ASPFU	Q4mpR8_aspergillus
401	26	81.2	467	2	Q6OM0C_CABER	474	26	81.2	680	2	Q9N9G7_9ASCI	Q9n9G7_phallusia m
402	26	81.2	467	2	Q5VR7S_ORYSA	475	26	81.2	687	2	Q4SMW1_TETNG	Q4smW1_tetradon n
403	26	81.2	474	2	Q4KLE2_XENLA	476	26	81.2	702	2	Q7QWT7_GITALA	Q7qwt7_giardia lam
404	26	81.2	479	2	Q4KLE2_XENLA	477	26	81.2	705	2	Q4QBC0_LEIMA	Q4qbc0_leishmania
405	26	81.2	480	1	YAAO_BACSU	478	26	81.2	706	2	Q5K1R8_CRYNE	Q5k1R8_cryptococcu
406	26	81.2	482	2	Q9C5H0_ARATH	479	26	81.2	707	2	Q5KCY1_CRYNE	Q5kcy1_cryptococcu
407	26	81.2	482	2	Q9C9M8_ARATH	480	26	81.2	707	2	Q4WV54_ASPFU	Q4wv54_caulobacter
408	26	81.2	483	2	Q9Z170_PSEST	481	26	81.2	713	2	Q9A472_CANCR	Q9a472_caulobacter
409	26	81.2	483	2	Q5ZMF7_CHICK	482	26	81.2	716	2	Q7PGN8_ANOGA	Q7pgn8_anopheles
410	26	81.2	487	2	Q9M343_ARATH	483	26	81.2	738	2	Q6NAX1_RHOPA	Q6nax1_rhodopseido
411	26	81.2	491	2	Q9M343_ARATH	484	26	81.2	739	2	Q90ZL7_BRARE	Q90zL7_brachydanio
412	26	81.2	504	2	Q71631_9HIV1	485	26	81.2	739	2	Q9YHZ4_BRARE	Q9yhz4_brachydanio
413	26	81.2	504	2	Q9A8F5_CANCR	486	26	81.2	739	2	Q502S0_BRARE	Q502s0_brachydanio
414	26	81.2	504	2	Q71394_9HIV1	487	26	81.2	748	2	Q9SKR5_ARATH	Q9skR5_arabidopsis
415	26	81.2	521	2	Q9S2N5_ARATH	488	26	81.2	753	2	Q6PUC1_ANOGA	Q6puc1_anopheles
416	26	81.2	522	2	Q7NG65_GLOVI	489	26	81.2	756	2	Q82TY2_NITEU	Q82ty2_nitrososoma
417	26	81.2	524	2	Q6NG59_CORDI	490	26	81.2	758	2	Q5AKM6_CANAL	Q5akM6_candida alb
418	26	81.2	525	2	Q6BNX0_MOUSE	491	26	81.2	763	2	Q4WYG4_ASPFU	Q4wYg4_aspergillus
419	26	81.2	528	2	Q6NRF1_CORDI	492	26	81.2	765	2	Q4H2R8_GIBZE	Q4h2R8_gibberella
420	26	81.2	533	2	Q6E1R9_XENLA	493	26	81.2	766	2	Q9J177_ARATH	Q9j177_arabidopsis
421	26	81.2	534	1	Q5GVK0_XANOR	494	26	81.2	777	2	Q9P939_SCHCO	Q9p939_schizopyll
422	26	81.2	536	2	Q6AF37_LERIX	495	26	81.2	778	2	Q86L41_DICDI	Q86l41_dicystostei
423	26	81.2	540	2	Q6AF37_LERIX	496	26	81.2	792	2	P71414_HALSA	P71414_halobacteri
424	26	81.2	545	2	Q9U3Z2_HYDAT	497	26	81.2	795	2	Q53N63_ORYSA	Q53n63_oryza sativ
425	26	81.2	545	2	Q81I18_MOUSE	498	26	81.2	797	2	Q59UQ3_CANAL	Q59uQ3_candida alb
426	26	81.2	547	2	Q4S513_TETNG	499	26	81.2	805	2	Q9P930_HALSA	Q9p930_halobacteri
427	26	81.2	549	2	Q9KLF8_VIBCH	500	26	81.2	810	2	Q4S6H1_TETNG	Q4s6H1_tetradon n
428	26	81.2	549	2	Q9W639_XENLA	501	26	81.2	812	2	Q51R86_MAGCR	Q51r86_magnaporthe
429	26	81.2	551	1	Q9W639_XENLA	502	26	81.2	812	2	Q86VU3_HUMAN	Q86vU3_homo sapien
430	26	81.2	551	1	Q6GTP6_MOUSE	503	26	81.2	814	2	Q8GGG0_9FUSO	Q8ggG0_fusobacteri
431	26	81.2	552	1	SMAD4_HUMAN	504	26	81.2	815	2	Q6C5W6_YARLI	Q6c5W6_yarrowia li
432	26	81.2	552	1	SMAD4_PIG	505	26	81.2	819	1	MAK2_HUMAN	MAK2_homo sapien
433	26	81.2	552	1	SMAD4_PIG	506	26	81.2	821	1	MAK2_MOUSE	MAK2_mouse
434	26	81.2	552	1	Q8WMS1_MUSVI	507	26	81.2	827	2	Q8BWO6_MOUSE	Q8bW06_mouse
435	26	81.2	556	2	Q5UQH6_MIMIV	508	26	81.2	827	2	Q8BJ70_MOUSE	Q8bj70_mouse
436	26	81.2	559	2	Q7USY0_RHOBA	509	26	81.2	840	2	Q8JXG2_HPBVO	Q8jxG2_hepatitis b
437	26	81.2	561	2	Q876R0_NEUPA	510	26	81.2	841	2	Q8R2U9_MOUSE	Q8r2U9_mouse
438	26	81.2	563	2	Q81OF1_DROME	511	26	81.2	843	2	Q5DNM7_HPBVO	Q5dNm7_hepatitis b
439	26	81.2	564	2	Q5S941_DICDI	512	26	81.2	843	2	Q8B6N0_HPBVO	Q8b6N0_hepatitis b
440	26	81.2	566	2	Q6NEP7_CORDI	513	26	81.2	843	2	Q8B6N6_HPBVO	Q8b6N6_hepatitis b
441	26	81.2	581	2	Q7R120_GITALA	514	26	81.2	843	2	Q8JMY7_HPBVO	Q8jmy7_hepatitis b
442	26	81.2	584	2	Q4N907_THERA	515	26	81.2	843	2	Q8JMY7_HPBVO	Q8jmy7_hepatitis b
443	26	81.2	587	2	Q9VHU6_DROME	516	26	81.2	843	2	Q8JMY7_HPBVO	Q8jmy7_hepatitis b
444	26	81.2	587	2	Q6DCG7_XENLA	517	26	81.2	843	2	Q8JMY7_HPBVO	Q8jmy7_hepatitis b
445	26	81.2	590	2	Q8Y3Y8_LISMO	518	26	81.2	843	2	Q8JMY7_HPBVO	Q8jmy7_hepatitis b
446	26	81.2	591	2	Q71W81_LISMP	519	26	81.2	844	2	Q565W1_9BACT	Q565w1_uncultured
447	26	81.2	591	2	Q58EP7_BRARE	520	26	81.2	855	2	Q9SYU9_ARATH	Q9syU9_arabidopsis
448	26	81.2	592	1	HYTB_PSESN	521	26	81.2	865	2	Q8BP62_ARATH	Q8bp62_arabidopsis
449	26	81.2	595	2	Q6GN80_XENLA	522	26	81.2	865	2	Q8BR72_MOUSE	Q8br72_mouse
450	26	81.2	601	2	Q7RU99_NEUCR	523	26	81.2	867	2	Q8VYD4_ARATH	Q8vyD4_arabidopsis
451	26	81.2	607	2	Q73HG5_WOLPM	524	26	81.2	872	2	Q9HCQ4_HUMAN	Q9hcQ4_homo sapien
452	26	81.2	608	2	Q73IA7_WOLPM	525	26	81.2	876	2	Q7PBJ4_RICSI	Q7pbJ4_rickettsia
453	26	81.2	612	2	Q9JMM7_9RICK	526	26	81.2	879	2	Q5U777_CRYNE	Q5u777_cryptococcu
454	26	81.2	610	2	Q9JMM7_9RICK	527	26	81.2	879	2	Q5U777_CRYNE	Q5u777_cryptococcu
455	26	81.2	611	2	Q9JMM7_9RICK	528	26	81.2	887	2	Q5V7F4_HALMA	Q5v7F4_haloarcula
456	26	81.2	612	1	PEXS_YEAST	529	26	81.2	891	2	Q2T1E6_RICCN	Q2t1E6_rickettsia
457	26	81.2	615	2	Q4X093_ASPFU	530	26	81.2	896	2	Q8TEH3_HUMAN	Q8teh3_homo sapien
458	26	81.2	616	2	Q4WUG1_ASPFU	531	26	81.2	897	2	Q4P5F7_USTMA	Q4p5F7_ustilago ma
459	26	81.2	617	2	Q5ARB9_EMMENI	532	26	81.2	902	2	Q7QRY4_GITALA	Q7qry4_giardia lam
460	26	81.2	634	2	Q54UJ4_DICDI	533	26	81.2	910	2	Q750U5_ASHGO	Q750u5_ashbya gos
461	26	81.2	634	2	Q54UJ4_DICDI	534	26	81.2	912	2	Q875V7_SACCA	Q875v7_saccharomyc
462	26	81.2	641	2	Q7RMRI_NEUCR	535	26	81.2	929	2	Q4ILU7_GIBZE	Q4ilU7_gibberella
463	26	81.2	643	2	Q5FMO1_XENLA	536	26	81.2	949	2	Q4PBD4_USTMA	Q4pbd4_ustilago ma
464	26	81.2	643	2	Q6M907_NEUCR	537	26	81.2	956	2	Q57YC3_PTRYP	Q57yc3_trypanosoma
465	26	81.2	648	2	Q8KMA3_9RHOA	538	26	81.2	970	2	Q86IM2_DICDI	Q86im2_dicystostei
466	26	81.2	648	2	P74899_THETH	539	26	81.2	970	2	Q8BDY17_STRAS	Q8bdY17_streptococc
467	26	81.2	652	2	Q5S1T6_THETH	540	26	81.2	975	2	Q9XTL6_CABER	Q9xtL6_caenorhabdi
468	26	81.2	652	2	Q72J67_THETH	541	26	81.2	995	2	Q6MLI1_BBABA	Q6mLI1_belliovibri
469	26	81.2	654	2	Q8N4A3_HUMAN	542	26	81.2	997	2	Q756Y1_ASHGO	Q756y1_ashbya gos

543	26	81.2	1000	2	Q8CET8_MOUSE	Q8cet8 mus musculus	616	25	78.1	71	2	Q5W3F1_9ZZZZ	Q5w3f1 plasmodi pb3
544	26	81.2	1009	2	Q5WVFO_HUMAN	Q5wvf0 homo sapien	617	25	78.1	72	1	YVDD_VACCC	P88478 vaccinia vi
545	26	81.2	1012	2	Q9LKKZ4_SOYBN	Q9lkkz4 glycine max	618	25	78.1	72	1	YVDD_VACCV	P88478 vaccinia vi
546	26	81.2	1012	2	Q9LKKZ5_SOYBN	Q9lkkz5 glycine max	619	25	78.1	72	2	Q77TK0_VACCT	Q77tk0 vaccinia vi
547	26	81.2	1020	2	Q4P7N6_USTMA	Q4p7n6 ustilago ma	620	25	78.1	72	2	Q8QO49_CAMPS	Q8qq49 camelpox vi
548	26	81.2	1033	2	Q4V0E4_XANCP	Q4v0e4 xanthomonas	621	25	78.1	82	1	YLGN_LACIA	Y00571 lactococcus
549	26	81.2	1055	2	Q4WTD9_ASPFU	Q4wtd9 aspergillus	622	25	78.1	85	1	RL31E_VIBCH	Q9ktm4 vibrio chol
550	26	81.2	1055	2	Q4WM62_ASPFU	Q4wm62 aspergillus	623	25	78.1	86	1	RL31B_VIBVU	Q8dbh7 vibrio vuln
551	26	81.2	1084	2	Q556B3_DICDI	Q556b3 dictyostell	624	25	78.1	88	2	RL31B_VIBVU	Q7mle7 vibrio vuln
552	26	81.2	1092	2	Q54099_STREO	Q54099 streptococc	625	25	78.1	88	1	Q50T75_ENTHI	Q50tt5 entamoeba h
553	26	81.2	1115	2	Q5CUA9_CRYPV	Q5cu99 cryptococci	626	25	78.1	104	2	Q6EQO4_ORYSA	Q6eqq4 oryza sativ
554	26	81.2	1117	2	Q53971_STRDY	Q53971 streptococc	627	25	78.1	104	2	Q74692_SACPS	Q74692 saccharomy
555	26	81.2	1161	2	Q692G5_MOUSE	Q692g5 mus musculu	628	25	78.1	109	2	Q5OUN8_ENTHI	Q5oun8 entamoeba h
556	26	81.2	1215	2	Q4H2P2_CIOIN	Q4h2p2 ciona inte	629	25	78.1	109	2	Q54935_STREN	Q54935 streptoc
557	26	81.2	1216	2	Q9C276_NEUCR	Q9c276 neurospora	630	25	78.1	109	2	Q82PL7_STRAM	Q82pl7 streptomy
558	26	81.2	1254	2	Q6FJW6_CANGA	Q6fjw6 candida gla	631	25	78.1	111	2	Q9YH05_MOUSE	Q9yhq6 giinglymoeto
559	26	81.2	1266	2	Q9WJG0_DROME	Q9wjg0 drosophila	632	25	78.1	111	2	Q9CX15_MOUSE	Q9cx15 mus musculu
560	26	81.2	1297	2	Q4WQV3_ASPFU	Q4wqv3 aspergillus	633	25	78.1	113	2	Q75CG5_ASHGO	Q75cgs ashbya gos
561	26	81.2	1310	2	Q8B473_STRAS	Q8b473 streptococc	634	25	78.1	114	2	Q5ASU9_EMENI	Q5asu9 aspergillus
562	26	81.2	1324	2	Q8MMQ2_DICDI	Q8mmq2 dictyostell	635	25	78.1	114	2	Q511Z3_ENTHI	Q511z3 entamoeba h
563	26	81.2	1351	2	Q6GDB9_STRAR	Q6gdb9 staphylococ	636	25	78.1	124	2	Q4TCNO_TETNG	Q4tcno tetradon n
564	26	81.2	1363	2	Q9F5K8_RHOSH	Q9f5k8 rhodobacter	637	25	78.1	126	2	Q83TL6_SHIDY	Q83tl6 shigella dy
565	26	81.2	1381	2	Q83V14_VIBCH	Q83v14 vibrio chol	638	25	78.1	127	2	Q83TL7_SHIBO	Q83tl7 shigella bo
566	26	81.2	1439	2	Q4PEF4_USTMA	Q4pef4 ustilago ma	639	25	78.1	127	2	Q83UA8_SHIBO	Q83ua8 shigella bo
567	26	81.2	1458	2	Q9VX48_DROME	Q9vx48 drosophila	640	25	78.1	127	2	Q83UW0_SHIFL	Q83uw0 shigella fl
568	26	81.2	1458	2	Q9F8Q4_STRTR	Q9f8q4 streptococc	641	25	78.1	127	2	Q83UW1_SHIDY	Q83uw1 shigella dy
569	26	81.2	1585	2	Q5ARK3_EMENI	Q5ark3 aspergillus	642	25	78.1	127	2	Q83XR1_SHIDY	Q83xr1 shigella dy
570	26	81.2	1667	2	Q4P4E1_USTMA	Q4p4e1 ustilago ma	643	25	78.1	127	2	Q83XR2_SHIBO	Q83xr2 shigella bo
571	26	81.2	1677	2	Q4FX65_LEIMA	Q4fx65 leishmania	644	25	78.1	127	2	Q83XR4_SHIFL	Q83xr4 shigella fl
572	26	81.2	1740	2	Q86B45_DROME	Q86b45 drosophila	645	25	78.1	127	2	Q83XR5_SHIFL	Q83xr5 shigella fl
573	26	81.2	1842	2	Q41696_GIBZE	Q41696 gibberella	646	25	78.1	128	2	Q5J1J3_PYROCO	Q511j3 pyrococcus
574	26	81.2	1842	2	Q6CUT9_KLUTA	Q6cut9 kluyveromy	647	25	78.1	128	2	Q517D1_ENTHI	Q517d1 entamoeba h
575	26	81.2	2085	2	Q7R322_GIILA	Q7r322 giardia lam	648	25	78.1	129	2	Q9YDS0_AERPE	Q9yds0 aeropyrum p
576	26	81.2	2095	1	RRLP_TQSV	P37800 toscana vir	649	25	78.1	130	2	Q91B93_COTJA	Q91b93 coturnix co
577	26	81.2	2216	1	YCF2_EPTVI	P30072 epifagus vi	650	25	78.1	132	2	Q83U24_SHIFL	Q83u24 shigella fl
578	26	81.2	2245	2	Q55008_CRYNE	Q55108 cryptococcu	651	25	78.1	133	2	Q50U55_ENTHI	Q50u55 entamoeba h
579	26	81.2	2245	2	Q5KCP4_STRAC	Q5kcp4 cryptococcu	652	25	78.1	135	2	Q50B11_SCHUA	Q50b11 schistosoma
580	26	81.2	2261	2	Q5HCP3_STRAC	Q5hcp3 staphylococ	653	25	78.1	136	2	Q517H0_ENTHI	Q517h0 entamoeba h
581	26	81.2	2271	2	Q7A362_STRAM	Q7a362 staphylococ	654	25	78.1	137	2	Q8NDU5_HUMAN	Q8ndu5 homo sapien
582	26	81.2	2271	2	Q99QY4_STRAM	Q99qy4 staphylococ	655	25	78.1	137	2	Q83XR3_SHISO	Q83xr3 shigella so
583	26	81.2	2275	2	Q6G620_STRAS	Q6g620 staphylococ	656	25	78.1	138	2	Q51C54_ENTHI	Q51c54 entamoeba h
584	26	81.2	2275	2	Q8NUJ3_STRAM	Q8nuj3 staphylococ	657	25	78.1	139	2	Q86TW5_HUMAN	Q86tw5 homo sapien
585	26	81.2	2283	2	Q8VQ99_STAHO	Q8vq99 ashbya gos	658	25	78.1	139	2	Q50MW1_ENTHI	Q50mw1 entamoeba h
586	26	81.2	2338	2	Q759S3_ASHGO	Q759s3 ashbya gos	659	25	78.1	140	1	ERG28_HUMAN	Q9ukr5 homo sapien
587	26	81.2	2535	2	Q8ZDR6_YERPE	Q8zdr6 yersinia pe	660	25	78.1	140	1	Q5R589_PONPY	Q5r589 pongo pygma
588	26	81.2	2550	2	Q669G0_YERPS	Q669g0 yersinia ps	661	25	78.1	140	2	Q5R589_PONPY	Q5r589 pongo pygma
589	26	81.2	2578	2	Q74184_YERPE	Q74184 yersinia pe	662	25	78.1	144	2	Q519A1_ENTHI	Q519a1 entamoeba h
590	26	81.2	2579	2	Q8DOR8_YERPE	Q8dor8 yersinia pe	663	25	78.1	144	2	Q51D59_ENTHI	Q51d59 entamoeba h
591	26	81.2	3079	1	IRA2_YEAST	P19158 saccharomy	664	25	78.1	146	2	Q71910_HUMAN	Q71910 homo sapien
592	26	81.2	3094	1	Q6UDW3_PLAFA	Q6udw3 plasmodium	665	25	78.1	146	2	Q8ZJ75_YERPE	Q8zj75 yersinia pe
593	26	81.2	4829	1	BIRC6_HUMAN	Q9nuf09 homo sapien	666	25	78.1	146	2	Q66G10_YERPS	Q66g10 yersinia ps
594	26	81.2	4845	2	Q88738_MOUSE	Q88738 mus musculu	667	25	78.1	147	2	Q6DB97_ERWCT	Q6db97 yerinia car
595	26	81.2	5017	2	Q6HKW5_BACHK	Q6hkws bacillus th	668	25	78.1	148	2	Q51OU0_ENTHI	Q51ou0 entamoeba h
596	26	81.2	5017	2	Q81FJ0_BACCR	Q81fj0 bacillus th	669	25	78.1	148	2	Q51OU0_ENTHI	Q51ou0 entamoeba h
597	26	81.2	5017	2	Q81SNO_BACAN	Q81sno bacillus an	670	25	78.1	151	2	Q5NYS0_AZOSE	Q5nyso azoarcus sp
598	26	81.2	5017	2	Q63DF3_BACCZ	Q63df3 bacillus ce	671	25	78.1	152	2	Q7N6J8_PROLL	Q7n6j8 phototrabu
599	26	81.2	8426	2	Q5YPH7_NOCFA	Q5yph7 nocardia fa	672	25	78.1	154	1	PFDA_HALNA	Q5ny26 haemophilus
600	25	78.1	45	2	Q9DIL8_9HRC	Q9dil8 hepatitis c	673	25	78.1	155	2	Q8VRCO_HAEIN	Q8vrc0 haemophilus
601	25	78.1	46	2	Q9A039_STRPY	Q9a039 streptococc	674	25	78.1	155	2	Q9WV53_CRIGR	Q9wv53 cricetulus
602	25	78.1	50	2	Q9TUX6_CANPA	Q9tux6 canis fami1	675	25	78.1	157	1	PSML_STN13	Q6jkt1 rickettsia
603	25	78.1	53	2	Q50872_ENTHI	P60459 methanosarc	676	25	78.1	158	2	Q8PNC2_XANAC	Q8pnc2 xanthomonas
604	25	78.1	55	1	SEGC_METMA	Q8px50 methanosarc	677	25	78.1	158	2	Q03668_RATRT	Q03668 rattus ratc
605	25	78.1	55	1	SEGC_METMA	Q8px50 methanosarc	678	25	78.1	162	2	Q50MS9_ENTHI	Q50ms9 entamoeba h
606	25	78.1	56	2	Q61HF6_DROME	Q61hp6 drosophila	679	25	78.1	163	2	Q7WYB6_RICETSA	Q7wyb6 rickettsia
607	25	78.1	57	2	Q519H2_ENTHI	Q519h2 entamoeba h	680	25	78.1	163	2	Q7WYB6_RICETSA	Q7wyb6 rickettsia
608	25	78.1	57	2	Q51B55_ENTHI	Q51b55 entamoeba h	681	25	78.1	163	2	Q7WYB6_RICETSA	Q7wyb6 rickettsia
609	25	78.1	59	2	Q5ZDU2_ORYSA	Q5zdu2 oryza sativ	682	25	78.1	166	2	Q41WQ0_AZAVO	Q41wq0 azotobacter
610	25	78.1	61	2	Q6PV50_YERRU	Q6pv50 yerinia ru	683	25	78.1	168	2	Q7POM1_CHRVO	Q7pom1 chromobacter
611	25	78.1	71	1	KLBP1_ECOLI	Q52729 escherichia	684	25	78.1	169	2	Q50NJI_ENTHI	Q50nj1 entamoeba h
612	25	78.1	71	2	Q76L1Y9_CONAC	Q76l1y9 commomonas a	685	25	78.1	170	2	Q7X4K5_RICPE	Q7x4k5 rickettsia
613	25	78.1	71	2	Q79BS8_PSSBD	Q79bs8 pseudomonas	686	25	78.1	170	2	Q63323_9NEOB	Q63323 buto exsul
614	25	78.1	71	2	Q4LCB3_9BACT	Q4lcb3 uncultured	687	25	78.1	170	2	Q63323_9NEOB	Q63323 buto viridi
615	25	78.1	71	2	Q6NSM8_RHOPA	Q6nsm8 rhodospseudo	688	25	78.1	170	2	Q63327_9NEOB	Q63327 buto verric

689	25	78.1	170	2	063329_9NEOB	063329	bufo andrew	762	25	78.1	245	2	08WB41_9NEOB	08WB41	bufo gariep
690	25	78.1	170	2	063331_BUPBG	063331	bufo bufu g	763	25	78.1	245	2	04SUG0_TETNG	04SUG0	tetraodon n
691	25	78.1	170	2	063332_BUPBG	063332	bufo bufu g	764	25	78.1	246	2	05VOM6_HALMA	05VOM6	haliaeetula n
692	25	78.1	170	2	063333_BUPBG	063333	bufo bufu g	765	25	78.1	246	2	05K1Y8_CRYNE	05K1Y8	cryptococcu
693	25	78.1	170	2	063957_BUPBG	063957	bufo bufu g	766	25	78.1	251	2	08FPQ2_BRAVA	08FPQ2	bradyrhizob
694	25	78.1	170	2	064012_9NEOB	064012	bufo andrew	767	25	78.1	252	2	07Y1B2_BRANA	07Y1B2	brasica na
695	25	78.1	173	2	0513T4_ENTHI	0513T4	entamoeba h	768	25	78.1	253	2	08C469_MOUSE	08C469	mus muscullu
696	25	78.1	173	2	086177_BACNO	086177	bacteroides	769	25	78.1	254	1	YVCN_BACSU	05LB76_BACFN	066977
697	25	78.1	174	2	08BDA4_VIBVU	08BDA4	vibriol vuln	770	25	78.1	256	2	064RM2_BACFR	064RM2	bacteroides
698	25	78.1	176	2	04J0O7_AZOVU	04J0O7	azotobacter	771	25	78.1	256	2	07OMO0_AMOGA	07OMO0	amonopelles g
699	25	78.1	176	2	0989O6_RHILLO	0989O6	rhizobium l	772	25	78.1	258	2	08TCH6_HUMAN	08TCH6	homo sapien
700	25	78.1	177	2	092VQ6_RHIME	092VQ6	rhizobium m	773	25	78.1	260	2	08TR97_CAEBR	08TR97	caenorhadi
701	25	78.1	177	2	070412_RAT	070412	rat	774	25	78.1	260	2	SILI_CYLPU	08YMK1_ANASP	08YMK1
702	25	78.1	178	2	054933_STRPN	054933	streplococc	775	25	78.1	265	2	0519Y5_ENTHI	0519Y5	entamoeba h
703	25	78.1	179	2	08IBS4_ARATH	08IBS4	arebidopsis	776	25	78.1	265	1	08YMK1_ANASP	08YMK1	anasp
704	25	78.1	179	2	09SKT5_ARATH	09SKT5	arebidopsis	777	25	78.1	268	2	07WGT0_BORBR	07WGT0	bordetella
705	25	78.1	181	2	08W4X3_METGX	08W4X3	metasequoia	778	25	78.1	270	2	06GEM5_STAR	06GEM5	staphylococ
706	25	78.1	181	2	09FSY0_CRYJA	09FSY0	cryptometria	779	25	78.1	271	2	05HEO0_STAC	05HEO0	staphylococ
707	25	78.1	181	2	07P2N6_FUSNV	07P2N6	fusobacteri	780	25	78.1	271	2	07A484_STANV	07A484	staphylococ
708	25	78.1	181	2	08RG57_FUSNN	08RG57	fusobacteri	781	25	78.1	271	2	09S6S5_STAMM	09S6S5	staphylococ
709	25	78.1	182	2	08LTT4_YVIRU	08LTT4	bacterioph	782	25	78.1	271	2	05DBE8_SCHAU	05DBE8	schistosoma
710	25	78.1	182	2	04K981_PSEFS	04K981	pseudomonas	783	25	78.1	273	2	08GAX4_STANU	08GAX4	staphylococ
711	25	78.1	185	2	07N1Q4_PHOHL	07N1Q4	photothadu	784	25	78.1	273	2	08WB38_9NEOB	08WB38	bufo donben
712	25	78.1	186	2	05USAO_9MONO	05USAO	avian pneum	785	25	78.1	273	2	08WB39_9NEOB	08WB39	bufo damara
713	25	78.1	188	2	08S5Q4_ORYSA	08S5Q4	oryza sativ	786	25	78.1	277	2	07ZJ3D_HUMAN	07ZJ3D	homo sapien
714	25	78.1	189	2	09FSW2_9CONI	09FSW2	dacrydium f	787	25	78.1	278	2	09CEV2_LACLA	09CEV2	lacina
715	25	78.1	190	2	05IGJ7_ENTHI	05IGJ7	entamoeba h	788	25	78.1	278	2	04WKJ4_ASPFU	04WKJ4	aspeygillus
716	25	78.1	190	2	052997_ECOLI	052997	escherichia	789	25	78.1	280	2	057NZ1_SALCH	057NZ1	salmonella
717	25	78.1	191	2	09FVPS_AGADA	09FVPS	agathis dam	790	25	78.1	281	2	05PHQ3_SALPA	05PHQ3	salmonella
718	25	78.1	192	2	09FPQ0_9RICX	09FPQ0	ricicetisla	791	25	78.1	281	2	08Z796_SALVT	08Z796	salmonella
719	25	78.1	196	1	YCDI_ECO57	YCDI	ecoli	792	25	78.1	281	2	08ZP77_SALTY	08ZP77	salmonella
720	25	78.1	196	1	YCDI_ECO57	YCDI	ecoli	793	25	78.1	281	2	08DI98_SYNEL	08DI98	synel
721	25	78.1	196	2	08S941_STILA	08S941	silene lati	794	25	78.1	281	1	HSLI_BACTN	05RFQ8_LACAC	05RFQ8
722	25	78.1	196	2	08RI44_ECOL6	08RI44	escherichia	795	25	78.1	283	2	05LAZ7_BACFR	05LAZ7	bacteroides
723	25	78.1	196	2	083RVA_SHIFL	083RVA	shigella fl	796	25	78.1	283	2	064R66_BACFR	064R66	bacteroides
724	25	78.1	198	2	08WB50_9NEOB	08WB50	bufo poweri	797	25	78.1	283	2	019902_CABEL	019902	caenorhadi
725	25	78.1	200	2	073R50_TREDE	073R50	treponema d	798	25	78.1	286	2	086PQ0_SARNE	086PQ0	sarcocystis
726	25	78.1	202	2	05IOW3_MAGGR	05IOW3	magnaporthe	799	25	78.1	287	2	06LW42_PROPR	06LW42	photobacter
727	25	78.1	202	2	087GE7_VIBPA	087GE7	vibrio para	800	25	78.1	290	2	09SBR9_ARATH	09SBR9	arebidopsis
728	25	78.1	203	2	08ZGQ1_YERPE	08ZGQ1	yersinia pe	802	25	78.1	291	2	Y347_HELPU	Y347	helpu
729	25	78.1	204	2	04Q5H7_LEITMA	04Q5H7	leishmania	803	25	78.1	293	1	Y347_HELPU	Y347	helpu
730	25	78.1	204	2	0829C9_SALTI	0829C9	salmonella	804	25	78.1	293	2	066O63_POLCB	066O63	polycyomce
731	25	78.1	205	2	04UBK7_THEAN	04UBK7	theileria a	805	25	78.1	294	2	09CP11_PASMU	09CP11	pasteurella
732	25	78.1	206	2	0973M7_SUITO	0973M7	sulfolobus	806	25	78.1	294	2	07XP96_ORYSA	07XP96	oryza sativ
733	25	78.1	206	2	09BUCI_HUMAN	09BUCI	homo sapien	807	25	78.1	295	2	SM1B1_CANFA	SM1B1	canis famli
734	25	78.1	209	2	06PGQ0_HUMAN	06PGQ0	homo sapien	808	25	78.1	296	1	Q4IID1_GIBZE	Q4IID1	gibberella
735	25	78.1	209	2	08D018_YERPE	08D018	yersinia pe	809	25	78.1	296	2	06LBS2_9ALPH	06LBS2	equid herpe
736	25	78.1	213	2	04HLV7_CAMLA	04HLV7	campylobact	810	25	78.1	296	2	072AB5_DESVH	072AB5	desulfovibr
737	25	78.1	213	2	05P789_AZOSE	05P789	azarcus sp	811	25	78.1	297	2	Y347_HELPU	Y347	helpu
738	25	78.1	214	1	DAMX_SEBMA	DAMX	sebacia ma	812	25	78.1	298	1	072V52_LEPIC	072V52	leptocypira
739	25	78.1	214	2	07SCN6_NEUCR	07SCN6	neurospora	813	25	78.1	299	2	08FPD4_LEPIC	08FPD4	leptocypira
740	25	78.1	214	2	06MKR3_BDBBA	06MKR3	bdeliovibri	814	25	78.1	299	2	06S574_9ALPH	06S574	9aliph
741	25	78.1	216	2	0519P6_ENTHI	0519P6	entamoeba h	815	25	78.1	299	2	077CB2_9ALPH	077CB2	bovine herp
742	25	78.1	216	2	04MRL7_BACCE	04MRL7	bacillus ce	816	25	78.1	300	2	06S581_9ALPH	06S581	bovine herp
743	25	78.1	219	2	06DTJ3_STRPN	06DTJ3	streplococc	817	25	78.1	300	2	0551A6_ENTHI	0551A6	entamoeba h
744	25	78.1	219	2	08WB42_9NEOB	08WB42	bufo panthe	818	25	78.1	302	2	05STP0_CRYNE	05STP0	cryptococcu
745	25	78.1	219	2	08WB45_BURRA	08WB45	bufo regalia	819	25	78.1	303	2	07WNL7_BORBR	07WNL7	bordetella
746	25	78.1	222	2	05DCC9_SCHUA	05DCC9	schistosoma	820	25	78.1	303	2	05BVN2_SCHUA	05BVN2	schistosoma
747	25	78.1	223	2	0511H7_ENTHI	0511H7	entamoeba h	821	25	78.1	306	2	07YTM9_CABEL	07YTM9	caenorhadi
748	25	78.1	226	2	05SRA32_PONPY	05SRA32	pongo pygma	822	25	78.1	306	2	09LL87_MAIZE	09LL87	zea mays (m
749	25	78.1	226	2	07YV17_BORPE	07YV17	bordetella	823	25	78.1	306	2	07ABCS_ECO57	07ABCS	escherichia
750	25	78.1	226	2	07WIM6_BORBR	07WIM6	bordetella	824	25	78.1	308	2	08X4S5_ECO57	08X4S5	escherichia
751	25	78.1	231	2	071EC6_AGRVI	071EC6	agrobacteri	825	25	78.1	308	2	06YTUI_MOUSE	06YTUI	mus muscullu
752	25	78.1	231	2	08WB49_9NEOB	08WB49	bufo poweri	826	25	78.1	309	2	07ND12_GLOVI	07ND12	gloeobacter
753	25	78.1	234	2	07QO53_9DIPT	07QO53	chironomus	827	25	78.1	313	2	08YUJ6_ANASP	08YUJ6	anabaena sp
754	25	78.1	235	2	05DYQ3_VIBFI	05DYQ3	vibriol fibc	828	25	78.1	313	2	08VTB1_HELPU	08VTB1	hellicobacte
755	25	78.1	236	2	05IG14_ENTHI	05IG14	entamoeba h	829	25	78.1	315	2	06AL45_DESPS	06AL45	desulfofate
756	25	78.1	236	2	0621C7_BURMA	0621C7	burkholderi	830	25	78.1	316	2	051YW3_MAGGR	051YW3	magnaporthe
757	25	78.1	236	2	063W80_BURPS	063W80	burkholderi	831	25	78.1	318	2	GUTQ_ECOLI	GUTQ	ecoli
758	25	78.1	237	2	08W972_9NEOB	08W972	bufo macula	832	25	78.1	321	1	08FEN7_ECOL6	08FEN7	escherichia
759	25	78.1	237	2	0880F6_PSESM	0880F6	pseudomonas	833	25	78.1	321	2	06W395_9CREN	06W395	uncultured
760	25	78.1	242	2	08WB37_9NEOB	08WB37	capensisbufo	834	25	78.1	322	2			

835	25	78.1	322	2	09T2M1_CABEL	09T2M1 caenorhabdi	908	25	78.1	366	2	05T120_CHICK	05T120 gallus gall
836	25	78.1	322	2	09JP89_RHOGE	09JP89 rhodocyclus	909	25	78.1	369	2	06ANG3_DRSPP	06ANG3 deullifotale
837	25	78.1	324	2	05W277_ARATH	05W277 arabidopsi	910	25	78.1	370	2	06M01_USEUD	06M01 paconia sp.
838	25	78.1	326	2	08C6V8_MOUSE	08C6V8 mus musculu	911	25	78.1	371	2	06B1Z9_9ROSI	06B1Z9 retnwardtia
839	25	78.1	327	2	063P96_BACCC	063P96 bacillus ce	912	25	78.1	372	2	07MSR1_9MICC	07MSR1 arthrobacte
840	25	78.1	328	2	0891J4_BRALJ	0891J4 bradyrhizob	913	25	78.1	372	2	089UV8_BRAJA	089UV8 bradyrhizob
841	25	78.1	331	1	BTUC_VIBPA	087939 vibrio para	914	25	78.1	373	2	003787_YEAST	003787 saccharomyc
842	25	78.1	331	1	BTUC_VIBPA	087939 vibrio para	915	25	78.1	375	2	044050_ARTGO	044050 arthrobacte
843	25	78.1	331	1	BTUC_VIBPA	087939 vibrio para	916	25	78.1	376	2	0528C1_ORYSA	0528C1 oryza sativ
844	25	78.1	331	1	BTUC_VIBPA	087939 vibrio para	917	25	78.1	377	2	09C0E5_HUMAN	09C0E5 homo sapien
845	25	78.1	333	2	06ZMF2_HUMAN	06ZMF2 homo sapien	918	25	78.1	377	2	09H013_HUMAN	09H013 homo sapien
846	25	78.1	333	2	08A2J3_BACTN	08A2J3 bacteroides	919	25	78.1	377	2	08C5T8_MOUSE	08C5T8 mus musculu
847	25	78.1	335	2	07NY79_CHYVO	07NY79 chromodact	920	25	78.1	378	2	09A8D5_CAUCH	09A8D5 caulobacter
848	25	78.1	335	2	06FEV3_ACIAD	06FEV3 acinetobact	921	25	78.1	379	2	06H193_9SACH	06H193 pichia fere
849	25	78.1	336	2	0669R8_YERPS	0669R8 yerinia pe	922	25	78.1	379	2	07R5P5_GIALA	07R5P5 giardia lam
850	25	78.1	336	2	08ZEP1_YERPE	08ZEP1 yerinia pe	923	25	78.1	381	2	0531U3_ORYSA	0531U3 oryza sativ
851	25	78.1	338	2	06C8V3_YARLI	06C8V3 yarrowia li	924	25	78.1	382	2	04ZTM4_PESBY	04ZTM4 pseudomonas
852	25	78.1	338	2	07N4U5_PHOLL	07N4U5 photorhabd	925	25	78.1	382	2	06B2J1_PBSRM	06B2J1 pseudomonas
853	25	78.1	339	2	06D2K0_BRWCT	06D2K0 erwina car	926	25	78.1	384	2	09X218_THEMA	09X218 thermotoga
854	25	78.1	340	2	09CLR3_PASMU	09CLR3 pasteurella	927	25	78.1	385	2	09VKX8_DROME	09VKX8 drosophila
855	25	78.1	341	2	08CD05_MOUSE	08CD05 mus musculu	928	25	78.1	385	2	08K0G1_MOUSE	08K0G1 mus musculu
856	25	78.1	342	2	05B769_EMENT	05B769 aspergillus	929	25	78.1	388	1	08CB17_MOUSE	08CB17 mus musculu
857	25	78.1	343	2	06NTE8_HUMAN	06NTE8 homo sapien	930	25	78.1	388	2	041927_MRY68	041927 murid herpe
858	25	78.1	343	2	08VTB7_HELPY	08VTB7 helicobacte	931	25	78.1	388	2	07RRG6_DROME	07RRG6 drosophila
859	25	78.1	343	2	08VTD4_HELPY	08VTD4 helicobacte	932	25	78.1	390	2	06TBB1_9ROSI	06TBB1 podostemum
860	25	78.1	343	2	08VTD6_HELPY	08VTD6 helicobacte	933	25	78.1	391	2	06LTQ1_PHOPR	06LTQ1 photobacter
861	25	78.1	343	2	08VTE4_HELPY	08VTE4 helicobacte	934	25	78.1	393	2	08ES39_CABEL	08ES39 caenorhabdi
862	25	78.1	343	2	08VTE6_HELPY	08VTE6 helicobacte	935	25	78.1	395	2	06Z310_ORYSA	06Z310 oryza sativ
863	25	78.1	343	2	08VTE9_HELPY	08VTE9 helicobacte	936	25	78.1	400	1	HCMD_ECOLI	HCMD escherichia
864	25	78.1	343	2	09ZNI5_HELPJ	09ZNI5 helicobacte	937	25	78.1	400	1	08XAT7_ECO57	08XAT7 escherichia
865	25	78.1	343	2	09G363_ACACP	09G363 acanthosaur	938	25	78.1	400	2	VE2_HPV1A	VE2 human papil
866	25	78.1	344	2	05VHL4_9NEOB	05VHL4 bufo melano	939	25	78.1	403	2	06YUJ2_MOUSE	06YUJ2 mus musculu
867	25	78.1	344	2	070ED4_9NEOB	070ED4 bufo melano	940	25	78.1	407	1	GCST_FLAN	GCST flaviera an
868	25	78.1	344	2	08MB40_9NEOB	08MB40 bufo gariel	941	25	78.1	407	1	GCST_FLAAP	GCST flaviera tr
869	25	78.1	344	2	08MB43_BURCA	08MB43 bufo caneru	942	25	78.1	407	1	GCST_FLAAP	GCST flaviera tr
870	25	78.1	344	2	08MB44_9NEOB	08MB44 bufo xeros.	943	25	78.1	408	2	06W4B5_DROSI	06W4B5 drosophila
871	25	78.1	344	2	08MB46_9NEOB	08MB46 bufo macula	944	25	78.1	408	2	06W4E7_DROSI	06W4E7 drosophila
872	25	78.1	344	2	08MB48_9NEOB	08MB48 bufo macula	945	25	78.1	408	2	06W4B9_DROSI	06W4B9 drosophila
873	25	78.1	344	2	08MB51_9NEOB	08MB51 bufo guttur	946	25	78.1	408	2	06W4F2_DROME	06W4F2 drosophila
874	25	78.1	344	2	08MB52_9NEOB	08MB52 bufo guttur	947	25	78.1	408	2	06W4G1_DROME	06W4G1 drosophila
875	25	78.1	344	2	08MB53_9NEOB	08MB53 bufo guttur	948	25	78.1	408	2	06W4G4_DROME	06W4G4 drosophila
876	25	78.1	347	2	09XC69_STRPR	09XC69 streptomyce	949	25	78.1	408	2	06W4G7_DROME	06W4G7 drosophila
877	25	78.1	347	2	04W8Q0_UROHA	04W8Q0 uromastix h	950	25	78.1	408	2	06W4H2_DROME	06W4H2 drosophila
878	25	78.1	348	2	07Z6N7_HUMAN	07Z6N7 homo sapien	951	25	78.1	408	2	06W4H2_DROME	06W4H2 drosophila
879	25	78.1	349	1	08DOP7_YERPE	08DOP7 yerinia pe	952	25	78.1	410	2	05GVF3_XANOR	05GVF3 xanthomonas
880	25	78.1	349	1	GNAT1_BOVIN	028300 bos taurus	953	25	78.1	410	2	04NMD4_9NICC	04NMD4 arthrobacte
881	25	78.1	349	1	GNAT1_CANFA	028300 canis famli	954	25	78.1	411	2	05R374_VIBRI	05R374 vibrio fise
882	25	78.1	349	1	GNAT1_HUMAN	P11488 homo sapien	955	25	78.1	411	2	06DHU2_BRARE	06DHU2 brachydanio
883	25	78.1	349	1	GNAT1_MOUSE	P20612 mus musculu	956	25	78.1	414	2	09SAV9_ARATH	09SAV9 arabidopsi
884	25	78.1	349	1	GNAT1_XENTIA	P38407 xenopus lae	957	25	78.1	414	2	07XPY1_ORYSA	07XPY1 oryza sativ
885	25	78.1	349	2	06OPT9_CABER	06OPT9 caenorhabdi	958	25	78.1	416	2	056HDX_ARATH	056HDX arabidopsi
886	25	78.1	349	2	08FDIO_ECOL6	08FDIO escherichia	959	25	78.1	420	2	08XMG4_DROME	08XMG4 drosophila
887	25	78.1	349	2	09YTI5_9HERP	09YTI5 atelina her	960	25	78.1	420	2	08MLG4_DROME	08MLG4 drosophila
888	25	78.1	350	2	04VEN2_HUMAN	04VEN2 homo sapien	961	25	78.1	420	2	088G61_PSEPK	088G61 pseudomonas
889	25	78.1	350	2	067YS8_ARATH	067YS8 arabidopsi	962	25	78.1	421	2	063TR4_BURMA	063TR4 burkholderi
890	25	78.1	350	2	08S3D6_ARATH	08S3D6 arabidopsi	963	25	78.1	421	2	062KM7_BURMA	062KM7 burkholderi
891	25	78.1	350	2	09ZUG9_ARATH	09ZUG9 arabidopsi	964	25	78.1	422	2	0562B6_RAT	0562B6 rattus norv
892	25	78.1	350	2	06QNB4_SALET	06QNB4 salmonella	965	25	78.1	424	2	05R716_PONPY	05R716 poncio pygma
893	25	78.1	350	2	057RK6_SALCH	057RK6 salmonella	966	25	78.1	425	2	08PUS6_METWA	08PUS6 methanosarc
894	25	78.1	350	2	05PEX4_SALPA	05PEX4 salmonella	967	25	78.1	425	2	097H04_CLOAB	097H04 clostridium
895	25	78.1	350	2	08ZMM8_SALTY	08ZMM8 salmonella	968	25	78.1	425	2	07NVV5_CHYVO	07NVV5 chromobacte
896	25	78.1	351	2	06F324_ORYSA	06F324 oryza sativ	969	25	78.1	426	2	09HEX7_SACPS	09HEX7 saccharomyc
897	25	78.1	351	2	09W0B8_MEIMA	09W0B8 neisseria m	970	25	78.1	426	2	051UX4_MAGGR	051UX4 magnaporthe
898	25	78.1	356	2	04PIU5_CABEL	04PIU5 caenorhabdi	971	25	78.1	426	2	04P8J6_USHMA	04P8J6 usuliago ma
899	25	78.1	358	2	ALP_YEAST	P14540 aspergillius	972	25	78.1	427	2	05SPW4_CRYNE	05SPW4 cryptococcu
900	25	78.1	358	2	04X132_ASPPU	04X132 aspergillius	973	25	78.1	427	2	05SDU5_CRYNE	05SDU5 cryptococcu
901	25	78.1	358	2	08OGV3_FUGRU	08OGV3 fugu rubrip	974	25	78.1	428	2	07S7L8_NEUCR	07S7L8 neuospora
902	25	78.1	359	1	LPFD_SALTY	P43663 salmonella	975	25	78.1	429	2	04M0X8_9BURK	04M0X8 burkholderi
903	25	78.1	359	2	0571T7_SALCH	0571T7 salmonella	976	25	78.1	429	2	07VFL6_HELHP	07VFL6 helicobacte
904	25	78.1	362	2	061S24_CABER	061S24 caenorhabdi	977	25	78.1	431	1	TRAI_RHISN	TRAI rhizobium s
905	25	78.1	362	2	04IJ24_DROSI	04IJ24 drosophila	978	25	78.1	431	1	084G45_RHILV	084G45 rhizobium l
906	25	78.1	365	2	04HV33_GIBZE	04HV33 gibberella	979	25	78.1	431	2	09KSVO_VIBCH	09KSVO vibrio chol
907	25	78.1	366	2	08VZQ2_ARATH	08VZQ2 arabidopsi	980	25	78.1	432	2	093UX6_9RHIZ	093UX6 agrobacteri

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981 25 78.1 432 2 Q9FSD2 AGNRH Q9FSD2 agrobacteri
982 25 78.1 432 2 Q6LB42 OLICA Q6LB42 oligotropha
983 25 78.1 433 1 TRBI AGRTU P54917 agrobacteri
984 25 78.1 433 2 Q6AMW2 DESPS Q6AMW2 desulfolate
985 25 78.1 435 2 Q64HT1 RHRET Q64HT1 rhizobium e
986 25 78.1 435 2 Q4LNK1 YBURL Q4LNK1 rhodospirill
987 25 78.1 435 2 Q7U118 RHODA Q7U118 rhodospirill
988 25 78.1 435 2 Q6XLY6 9PHYC Q6XLY6 feildmannia
989 25 78.1 437 2 Q9RT97 DEIRA Q9RT97 deinococcus
990 25 78.1 438 2 Q4Q1B6 LEIMA Q4Q1B6 leishmania
991 25 78.1 438 2 Q66179 9RHIZ Q66179 agrobacteri
992 25 78.1 438 2 Q9Z482 9RHIZ Q9Z482 agrobacteri
993 25 78.1 438 2 Q7D201 AGRTS Q7D201 agrobacteri
994 25 78.1 440 2 Q75G29 LEPIC Q75G29 leptospira
995 25 78.1 440 2 Q8BY10 LEPIN Q8BY10 leptospira
996 25 78.1 442 2 Q6S522 ORYSA Q6S522 oryza sativ
997 25 78.1 442 2 Q7SYJ3 BRARE Q7SYJ3 brichydanio
998 25 78.1 446 1 DYP8 CAEEL Q09276 caenothabdi
999 25 78.1 447 2 Q5TS52 ANOGA Q5TS52 anopheles g
1000 25 78.1 448 2 Q7PWW7 ANOGA Q7PWW7 anopheles g

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ALIGNMENTS

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RESULT 1
KV01_RAT STANDARD; PRT; 109 AA.

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AC P01681;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE IG kappa chain V region S211.
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=Louisian;
RC MEDLINE=75212238; PubMed=807630;
RT "The primary structure of a rat kappa Bence Jones protein:
RT phylogenetic relationships of V- and C-region genes."
RT J. Immunol. 115:55-62(1975).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01944; KVRT21.
DR HSSP; P01625; 1LVE.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003586; IG_V.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 35 Complementarity-determining-1.
FT REGION 36 50 Framework-2.
FT REGION 51 57 Complementarity-determining-2.
FT REGION 58 89 Framework-3.
FT REGION 90 98 Complementarity-determining-3.
FT REGION 99 108 Framework-4.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11948 MW; A25BFB9FDE5CBAC6 CRC64;

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Query Match 100.0%; Score 32; DB 1; Length 109;

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Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTLOS 7
Db 51 SGSTLOS 57

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RESULT 2

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Q4HCC8_9DEIO PRELIMINARY; PRT; 294 AA.
AC Q4HCC8;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DgeodRAFT_2124;
OS Deinococcus geothermalis DSM 11300.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=319795;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Plutck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Deinococcus geothermalis
RT DSM 11300."
RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Lartner F., Land M.;
RT "Annotation of the draft genome assembly of Deinococcus geothermalis
RT DSM 11300."
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAHE0100001; EAL84018.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 294 AA; 32036 MW; 1D6FB29BCDAJFC29 CRC64;

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Query Match 100.0%; Score 32; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTLOS 7
Db 288 SGSTLOS 294

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RESULT 3

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Q757S8 ASHGO PRELIMINARY; PRT; 630 AA.
AC Q757S8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE AEL066CD.
GN Name=AEL066C;
GN Ashyia gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,

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RA Gaffney T.D., Philippsen P.;
RT "The *Asphyx gossypii* genome as a tool for mapping the ancient
RT *Saccharomyces cerevisiae* genome.";
RL Science 304:304-307(2004).
DR EMBL; AE016818; AAS52619.1; -; Genomic_DNA.
DR AGD; AEL066C; -.
KW Complete proteome.
SQ SEQUENCE 690 AA; 78639 MW; BF2BC6BC21521CEF CRC64;

Query Match 100.0%; Score 32; DB 2; Length 690;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGGTLOS 7
| | | | |
Db 492 SGGTLOS 498

RESULT 4
06DFCS_XENLA PRELIMINARY; PRT; 361 AA.
ID 06DFCS_XENLA PRELIMINARY; PRT; 361 AA.
AC 06DFCS; 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Abhd5-prov protein.
GN Name-abhd5-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RX Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076814; AAH76814.1; -; mRNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.

DR InterPro; IPR000073; A/b_hydrolase.
DR InterPro; IPR003089; AB_hydrolase.
DR InterPro; IPR000639; Epox_hydrolase.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
DR PRINTS; PR00412; EPOXYHYDROLASE.
KW Hydrolase.
SQ SEQUENCE 361 AA; 40313 MW; D611F2CDA62E651B CRC64;

Query Match 93.8%; Score 30; DB 2; Length 361;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGGTLOS 7
| | | | |
Db 316 SGGTLOS 322

RESULT 5
05BK12_XENLR PRELIMINARY; PRT; 371 AA.
ID 05BK12_XENLR PRELIMINARY; PRT; 371 AA.
AC 05BK12; 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Xenopus tropicalis (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_Taxid=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole body;
RX Klein S., Gerhard D.S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091064; AAH91064.1; -; mRNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000073; A/b_hydrolase.
DR InterPro; IPR003089; AB_hydrolase.
DR InterPro; IPR000639; Epox_hydrolase.
DR Pfam; PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
DR PRINTS; PR00412; EPOXYHYDROLASE.
KW Hydrolase, Hypothetical protein.
SQ SEQUENCE 371 AA; 41475 MW; BB3BEF82849670D CRC64;

Query Match 93.8%; Score 30; DB 2; Length 371;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTLOS 7
 |||:|
 Db 326 SGATLOS 332

RESULT 6
 Q7XC80_ORYSA PRELIMINARY; PRT; 144 AA.

AC Q7XC80;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=OSJNB0042H09.25;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCB1_TaxID=39947;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA The Rice Chromosome 10 Sequencing Consortium;
 RT "In-depth view of structure, activity, and evolution of rice
 RT chromosome 10.";
 RL Science 300:1566-1569 (2003).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Wang R.A., McCombie W.R., Messing J., Yuan Q.,
 RA Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017119; AAP54994.1; -; Genomic_DNA.
 DR Gramene; Q7XC80; -;
 KW Hypothetical protein.
 SQ SEQUENCE 144 AA; 15076 MW; 7E46E527E4624C9E CRC64;

Query Match 90.6%; Score 29; DB 2; Length 144;
 Best Local Similarity 85.7%; Pred. No. 94;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTLOS 7
 |||:|
 Db 18 SGATLOS 24

RESULT 7
 Q8SB90_ORYSA PRELIMINARY; PRT; 144 AA.

AC Q8SB90;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein OSJNB0042H09.25.
 GN Name=OSJNB0042H09.25;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCB1_TaxID=4530;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
 RA Ganabinger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
 RA Teitelin T., Riggs F., Hejao J., Ziemann V., Blunt S., Pai G.,
 RA Vanden S.E., Utecherback T.R., Feldblum T.V., Kalb E., Quackenbush J.,
 RA Salberg S.L., White O., Fraser C.M.;
 RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell R.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC079874; AAL79806.1; -; Genomic_DNA.
 DR Gramene; Q8SB90; -;
 KW Hypothetical protein.
 SQ SEQUENCE 144 AA; 15076 MW; 7E46E527E4624C9E CRC64;

Query Match 90.6%; Score 29; DB 2; Length 144;
 Best Local Similarity 85.7%; Pred. No. 94;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTLOS 7
 |||:|
 Db 18 SGATLOS 24

RESULT 8
 Q57FL6_BRUAB PRELIMINARY; PRT; 197 AA.

AC Q57FL6;
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE YfiA, ribosomal subunit interface protein.
 GN Name=YfiA; OrderedLocustNames=Brubd1_0156;
 OS Brucella abortus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OC NCB1_TaxID=235;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=9-941 / Biovar 1;
 RX PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
 RA Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuercher R.L.,
 RA Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
 RT "Completion of the genome sequence of Brucella abortus and comparison
 RT to the highly similar genomes of Brucella melitensis and Brucella
 RT suis.";
 RL J. Bacteriol. 187:2715-2726 (2005).
 DR EMBL; AE017223; AAX73568.1; -; Genomic_DNA.
 KW Complete Proteome.
 SQ SEQUENCE 197 AA; 21628 MW; 9CE9C00D49B345A2 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 197;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTLOS 7
 |||:|
 Db 59 SGATLOS 65

RESULT 9
 Q8G2Z7_BRUSU PRELIMINARY; PRT; 197 AA.

AC Q8G2Z7;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Ribosomal subunit interface protein.
 GN Name=YfiA; OrderedLocustNames=BR0160;
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OC NCB1_TaxID=29461;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=2247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
 RA Paulsen I.T., Seehadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
 RA Van Aken S.E., Riedmuller S., Tettein H., Gill S.R., White O.,

RA Salberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
 RA Frazer C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014291; AAN29113.1; -; Genomic_DNA.
 DR TIGR; BR0160; -;
 DR InterPro; IPR003489; Ribosomal S30S54.
 DR Pfam; PF02482; Ribosomal S30AB; 1.
 DR TIGRFAM; TIGR00741; yf1a; 1.
 KW Complete proteome.
 SQ SEQUENCE 197 AA; 21570 MW; 20E5F175168C4651 CRC64;

QY 1 SGGSTLOS 7
 ||:||||
 Db 59 SGGSTLOS 65

Query Match 90.6%; Score 29; DB 2; Length 197;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 O8YEU0 BRUME PRELIMINARY; PRT; 197 AA.
 ID O8YEU0;
 AC O8YEU0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DE Putative sigmas54 modulation protein / SSU ribosomal protein S30P.
 GN OrderedlocusNames=BME11787;
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=16M / ATCC 23456 / Biotype 1;
 RX PubMed=11756688; DOI=10.1073/pnas.221575398;
 RA DelVecchio V.G., Kapratral V., Redkar R.J., Petra G., Mujar C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,
 RA Jablonksi L., Larsen N., D'Souza M., Bernal A., Goldsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrides N.C., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 RT Brucella melitensis.";
 RT Brucella melitensis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL; AE009611; AAL52968.1; -; Genomic_DNA.
 DR PIR; AB3475; AB3475.
 DR InterPro; IPR003489; Ribosomal S30S54.
 DR Pfam; PF02482; Ribosomal S30AB; 1.
 DR TIGRFAM; TIGR00741; yf1a; 1.
 KW Complete proteome.
 SQ SEQUENCE 197 AA; 21628 MW; 9CE9C00D49B345A2 CRC64;

QY 1 SGGSTLOS 7
 ||:||||
 Db 59 SGGSTLOS 65

Query Match 90.6%; Score 29; DB 2; Length 197;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 Q9L0H5 STRCO PRELIMINARY; PRT; 219 AA.
 ID Q9L0H5;
 AC Q9L0H5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative integral membrane protein.
 GN OrderedlocusNames=SC04782; ORFNames=SCD63.14c;

OG Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=A3(2) / M45;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser I., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinovitch E., Rajadream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939121; CAB82021.1; -; Genomic_DNA.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 KW Complete proteome.
 SQ SEQUENCE 219 AA; 22701 MW; C65145904239FF50 CRC64;

QY 1 SGGSTLOS 7
 ||:||||
 Db 35 SGGSTLOS 41

Query Match 90.6%; Score 29; DB 2; Length 219;
 Best Local Similarity 85.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 Q739H5_BACCI PRELIMINARY; PRT; 292 AA.
 ID Q739H5;
 AC Q739H5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 GN OrderedlocusNames=BCE2166;
 OS Bacillus cereus (strain ATCC 10987).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=222523;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=14960714; DOI=10.1093/nar/gkh258;
 RA Raeko D.A., Ravel J., Oksstad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
 RA Nelson W.C., Koltoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
 RT adaptations and a large plasmid related to Bacillus anthracis pXO1.";
 RL Nucleic Acids Res. 32:977-988(2004).
 DR EMBL; AE017271; AAS41087.1; -; Genomic_DNA.
 DR TIGR; BCE2166; -;
 KW Complete proteome; Hypothetical protein; Nucleotide-binding.
 SQ SEQUENCE 292 AA; 33346 MW; A90F638795045DB8 CRC64;

QY 1 SGGSTLOS 7
 ||:||||
 Db 106 TGGSTLOS 112

Query Match 90.6%; Score 29; DB 2; Length 292;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 Q9HXJ3_PSEAE

ID Q9HXJ3 PSEAE PRELIMINARY; PRT; 347 AA.
AC Q9HXJ3
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedlocusNames=PA3804;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lapid G., Lam R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Sater M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.,
RT Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964 (2000).
DR EMBL; AE004798; AAG07191.1; -; Genomic_DNA.
DR PIR; G83171; G83171.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001387; HTH_3.
DR InterPro; IPR000943; Sigma_70.
DR SMART; SM00530; HTH_XRE; 1.
DR PROSITE; PS50943; HTH_CROCI; 1.
DR PROSITE; PS00716; SIGMA70_2; UNKNOWN 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 347 AA; 36102 MW; 4ECC03528FD97126 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 347;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
DB 95 SGSTVQS 101

RESULT 14
Q7PZDI ANOGA PRELIMINARY; PRT; 355 AA.
ID Q7PZDI ANOGA PRELIMINARY; PRT; 355 AA.
AC Q7PZDI;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE ENSANGP00000021274.
GN ORFNames=ENSANG00000018785;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Megaloptera; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=80454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008986; EAA00521.2; -; Genomic_DNA.

DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR004210; BSSS_motif.
DR InterPro; IPR006578; MADF.
DR Pfam; PF02944; BSSS; 1.
DR SMART; SM00595; MADF; 1.
SQ SEQUENCE 355 AA; 40404 MW; 33104FF93B67C95 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 355;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
DB 231 TGSTLOS 237

RESULT 15
Q6ACF0 LEIXX PRELIMINARY; PRT; 372 AA.
ID Q6ACF0 LEIXX PRELIMINARY; PRT; 372 AA.
AC Q6ACF0;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Phosphoribosylformylglycinamide cyclase.
GN Name=purM; OrderedlocusNames=lxr22750;
OS Leifsonia xyli (subsp. xyli).
OC Bacteria; Actinobacteria; Actinobacteriales; Leifsonia.
OC Micrococciaceae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CTCB07.
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Harkava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F. Jr., Carter H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.B., Lemos B.G.M.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.,
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyli subsp. xyli."
RL MCL Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AE016822; AAT89943.1; -; Genomic_DNA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0016874; F:Ligase activity; IEA.
DR GO; GO:0004641; F:phosphoribosylformylglycinamide cyclase; IEA.
DR GO; GO:0006189; P:de novo IMP biosynthesis; IEA.
DR GO; GO:0006164; P:purine nucleotide biosynthesis; IEA.
DR InterPro; IPR000728; AIR_synth.
DR InterPro; IPR010918; AIR_synth_C.
DR InterPro; IPR004733; purM_c1igase.
DR Pfam; PF00586; AIRS; 1.
DR Pfam; PF02769; AIRS_C; 1.
DR TIGRFAMs; TIGR00878; purM; 1.
KM Complete proteome; Ligase.
SQ SEQUENCE 372 AA; 37505 MW; 89A1DF9886F873CD CRC64;

Query Match 90.6%; Score 29; DB 2; Length 372;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
DB 236 SGSTLES 302

RESULT 16
Q4P349 USTWA PRELIMINARY; PRT; 378 AA.
ID Q4P349 USTWA PRELIMINARY; PRT; 378 AA.

AC Q4P349;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=UW05464.1;
 OS Ustilago maydis 521.
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OK NCBI_TaxID=237631;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=521;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Alt-rabha M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Ambuster J., Bachanteang P., Baldwin J., Barry A.,
 RA Bayul T., Blichstein B., Bloom T., Bye J., Boguslavsky L.,
 RA Borowsky M., Boukhalter B., Brumache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Chesnatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook K., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Dufey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Garth G., Gnerre S.,
 RA Gutke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyssele M., Karlsson E.,
 RA Kells C., Kieu A., Klesner P., Kodira C., Kulbokas E., Labucci K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Maraballa R., Maru K., Matthews C., Mancelli E.,
 RA Mccartov J., McDonough S., Mcghee T., Meldrim J., Menes L.,
 RA Mesitov J., Mhalley A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunhang P., Pigani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Steeson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoutang Y., Topham K.,
 RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wengai T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Zander E.;
 RT "The genome sequence of Ustilago maydis."
 RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL, AACP0100197; EAK6397.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 378 AA; 41595 MW; F71AD1EA65869BE8 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 378;
 Best Local Similarity 85.7%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
 :|||||
 Db 66 TGGTLOS 72

RESULT 17
 OS1CUG_ENTH1
 ID OS1CUG_ENTH1 PRELIMINARY; PRT; 406 AA.
 AC OS1CUG;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE WD repeat protein.
 GN ORFNames=18 t00050;
 OS Entamoeba histolytica HM-1:IMNS.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OK NCBI_TaxID=294381;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HM-1:IMNS;
 RA PubMed=15729342; DOI=10.1038/nature03291;
 RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
 RA Amdeo P., Roncaglia P., Berriaman M., Hart R.P., Mann B.J., Nozaki T.,
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leijpe M.,
 RA Hofer M., Bruchhaus I., Willhoef U., Bhattacharya A.,
 RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
 RA Jagals K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
 RA Quail M.A., Rabinowitz B., Norbertczak H., Price C., Wang Z.,
 RA Guillen N., Lichter C., Strop S.E., Bhattacharya S., Lohia A.,
 RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
 RA Fraser C.M., Hall N.;
 RT "The genome of the protist parasite Entamoeba histolytica";
 RL Nature 433:865-868 (2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL, AAFB0100087; EAL50669.1; -; Genomic_DNA.
 DR InterPro; IPR011993; PH type.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 3.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR ProDom; PD000018; WD40; 1.
 DR SMART; SM00320; WD40; 6.
 DR PROSITE; PS00678; WD_REPEATS_1; 3.
 DR PROSITE; PS50082; WD_REPEATS_2; 3.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Cytokeleton; Repeat; WD repeat.
 SQ SEQUENCE 406 AA; 44778 MW; 2E753F50C60E32CB CRC64;

Query Match 90.6%; Score 29; DB 2; Length 406;
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
 :|||||
 Db 220 SGGTLOS 226

RESULT 18
 INXS_DROME
 ID INXS_DROME STANDARD; PRT; 419 AA.
 AC Q9VWD5; Q8MZL3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Innexin inxs
 GN Name=inx5; ORFNames=CG7537;
 OS Drosophila melanogaster (Fruit Fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OK NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
 RA MEDLINE=21959302; PubMed=11960713; DOI=10.1016/S0925-4773(02)00025-4;
 RA Stebbings L.A., Todman M.G., Phillips R., Greer C.E., Tam J.,
 RA Phelan P., Jacobs K., Bacon J.P., Davies J.A.;
 RT "Gap junctions in Drosophila: developmental expression of the entire
 RT innexin gene family";
 RL Mech. Dev. 113:197-205 (2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN-Berkeley;
 RX MEDLINE:20196006; PubMed10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams W.D., Ceiniker S.E., Holt R.A., Evans C.A., Gockyne J.D.,
 RA Amatiides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abiri J.F., Adiyani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borova D., Botchan M.R., Bouck J., Brockett P., Broctier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Ditzel S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei W.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merilov G., Milshina N.V., Moberly C., Morris J., Mostreli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacble J.M.,
 RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitlska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Waasman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP GENOME REANNOTATION.
 RX MEDLINE:22426069; PubMed12537572;
 RA Miura S., Crosby M.A., Mungall C.U., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochman S.B.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Ceiniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.22(2002).
 CC -1- FUNCTION: Structural component of the gap junctions (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in the cortex of the pupal CNS and
 CC at low levels in the wing imaginal disk.
 CC -1- DEVELOPMENTAL STAGE: Little or no embryonic expression.
 CC -1- SIMILARITY: Belongs to the pannexin family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL: A1057372; A125820.1; -; mRNA.
 DR EMBL: AE003511; AAF48923.2; -; Genomic DNA.
 DR Ensembl: CG7537; Drosophila melanogaster.
 DR FlyBase: FBgn0030989; Infs.
 DR GO: GO:0005921; C:gap junction; IEP.

DR GO: GO:0016021; C:Integral to membrane; NAS.
 DR GO: GO:0015286; F:Innexin channel activity; IEP.
 DR InterPro: IPR000990; Innexin.
 DR PANTHER: PTHR11993; Innexin; 2.
 DR Pfam: PF00876; Innexin; 1.
 DR PRINTS: PRO1262; INNEXIN.
 DR PROSITE: PS51013; PANNEXIN; 1.
 KW Gap junction; Transmembrane.
 FT TOPO_DOM 1 21
 FT TRANSMEM 2 42
 FT TOPO_DOM 43 162
 FT TRANSMEM 163 183
 FT TOPO_DOM 184 238
 FT TRANSMEM 239 259
 FT TOPO_DOM 260 320
 FT TRANSMEM 321 341
 FT TOPO_DOM 342 419
 FT SEQUENCE 419 AA; 48978 MW; 990C17B9ECABA209 CRC64;
 SQ
 Query Match 90.6%; Score 29; DB 1; Length 419;
 Best Local Similarity 85.7%; Pred. No. 3.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTLOS 7
 DB 411 SGSTLES 417
 RESULT 19
 Q6BCG8 EDWIC
 ID Q6BCG8 EDWIC PRELIMINARY; PRT; 438 AA.
 AC Q6BCG8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Edwardsiella ictaluri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Edwardsiella.
 OX NCBI_TaxID=67780;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Thune R.L., Fernandez D.H., Benoit J.L., Kelly-Smith M., Rogge M.L.,
 RA Boock N.J., Bologna R.A.;
 RT "Identification of Virulence Factors Involved in the Pathogenesis of
 RT Edwardsiella ictaluri Using Signature Tagged Mutagenesis.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY667437; AAT77726.1; -; Genomic DNA.
 DR InterPro: IPR001646; 5peptide_repeat.
 DR InterPro: IPR002885; PPR.
 DR Pfam: PF00805; Pentapeptide; 6.
 DR TIGRFAMs: TIGR00756; PPR; 1.
 KW Hypothetical protein.
 SQ
 Query Match 90.6%; Score 29; DB 2; Length 438;
 Best Local Similarity 85.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTLOS 7
 DB 320 SGATLOS 326
 RESULT 20
 Q4KYN6 PECFR
 ID Q4KYN6; PECFR PRELIMINARY; PRT; 448 AA.
 AC Q4KYN6;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Flagellin.
 GN Name=flaA;

```

OS Pectinatus frisingensis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Acidimicrococcaceae;
OC Pectinatus.
OX NCBI_TaxID=865;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 20465;
RA Chaban B., Deneer T., Deneer H., Hymer J., Ziola B.;
RT "Identification and Characterization of the Flagellin Gene and Protein
from the Genus Pectinatus.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY659943; AAT70054.1; -; Genomic_DNA.
KW Flagellum.
SQ SEQUENCE 448 AA; 46751 MW; 8E0B023FAE63CE0A CRC64;

Query Match 90.6%; Score 29; DB 2; Length 448;
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
DB 204 SGTLOS 210

RESULT 21
07SECG_ASHGO PRELIMINARY; PRT; 481 AA.
ID 07SECG;
AC 07SECG;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE AAR151WP.
GN Name=AAR151W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RA Pubmed=15001715; DOI=10.1126/science.1095781;
RA Dierich F.S., Voegel S., Brachat S., Lerch A., Gates K., Steiner S.,
Mohr C., Pohlmann R., Luedi P., Chol S., Wang R.A., Flavler A.,
Gaffney T.D., Phillipsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
DR EMBL; AE016814; AAS50518.1; -; Genomic_DNA.
DR HSSP; P09012; LAUD.
DR AGD; AAR151W; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0000398; F:nuclear mRNA splicing, via spliceosome; IEA.
DR InterPro; IPR012677; a_b_plalt_nuc_bd.
DR InterPro; IPR000504; RNPI_RNA_bd.
DR Pfam; PF00076; RRM_1; 2.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PS50102; RKM; 2.
KW Complete proteome.
SQ SEQUENCE 481 AA; 51096 MW; E4978F3587FC7112 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 481;
Best Local Similarity 85.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
DB 148 SGTLOS 154

RESULT 22
04SL06_TETNG
ID 04SL06_TETNG PRELIMINARY; PRT; 530 AA.
AC 04SL06;

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DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Chromosome 15 SCAFL14556, whole genome shotgun sequence.
GN ORNames=GSTENG00016129001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99863;
RN
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicod S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Saloubat M., Levy M., Boudet N., Castellano S.,
Antouard V., Jubin C., Castelli V., Karinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Beraudins V.,
Craud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosaak S.,
Kellis M., Volff JN., Guigo R., Zody M.C., Mestrov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetradon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CA601014556; CAP98426.1; -; Genomic_DNA.
SQ SEQUENCE 530 AA; 60724 MW; E4631908A65D3FA8 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 530;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
DB 223 SGTLOS 229

RESULT 23
GUP2_YEAST
ID GUP2_YEAST STANDARD; PRT; 609 AA.
AC 008929;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Glycero1 uptake protein 2.
GN Name=GUP2; OrderedLocustNames=YPL189W;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansong W.,
Aratijo R., Aparicio A., Bartell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung B., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dierich F.S., Delius H., Dipolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
Hall J., Hedling U., Heumann K., Hilbert H., Hillier L.W.,
RA Hunnicke-Smith S., Hyman R.W., Johnston M., Kalman S., Kleine K.,
Komp C., Kurd O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,

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RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Mosecl D.,
 RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
 RA Petzel F.X., Pohl T.M., Purrelle B., Rajandream M.A., Reichmann S.,
 RA Rieger M., Riles L., Roberts D., Schaefer M., Scharte M., Scherens B.,
 RA Schramm S., Schroeder M., Sidic A.-M., Teitelin H., Ureastarazu L.A.,
 RA Ushinsky S., Viereckels F., Vissers S., Voss H., Walsh S.V.,
 RA Wamburt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.-W.,
 RA Zollner A., Vo D.H., Hant J.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XVI.",
 RT Nature 387:103-105 (1997).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=20392443; PubMed=10931309;
 RA Holat B., Lunde C., Lages F., Oliveira R., Lucas C.,
 RA Kiehlend Brandt M.C.;
 RT "GUP1 and its close homologue GUP2, encoding multimer-spanning
 RT proteins involved in active glycerol uptake in *Saccharomyces
 cerevisiae*.";
 RT Mol. Microbiol. 37:108-124 (2000).
 RL -1- FUNCTION: Involved in active uptake of glycerol driven by
 CC electrogenic proton symport.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- SIMILARITY: Belongs to the membrane-bound acyltransferase family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; Z73545; CAA97902.1; -; Genomic DNA.
 CC EMBL; Z73544; CAA97901.1; -; Genomic DNA.
 CC PIR; S65208; S65208.
 CC Ensembl; YPL189W; *Saccharomyces cerevisiae*.
 DR SGD; S000006110; GUP2.
 DR GO; GO:0015793; P:glycerol transport; IGT.
 DR InterPro; IPR004299; MBOAT_fam.
 DR Pfam; PF03062; MBOAT; 1.
 DR Complete proteome; Symport; Transmembrane; Transport.
 KM FT TRANSMEM 76 95 Potential.
 KM FT TRANSMEM 129 151 Potential.
 KM FT TRANSMEM 164 186 Potential.
 KM FT TRANSMEM 201 218 Potential.
 KM FT TRANSMEM 323 345 Potential.
 KM FT TRANSMEM 365 387 Potential.
 KM FT TRANSMEM 408 427 Potential.
 KM FT TRANSMEM 501 523 Potential.
 KM FT TRANSMEM 535 557 Potential.
 KM FT TRANSMEM 577 594 Potential.
 KM ACT SITE 496 496 Potential.
 SQ SEQUENCE 609 AA; 71289 MW; 346B7BBD7E3B5830 CRC64;

Query Match 90.6%; Score 29; DB 1; Length 609;
 Best Local Similarity 85.7%; Pred. No. 4.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
 ID |||||:
 DB 293 SGGTLOT 299

RESULT 24
 Q23266 CAEEL PRELIMINARY; PRT; 613 AA.
 AC Q23266;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein ZC374.2;
 GN ORFNames=ZC374.2;
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology.";
 RT Science 282:2012-2018 (1998).
 RL EMBL; Z72518; CAA96700.1; -; Genomic DNA.
 DR PIR; T27528; T27528.
 DR Ensembl; ZC374.2; *Caenorhabditis elegans*.
 DR WormBase; WBGene00013872; ZC374.2.
 DR WormPeP; ZC374.2; CE03804.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR InterPro; IPR003961; FN_III.
 DR Pfam; PF00041; FN3; 3.
 DR SMART; SM0060; FN3; 4.
 DR PROSITE; PS50853; FN3; 5.
 KM Complete proteome; Hypothetical protein; Repeat; Transmembrane.
 SQ SEQUENCE 613 AA; 69659 MW; F107AEFD229F94D0 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 613;
 Best Local Similarity 85.7%; Pred. No. 4.9e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
 ID |||||:
 DB 233 SGGTLOT 239

RESULT 25
 NR1_YEAST
 ID NR1_YEAST STANDARD; PRT; 672 AA.
 AC P32831;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Negative growth regulatory protein NGR1 (RNA-binding protein RBP1).
 DE Name=NGR1; Synonyms=RB1; OrderedLocustNames=YBR212W; ORFNames=YBR1459;
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; *Saccharomycotina*; *Saccharomycetes*;
 OC *Saccharomycetales*; *Saccharomycetaceae*; *Saccharomyces*.
 OX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93315487; PubMed=8325883;
 RT Lee F.-U.S., Mose U.;
 RT "An RNA-binding protein gene (RBP1) of *Saccharomyces cerevisiae*
 RT encodes a putative glucose-repressible protein containing two RNA
 RT recognition motifs.";
 RT J. Biol. Chem. 268:15080-15087 (1993).
 RN [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=S288c;
 RX MEDLINE=95112788; PubMed=7813418;
 RA Feldmann H., Aigle M., Aljinovic G., Andre B., Baclet M.C., Barthe C.,
 RA Baur A., Becam A.-M., Bileau N., Boles B., Brandt T., Brendel M.,
 RA Bruckner M., Busseron F., Christensen C., Contreras R., Crouzet M.,
 RA Czapluch C., Demolis N., Delaveau T., Dougon F., Domdey H.,
 RA Duesterhus S., Fiers W., Fobo G.M., Fritz C., Gassenhuber H.,
 RA Glandsdorff N., Goffeau A., Grivell L.A., de Haan M., Hein C.,
 RA Herbert C.J., Hollenberg C.P., Holmstrom K., Jacq C., Jacquet M.,
 RA Jauniaux J.-C., Jomiaux J.-L., Kalliesse T., Kieau P., Kirchsch L.,
 RA Koetter P., Korol S., Liebl S., Loggne M., Lohan A.J.E., Louis B.J.,
 RA Li Z.-Y., Maat M.J., Mallet L., Mamhaupt G., Messenguy F., Miesha T.,
 RA Molmans F., Mueller S., Nasr F., Obermaier B., Pera J., Plerard A.,
 RA Piravandi E., Pohl F.M., Pohl T.M., Potter S., Proft M., Purrelle B.,
 RA Ramerant Rad M., Rieger M., Rose M., Schaaff-Gerschenlaeger I.,
 RA Scherens B., Schwartzlose C., Skala U., Slonimski P.P., Smits P.H.M.,
 RA Soulet J.-L., Steensma H.Y., Stucka R., Ureastarazu L.A.,
 RA van der Aart Q.J.M., Van Dyck L., Vaasartot A., Velter I.,

RA Vierendeels F., Viassers S., Wagner G., de Wergifosse P., Wolle K.H.,
 RA Zagalski M., Zimmermann F.K., Mewes H.-W., Kleine K.,
 RT "Complete DNA sequence of yeast chromosome II.";
 RL EMBL J. 13:5795-5809(1994).
 CC -1- FUNCTION: May be an RNA-binding protein involved in control of an
 CC RNA processing pathway that influences the regulation of cell
 CC growth in early log phase. Can bind to RNA and single-stranded DNA
 CC but not double-stranded DNA.
 CC -1- INTERACTION:
 CC P32770:NRPI; NbExp=1; IntAct=EBI-12002, EBI-12260;
 CC -1- SIMILARITY: Contains 3 RRM (RNA recognition motif) domains.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; Z14097; CAA78478.1; -; Genomic DNA.
 CC EMBL; Z36081; CAA65176.1; -; Genomic DNA.
 CC PIR; S46086; S46086.
 CC HSSP; 061474; 2MST.
 CC -----
 CC IntAct; P32831;
 CC GenomLine; 136755; -;
 CC DR GenomLine; YBR212W; Saccharomyces cerevisiae.
 CC DR SGD; S000000416; NGR1.
 CC DR GO; GO:0048471; C:perinuclear region; IDA.
 CC DR GO; GO:0003723; F:RNA binding; IDA.
 CC DR GO; GO:0003697; F:single-stranded DNA binding; IDA.
 CC DR GO; GO:0045182; F:translation regulator activity; IMP.
 CC DR GO; GO:007005; P:mitochondrion organization and biogenesis; IMP.
 CC DR GO; GO:0040008; P:regulation of growth; IMP.
 CC DR InterPro; IPR012677; a b plait nuc_bd.
 CC DR InterPro; IPR005054; RNP_RNA_bd.
 CC DR Pfam; PF00076; RRM_1; 2.
 CC DR SMART; SM00360; RRM; 2.
 CC DR PROSITE; PS50102; RRM; 2.
 CC KW Complete proteome; Repeat; RNA-binding.
 CC FT DOMAIN 36 159 RRM 1.
 CC FT DOMAIN 192 271 RRM 2.
 CC FT DOMAIN 360 432 RRM 3.
 CC FT COMPBIAS 278 295 Gln-rich.
 CC FT COMPBIAS 485 495 Poly-Gln.
 CC FT COMPBIAS 566 672 Asn/Met-rich.
 CC FT COMPBIAS 322 322 P -> S (in Ref. 1).
 CC FT CONFLICT 568 568 T -> N (in Ref. 1).
 CC FT CONFLICT 585 585 P -> S (in Ref. 1).
 CC SQ SEQUENCE 672 AA; 75024 MW; 12F64EC4C5716750 CRC64;
 CC -----
 CC Query Match 90.6%; Score 29; DB 1; Length 672;
 CC Best Local Similarity 85.7%; Pred. No. 5.5e+02;
 CC Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 SGGTQGS 7
 CC DB 178 SGGTQGS 184
 CC -----
 CC RESULT 26
 CC ID 0623A3 CAEBR PRELIMINARY; PRT; 680 AA.
 CC AC 0623A3;
 CC DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 CC DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 CC DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 CC DE Hypothetical protein CBG01939.
 CC GN Name=CBG01939;
 CC OS Caenorhabditis briggsae.
 CC OC Caenorhabditis briggsae.
 CC OC Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 CC OC Rhabditidae; Pelodierinae; Caenorhabditis.
 CC OX NCBI_TaxId=6238;
 CC RN [1]
 CC RP NUCLEOTIDE SEQUENCE.

RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC DR EMBL; CAC0100010; CA58749.1; -; Genomic DNA.
 CC DR InterPro; IPR003961; FN_III.
 CC DR Pfam; PF00041; fn3; 3.
 CC DR SMART; SM00060; FN3; 4.
 CC DR PROSITE; PS50853; FN3; 5.
 CC KW Hypothetical protein; Repeat; Transmembrane.
 CC SQ SEQUENCE 680 AA; 76492 MW; D9BC5FCALDCRB6AF CRC64;
 CC -----
 CC Query Match 90.6%; Score 29; DB 2; Length 680;
 CC Best Local Similarity 85.7%; Pred. No. 5.6e+02;
 CC Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 SGGTQGS 7
 CC DB 236 SGGTQGS 242
 CC -----
 CC RESULT 27
 CC ID 04MAD5 ASPPU PRELIMINARY; PRT; 757 AA.
 CC AC 04MAD5;
 CC DT 13-SEP-2005 (T-EMBLrel. 31, Created)
 CC DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 CC DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
 CC DE Peptide transporter MTD1.
 CC GN ORFNames=AtUg90910;
 CC OS Aspergillus fumigatus Af293.
 CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 CC OX NCBI_TaxId=330879;
 CC RN [1]
 CC RP NUCLEOTIDE SEQUENCE.
 CC RC STRAIN=AF293;
 CC RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
 RA Artzy A., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Foster G.H., Fraser A., Garcia J.L., Garcia M.J., Godle A.,
 RA Goldman G.H., Goni K., Griffith-Jones S., Guilliam R., Haas B.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
 RA Majoros W.H., May G.S., Miller L.V., Mohamoud Y., Molina M., Monod M.,
 RA Mouyia I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
 RA Penava M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitch E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Remington H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Rensing C.M., Ruter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B., Denning D.W.;
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT Aspergillus fumigatus."
 RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC DR EMBL; AAH0100015; EAL64801.1; -; Genomic DNA.
 CC SQ SEQUENCE 757 AA; 84174 MW; 84FBBA86CT51E25A CRC64;
 CC -----
 CC Query Match 90.6%; Score 29; DB 2; Length 757;
 CC Best Local Similarity 85.7%; Pred. No. 6.3e+02;
 CC Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 1 SGGTQGS 7
 CC DB 605 SGGTQGS 611

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RESULT 28
O6FMN2_CANGA
ID O6FMN2_CANGA PRELIMINARY; PRT; 802 AA.
AC O6FMN2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Candida glabrata strain CBS138 chromosome K complete sequence.
GN OrderedLocusNames=CAGL0R06655g;
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
(1)
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 2001 / CBS 138;
RC PubMed=15229592; DOI=10.1038/nature02579;
RX Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
  Latourelle I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
  Goffard N., Francaul L., Aigle M., Anhouard V., Badoir A., Baïde V.,
  Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
  Boileau A., Boyer J., Catolico L., Confantoni F., de Darvar A.,
  Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
  Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
  Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Müller H.,
  Nicoud J.-M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,
  Pellens S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
  Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
  Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
  Bouchier C., Caudon B., Scarpelli C., Galliard C., Weissenbach J.,
  Wincker P., Souciet J.-L.,
  "Genome evolution in yeasts.";
RT Nature 430:35-44(2004).
DR EMBL; CR380957; CAG61473.1; -; Genomic DNA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0003981; P:nuclear mRNA splicing, via spliceosome; IEA.
DR InterPro; IPR012677; a b plat nuc_bd.
DR InterPro; IPR005054; RNP_RNA_Bd.
DR Pfam; PF00076; RRM_1; 2.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PS50102; RRM; 2.
KW Complete proteome.
SQ
SEQUENCE 802 AA; 88237 MW; 38D528A92962E5B2 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 802;
Best Local Similarity 85.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 220 SGGTLOS 226

RESULT 29
O4J6T1_SULAC
ID O4J6T1_SULAC PRELIMINARY; PRT; 879 AA.
AC O4J6T1;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Scd1_2215;
OS Sulfolobus acidocaldarius.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2285;
(1)
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 33909 / NCIB 11770 / DSM 639;
RC PubMed=15995215; DOI=10.1128/JB.187.14.4992-4999.2005;
RX Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarinson E.,

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RA Greve B., Awayez M., Zibat A., Klenk H.-P., Garrett R.A.;
RT "The genome of Sulfolobus acidocaldarius, a model organism of the
  Crenarchaeota.";
RL J. Bacteriol. 187:4992-4999(2005).
DR EMBL; CP000077; AA01501.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 879 AA; 93653 MW; 77081EB79751DC1C CRC64;

Query Match 90.6%; Score 29; DB 2; Length 879;
Best Local Similarity 85.7%; Pred. No. 7.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 720 SGGTLOS 726

RESULT 30
O4HYT6_GIBZE
ID O4HYT6_GIBZE PRELIMINARY; PRT; 927 AA.
AC O4HYT6;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG09872.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocortemycetidae; Hypocortemycetes; Nectriciaceae; Gibberella.
OX NCBI_TaxID=229533;
(1)
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PH-1;
RC Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
  Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
  Boudgallier B., Butler J., Calvo S.E., Camarata J., Chang U.,
  Chepel Y., Collymore A., Cook A., Cooke P., Corum B., Develiano K.,
  Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
  Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
  Gardina S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
  Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
  Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
  Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Liu A.,
  Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
  Matthews C., Mauceli E., McCarthy M., Meldrum J., Menus L.,
  Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
  Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
  Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
  Rachupka A., Ramsamy U., Raymond C., Reta R., Rise C., Rogov P.,
  Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
  Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M.,
  Talmas J., Tesfaye S., Theodore J., Topham K., Travers M.,
  Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
  Wu X., Wyman D., Young G., Zainoun J., Zemke L., Zimmer A., Zody M.,
  Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
DR EMBL; AACM0100409; EAA67756.1; -; Genomic DNA.
KW Hypothetical protein.
SQ
SEQUENCE 927 AA; 102248 MW; 3E120C6A16C28B5 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 927;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 816 SGGTLOS 822

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RESULT 31
Q9H5J5 HUMAN
ID Q9H5J5 HUMAN PRELIMINARY; PRT; 1117 AA.
AC Q9H5J5
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ23377.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RA Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Oka T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RL Submitted (JUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK027030; BAB15631.1; -; mRNA.
SQ SEQUENCE 1117 AA; 126894 MW; 09C16CAE9CCAC674 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 1117;
Best Local Similarity 85.7%; Pred. No. 9.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
Db 226 NGSTLOS 232

RESULT 32
Q4RLJ2 TETNG
ID Q4RLJ2 TETNG PRELIMINARY; PRT; 1221 AA.
AC Q4RLJ2
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAP15024, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0032669001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetradon.
NCBI_TaxID=99883;
RN NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Poulain J., De Berardinis V.,
RA Biemont C., Skalli Z., Cartolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Couranceau J.P., Gouay J.,
RA Perria G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Keills M., Volif J.N., Birren B., Nussbaum C., Kahn D., Robinson-Rechavi M.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "genome duplication in the teleost fish Tetradon nigroviridis reveals
the early vertebrate proto-karyotype.";
NCBI_TaxID=946-957(2004).
RN NUCLEOTIDE SEQUENCE.
RA Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: CAAE01015024; CAG10900.1; -; Genomic_DNA.
FT NON_TER 1

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SQ SEQUENCE 1221 AA; 130940 MW; 978D14EDC27B2CB3 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 1221;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
Db 544 SGSTLOS 550

RESULT 33
Q9NSI4 HUMAN
ID Q9NSI4 HUMAN PRELIMINARY; PRT; 1254 AA.
AC Q9NSI4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein DKFZP761N1024 (OTTHUMP0000017984)
DE (Fragment).
GN Name=DKFZP761N1024; ORFNames=RP1-202D23.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RA Sehra H.;
RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL162056; CAB82395.1; -; mRNA.
DR EMBL: AL121716; CA142425.1; -; Genomic_DNA.
DR PIR: T47141; T47141.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 1254 AA; 141862 MW; 7E1F86128B6CD16 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 1254;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
Db 363 NGSTLOS 369

RESULT 34
Q9UPN5 HUMAN
ID Q9UPN5 HUMAN PRELIMINARY; PRT; 1558 AA.
AC Q9UPN5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIAA117 protein (Fragment).
GN Name=KIAA117;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RA TISSUE=Brain;
RX MEDLINE=99397452; PubMed=10470851;
RA Kikuno R., Nagase T., Ishikawa K.-I., Hirosewa M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
The complete sequences of 100 new cDNA clones from brain which code

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RT for large proteins in vitro."
 RL DNA Ref. 6:197-205 (1999).
 DR EMBL; AB029040; BAA83069.2; -; mRNA.
 DR EMBL; ENSG0000083097; Homo sapiens.
 DR HGNC; HGNC:21194; KIAA1117.
 FT NON TER
 SQ SEQUENCE 1558 AA; 175803 MW; 49D7EBF32F67D1 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 1558;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTQVS 7
 :|||||
 Db 667 NGSTLQS 673

RESULT 35
 OSMZMS SYN6 PRELIMINARY; PRT; 1568 AA.

AC OSMZMS;
 DT 01-FEB-2005 (TRENBLrel. 29, Created)
 DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
 DE Hypothetical protein.
 GN OrderedCusNames=svc2305 G;
 OS Synchococcus sp. (strain PCC 6301) (Anacystis nidulans).
 OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
 NCBI_TaxID=269084;
 RX NCB1_TaxID=269084;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCC6301;
 RA Sugita M.;
 RT "Complete genome structure of the unicellular cyanobacterium Anacystis
 nidulans 6301 (Synchococcus sp. PCC6301).";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB008231; BAD80495.1; -; Genomic_DNA.
 DR InterPro; IPR007452; DUF490.
 DR Pfam; PF04357; DUF490; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 1568 AA; 169357 MW; 37DAFBA0D1F15DCP CRC64;

Query Match 90.6%; Score 29; DB 2; Length 1568;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTQVS 7
 :|||||
 Db 1372 SGSTLQT 1378

RESULT 36
 OSTA12 HUMAN PRELIMINARY; PRT; 2369 AA.

AC OSTA12;
 DT 01-FEB-2005 (TRENBLrel. 29, Created)
 DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE OTTHMP0000017983.
 GN Name=KIAA1117; ORFNames=RP1-202D23.2-001;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX NCB1_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RA Laird G.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RA Sehra H.;
 RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL139333; CA115284.1; -; Genomic DNA.
 DR EMBL; AL121716; CA142426.1; -; Genomic DNA.
 DR EMBL; AL121716; CA115284.1; JOINED; Genomic DNA.
 DR EMBL; AL139333; CA142426.1; JOINED; Genomic DNA.
 DR EMBL; ENSG0000083097; Homo sapiens.
 DR HGNC; HGNC:21194; KIAA1117.
 DR InterPro; IPR007249; Dozey N.
 DR Pfam; PF04118; Dozey N; 1.
 SQ SEQUENCE 2369 AA; 266560 MW; C6C8CFC70F1D9B64 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 2369;
 Best Local Similarity 85.7%; Pred. No. 2.3e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTQVS 7
 :|||||
 Db 1555 NGSTLQS 1561

RESULT 37
 O4OHG5 LEIMA PRELIMINARY; PRT; 6735 AA.

AC O4OHG5;
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=LmjF10_0500;
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 NCBI_TaxID=5664;
 RX NCB1_TaxID=5664;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=Friedlin;
 RA Peacock C.S.; Murphy L.; Ivens A.C.; Berriman M.; Blackwell J.;
 RA Smith D.; Collins M.; Foster N.; Harris D.; Oliver K.; O'Neill S.;
 RA Saunders D.; Seeger K.; Warren T.; Rajandream M.; and Barrell B.G.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CT005249; CAJ02617.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 6735 AA; 706908 MW; D89D718AABPBPEBA CRC64;

Query Match 90.6%; Score 29; DB 2; Length 6735;
 Best Local Similarity 85.7%; Pred. No. 7.8e+03;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTQVS 7
 :|||||
 Db 186 SGSTVQS 192

RESULT 38
 Q9CUZ6 MOUSE PRELIMINARY; PRT; 37 AA.

AC Q9CUZ6;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched
 library, clone:231081G03 product:FRIZZLED 7 (FRIZZLED-7) (FZ-7)
 DE (MF27) homolog (Fragment).
 GN Name=Fzd7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX NCB1_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P.; Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."

RL Mech. Enzymol. 303:19-44 (1999).
 [2]
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.O., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
 RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 [3]
 RC NUCLEOTIDE SEQUENCE.
 RX STRAIN=C57BL/6J; TISSUE=Tongue;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 [4]
 RC NUCLEOTIDE SEQUENCE.
 RX STRAIN=C57BL/6J; TISSUE=Tongue;
 RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 [5]
 RC NUCLEOTIDE SEQUENCE.
 RX STRAIN=C57BL/6J; TISSUE=Tongue;
 RA MEDLINE=20530913; PubMed=11076861; DOI=10.1101/9r.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsuki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 [6]
 RC NUCLEOTIDE SEQUENCE.
 RX STRAIN=C57BL/6J; TISSUE=Tongue;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Konda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muraumatsu M., Hayashizaki Y.;
 RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AK010239; BAB26790.1; -, mRNA.
 MGI, MGI:108570; Fzd7.

DR GO: 0005615; C:extracellular space; TAS.
 DR GO: 0016021; C:integral to membrane; TAS.
 DR InterPro: IPR000539; Trizzled.
 DR Pfam: PF01534; Trizzled. 1.
 FT NON TER 1
 SQ SEQUENCE 37 AA; 4307 MW; DA16B87F74D21286 CRC64;
 Query Match 87.5%; Score 28; DB 2; Length 37;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SGGTLOS 7
 DB 13 SGGTLOS 19
 RESULT 39
 Q5DMW8_9PRO1 PRELIMINARY; PRT; 92 AA.
 ID Q5DMW8;
 AC Q5DMW8;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DT PHYC (Fragment).
 GN Name=PHYC;
 OS Petalodiscus bojerianus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Malpighiales; Phyllanthaceae; Wielandiales;
 OC Petalodiscus.
 OC NCBI_TaxID=283144;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RS_PHY1;
 RA Samuel R., Kachararachchi H., Hoffmann P., Barfuss M., Murrack K.J.,
 RA Davis C., Chase M.W.;
 RT "Molecular phylogenetics of Phyllanthaceae: evidence from plastid MATK
 RT and nuclear PHYC sequences.";
 RL Am. J. Bot. 92:132-141 (2005).
 DR EMBL: AY579860; AAU12418.1; -, Genomic DNA.
 DR GO: 0008020; F:G-protein coupled photoreceptor activity; IEA.
 DR GO: 0018298; F:protein-chromophore linkage; IEA.
 DR GO: 0009585; F:red, far-red light phototransduction; IEA.
 DR GO: 0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001294; Phytochrome.
 DR PROSITE: PS00245; PHYTOCHROME_1; 1.
 DR PROSITE: PS50046; PHYTOCHROME_2; 1.
 KW Chromophore; Photoreceptor protein; Phytochrome.
 FT NON TER 1
 FT NON TER 92
 SQ SEQUENCE 92 AA; 10319 MW; 053F5A0915BAECA CRC64;
 Query Match 87.5%; Score 28; DB 2; Length 92;
 Best Local Similarity 85.7%; Pred. No. 99;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGGTLOS 7
 DB 41 SGGTLOS 47
 RESULT 40
 Q39765_GINBI PRELIMINARY; PRT; 114 AA.
 ID Q39765;
 AC Q39765;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DT Phytochrome (Fragment).
 GN Name=PHY;
 OS Ginkgo biloba (Ginkgo).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

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OX NCB1_TaxID=3311;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Mathews S., Lavin M., Sharrock R.A.;
RT "Evolution of the phytochrome gene family and its utility for
   phylogenetic analyses of angiosperms."
RL Ann. Mo. Bot. Gard. 82:296-321(1995).
DR EMBL: U08163; AAA17807.1; -; Genomic DNA.
DR GO: GO:0008020; P:G-protein coupled photoreceptor activity; IEA.
DR GO: GO:0016301; P:kinase activity; IEA.
DR GO: GO:0016740; P:transferase activity; IEA.
DR GO: GO:0018298; P:protein-chromophore linkage; IEA.
DR GO: GO:0009585; P:red, far-red light phototransduction; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO: GO:0007600; P:sensory perception; IEA.
DR GO: GO:0007601; P:visual perception; IEA.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR001294; Phytochrome.
DR PROSITE: PS50046; PHYTOCHROME_2; 1.
KW Phytochrome.
FT NON_TER
FT NON_TER
SQ SEQUENCE 114 AA; 12651 MW; EA789428F594AB6E CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 114;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSTLOS 7
DB 47 GSTLOS 52

RESULT 41
Q6ZP90_HUMAN PRELIMINARY; PRT; 168 AA.
AC Q6ZP90;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ26218.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=adrenal gland;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK129729; BAC85229.1; -; mRNA.
SQ SEQUENCE 168 AA; 18201 MW; A52070DA8DE8AEB2 CRC64;

Query Match
Best Local Similarity 87.5%; Score 28; DB 2; Length 168;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
DB 119 SGSTLOS 125

RESULT 42
Q9CHH7_LACTA PRELIMINARY; PRT; 171 AA.
AC Q9CHH7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein yhgB.
GN Name=yhgB; OrderedLocustNames=IL0754;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OK NCB1_TaxID=1360;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr-16979;
RA Bolotin A., Wincker P., Manger S., Jallion O., Matarne K.,
RA Welserbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
   lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
DR EMBL: AB006309; AAK04852.1; -; Genomic DNA.
DR PIR: B86719; B86719.
DR InterPro: IPR001646; Speptide_repeat.
DR Pfam: PF00805; Pentapeptide_2.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 171 AA; 19655 MW; E89A5D722E220AB2 CRC64;

Query Match
Best Local Similarity 87.5%; Score 28; DB 2; Length 171;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
DB 85 SGSTLOS 91

RESULT 43
Q9FD01_ERWST PRELIMINARY; PRT; 182 AA.
AC Q9FD01;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HrpL.
GN Name=hrpL;
OS Erwinia stewartii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pantoea.
OK NCB1_TaxID=66271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SS104;
RX MEDLINE=21517631; PubMed=11605961;
RA Frederick R.D., Ahmad M., Majerczak D.R., Arroyo-Rodriguez A.S.,
RA Mannila S., Coplin D.L.;
RT "Genetic organization of the Pantoea stewartii subsp. stewartii hrp
   gene cluster and sequence analysis of the hrpA, hrpC, hrpN, and wtsB
   operons."
RL Mol. Plant Microbe Interact. 14:1213-1222(2001).
DR EMBL: AF282857; AAG01453.1; -; Genomic DNA.
DR GO: GO:0003893; F:DNA-directed RNA polymerase activity; IEA.
DR GO: GO:0006987; F:sigma factor activity; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006457; P:protein folding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO: GO:0006986; P:response to unfolded protein; IEA.
DR GO: GO:0006352; P:transcription initiation; IEA.
DR InterPro: IPR007627; Sigma70_r2.
DR Pfam: PF04542; Sigma70_r2; 1.
SQ SEQUENCE 182 AA; 21305 MW; 1195180C764C8918 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 182;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSTLOS 7

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Db 124 GSSTLQS 129

RESULT 44

Q9W2Z1_DROME

ID Q9W2Z1_DROME PRELIMINARY; PRT; 186 AA.

AC Q9W2Z1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)

DE CG15131-PA.

GN Name=CG15131; ORFNames=CG15131;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OC NCB1_TaxID=7227;

OX NCB1_TaxID=7227;

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P., Burris K.C., Busam D.A., Butler H., Cadieu L.B., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W., Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K., Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ijzerman C., Jaitai M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laske P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M.D., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasmann D.A., Weinstein G.M., Weisenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of *Drosophila melanogaster*."

RT Science 287:2185-2195(2000).

RL [2]

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=22426065; PubMed=12537572;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R., Pacle J.M., Park S., Pfeiffer B.D., Richardson S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila melanogaster* euchromatic genome sequence."

RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RL [3]

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;

RT "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomic perspective."

RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).

RL [4]

RP NUCLEOTIDE SEQUENCE.

RP MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Bertencourt B.R., Celniker S.E., de Grey A.D.N.-J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;

RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review."

RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

RL [5]

RP NUCLEOTIDE SEQUENCE.

RP Berkeley *Drosophila* Genome Project;

RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R., Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E., Yu C., Rubin G.;

RT "Drosophila melanogaster release 4 sequence."

RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RL [6]

RP NUCLEOTIDE SEQUENCE.

RP FlyBase;

RG Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

RL EMBL; AE003449; AAF46546.1; -; Genomic DNA.

DR Ensemble; CG15131; Drosophila melanogaster.

DR FlyBase; FBgn0030173; CG15131.

DR GO; GO:000576; C:extracellular region; IEA.

DR GO; GO:0008061; P:chitin binding; IEA.

DR GO; GO:0006030; P:chitin metabolism; IEA.

DR InterPro; IPR002557; Chitin_bind_Pera.

DR Pfam; PF01607; CBM_14; 1.

DR SMART; SM00494; ChIBD2; 1.

DR SOURCE; PSS0940; CHIT BIND II; 1.

DR SEQUNCE 186 AA; 20609 MW; EPEDEK428914952EA CRC64;

SQ

Query Match 87.5%; Score 28; DB 2; Length 186;

Best local Similarity 85.7%; Pred. No. 2.2e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 36 GSSTLQS 42

QY 1 GSSTLQS 7

DB 36 GSSTLQS 42

RESULT 45

Q5DMZ1_GROSI

ID Q5DMZ1_GROSI PRELIMINARY; PRT; 193 AA.

AC Q5DMZ1;

DT 10-MAY-2005 (TrEMBLrel. 30, Created)

DT 10-MAY-2005 (TrEMBLrel. 30, last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, last annotation update)

DE PHYC (Fragment).

GN Name=PHYC;

OS Melnickia phyllanthoides.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eusteroids I; Malpighiales; Phyllanthaceae; Phyllanthaceae; Melnickia.

OX NCB1_TaxID=283128;

RL [1]

RP NUCLEOTIDE SEQUENCE.

RP STRAIN=RS_PHY28;

RA Samuel R., Kattrirachchi H., Hofmann P., Barfuss M., Wurdack K.J., Davis C., Chase M.W.;

RT "Molecular phylogenetics of Phyllanthaceae: evidence from plastid MATK

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RT and nuclear PHYC sequences." ;
RL Am. J. Bot. 92:132-141(2005).
GN Name=PHYC;
OS Gonatogyne brasiliensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids I; Malpighiales; Phyllanthaceae; Wielandiae;
OC Gonatogyne.
OX NCBI_TaxID=179686;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RS_PHY21;
RA Samuel R., Kathiraratchchi H., Hoffmann P., Barfuss M., Wurdack K.J.,
RA Davis C., Chae M.W.;
RT "Molecular phylogenetics of Phyllanthaceae: evidence from plastid MATK
RT and nuclear PHYC sequences." ;
RL Am. J. Bot. 92:132-141(2005).
EMBL; AY579861; AAU12415.1; -, Genomic_DNA.
DR GO; GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
DR GO; GO:0018298; P:protein-chromophore linkage; IEA.
DR GO; GO:0009585; P:red, far-red light phototransduction; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR001294; Phytochrome.
DR PRINTS; PR01033; PHYTOCHROME.
DR PROSITE; PS50046; PHYTOCHROME_2; 1.
KM Chromophore; Photoreceptor protein; Phytochrome.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 193 AA; 21939 MW; A662242637106EE CRC64;

Query Match
Best Local Similarity 87.5%; Score 28; DB 2; Length 193;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 32 SGGTLOS 38

RESULT 46
Q4VMK1_9PRO1 PRELIMINARY; PRT; 200 AA.
ID Q4VMK1_9PRO1 PRELIMINARY; PRT; 200 AA.
AC Q4VMK1;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE PHYC (Fragment).
GN Name=PHYC;
OS Reverchonina arenaria.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids I; Malpighiales; Phyllanthaceae; Phyllanthaceae;
OC Reverchonina.
OX NCBI_TaxID=300956;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Published=15904861; DOI=10.1016/j.ympev.2004.12.002;
RA Kathiraratchchi H., Hoffmann P., Samuel R., Wurdack K.J., Chae M.W.;
RT "Molecular phylogenetics of Phyllanthaceae inferred from five genes
RT (plastid atpB, matK, 3' rnhF, rbcL, and nuclear PHYC)." ;
RL Mol. Phylogenet. Evol. 36:112-134(2005).
EMBL; AY830380; AAX48138.1; -, Genomic_DNA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR001294; Phytochrome.
DR PRINTS; PR01033; PHYTOCHROME.
DR PROSITE; PS00245; PHYTOCHROME_1; 1.
KM Chromophore; Photoreceptor protein; Phytochrome.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 200 AA; 22555 MW; 6D449C5A63C9E96 CRC64;

Query Match
Best Local Similarity 87.5%; Score 28; DB 2; Length 200;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 34 SGGTLOS 40

RESULT 47
Q5DMZ7_9PRO1 PRELIMINARY; PRT; 206 AA.
ID Q5DMZ7_9PRO1 PRELIMINARY; PRT; 206 AA.
AC Q5DMZ7;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)

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DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE PHYC (Fragment).
GN Name=PHYC;
OS Gonatogyne brasiliensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids I; Malpighiales; Phyllanthaceae; Wielandiae;
OC Gonatogyne.
OX NCBI_TaxID=179686;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RS_PHY21;
RA Samuel R., Kathiraratchchi H., Hoffmann P., Barfuss M., Wurdack K.J.,
RA Davis C., Chae M.W.;
RT "Molecular phylogenetics of Phyllanthaceae: evidence from plastid MATK
RT and nuclear PHYC sequences." ;
RL Am. J. Bot. 92:132-141(2005).
EMBL; AY579861; AAU12415.1; -, Genomic_DNA.
DR GO; GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
DR GO; GO:0018298; P:protein-chromophore linkage; IEA.
DR GO; GO:0009585; P:red, far-red light phototransduction; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR001294; Phytochrome.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 206 AA; 23079 MW; 50CA2761A9F49CB1 CRC64;

Query Match
Best Local Similarity 87.5%; Score 28; DB 2; Length 206;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 41 SGGTLOS 47

RESULT 48
Q5DMY7_9PRO1 PRELIMINARY; PRT; 221 AA.
ID Q5DMY7_9PRO1 PRELIMINARY; PRT; 221 AA.
AC Q5DMY7;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE PHYC (Fragment).
GN Name=PHYC;
OS Petalodiscus platyrachis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eustosids I; Malpighiales; Phyllanthaceae; Wielandiae;
OC Petalodiscus.
OX NCBI_TaxID=283147;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RS_PHY32;
RA Samuel R., Kathiraratchchi H., Hoffmann P., Barfuss M., Wurdack K.J.,
RA Davis C., Chae M.W.;
RT "Molecular phylogenetics of Phyllanthaceae: evidence from plastid MATK
RT and nuclear PHYC sequences." ;
RL Am. J. Bot. 92:132-141(2005).
EMBL; AY579861; AAU12415.1; -, Genomic_DNA.
DR GO; GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
DR GO; GO:0018298; P:protein-chromophore linkage; IEA.
DR GO; GO:0009585; P:red, far-red light phototransduction; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR001294; Phytochrome.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 221 AA; 23079 MW; 50CA2761A9F49CB1 CRC64;

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DR Pfam; PF00360; Phytochrome; 1.
 DR PRINTS; PR01033; PHYTOCHROME.
 DR PROSITE; PS00245; PHYTOCHROME_1; 1.
 DR PROSITE; PS50046; PHYTOCHROME_2; 1.
 KM Chromophore; Photoreceptor protein; Phytochrome.
 FT NON_TER 1
 FT NON_TER 221
 SQ SEQUENCE 221 AA; 24717 MW; 54D7055C4B4FD6D3 CRC64;

Query Match 87.5%; Score 28; DB 2; Length 221;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
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 DB 41 SGSTLRS 47

RESULT 49
 OSNM10_9PRO1 PRELIMINARY; PRT; 223 AA.
 ID OSDN10;
 AC OSDN10;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE PHYC (Fragment).
 GN Name=PHYC;
 OS Baccaurea javanica.
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eustosids I; Malpighiales; Phyllanthaceae; Dypeteae;
 OC Baccaurea.
 OC NCBI_Taxid=287980;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RS_PHY7;
 RA Samuel R., Kattriarachchi H., Hoffmann P., Barfuss M., Murdack K.J.,
 RA Davis C., Chase M.W.;
 RT "Molecular phylogenetics of Phyllanthaceae: evidence from plastid MATK
 and nuclear PHYC sequences";
 RL Am. J. Bot. 92:132-141(2005).
 DR EMBL; AY579836; AAU12396.1; -; Genomic_DNA.
 DR GO; GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
 DR GO; GO:0018298; P:protein-chromophore linkage; IEA.
 DR GO; GO:0009585; P:red, far-red light phototransduction; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR001294; Phytochrome.
 DR Pfam; PF01590; GAF; 1.
 DR Pfam; PF00360; Phytochrome; 1.
 DR PRINTS; PR01033; PHYTOCHROME.
 DR PROSITE; PS00245; PHYTOCHROME_1; 1.
 DR PROSITE; PS50046; PHYTOCHROME_2; 1.
 KM Chromophore; Photoreceptor protein; Phytochrome.
 FT NON_TER 1
 FT NON_TER 223
 SQ SEQUENCE 223 AA; 24966 MW; F40F5C4C2479CDB1 CRC64;

Query Match 87.5%; Score 28; DB 2; Length 223;
 Best Local Similarity 85.7%; Pred. No. 2.7e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
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 DB 41 SGSTLRS 47

RESULT 50
 OSDMY6_9PRO1 PRELIMINARY; PRT; 224 AA.
 ID OSDMY6;
 AC OSDMY6;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE PHYC (Fragment).
 GN Name=PHYC;
 OS Petalodiscus leandrianus.
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eustosids I; Malpighiales; Phyllanthaceae; Wielanditeae;
 OC Petalodiscus.
 OC NCBI_Taxid=283146;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RS_PHY33;
 RA Samuel R., Kattriarachchi H., Hoffmann P., Barfuss M., Murdack K.J.,
 RA Davis C., Chase M.W.;
 RT "Molecular phylogenetics of Phyllanthaceae: evidence from plastid MATK
 and nuclear PHYC sequences";
 RL Am. J. Bot. 92:132-141(2005).
 DR EMBL; AY579862; AAU12420.1; -; Genomic_DNA.
 DR GO; GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
 DR GO; GO:0018298; P:protein-chromophore linkage; IEA.
 DR GO; GO:0009585; P:red, far-red light phototransduction; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR001294; Phytochrome.
 DR Pfam; PF01590; GAF; 1.
 DR Pfam; PF00360; Phytochrome; 1.
 DR PRINTS; PR01033; PHYTOCHROME.
 DR PROSITE; PS00245; PHYTOCHROME_1; 1.
 DR PROSITE; PS50046; PHYTOCHROME_2; 1.
 KM Chromophore; Photoreceptor protein; Phytochrome.
 FT NON_TER 1
 FT NON_TER 224
 SQ SEQUENCE 224 AA; 24998 MW; 81AB4D1D6D4FD9F8 CRC64;

Query Match 87.5%; Score 28; DB 2; Length 224;
 Best Local Similarity 85.7%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
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 DB 41 SGSTLRS 47

Search completed: January 17, 2006, 12:06:38
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102	27	84.4	1176	4	PCR-US93-11405A-10	Sequence 10, Appl	175	25	78.1	147	2	US-09-854-133-99	Sequence 99, Appl
103	27	84.4	1176	4	US-08-835-160-2	Sequence 2, Appl	176	25	78.1	159	2	US-09-370-838-98	Sequence 98, Appl
104	27	84.4	1177	2	US-08-855-160-6	Sequence 8, Appl	177	25	78.1	159	2	US-09-854-133-98	Sequence 98, Appl
105	27	84.4	1177	2	US-08-855-160-8	Sequence 6, Appl	178	25	78.1	164	2	US-09-949-016-7480	Sequence 7480, Ap
106	27	84.4	1177	2	US-08-855-160-6	Sequence 8, Appl	179	25	78.1	164	2	US-09-488-039A-14040	Sequence 14040, A
107	27	84.4	1181	1	US-07-951-715A-11	Sequence 11, Appl	180	25	78.1	196	2	US-09-252-991A-32026	Sequence 32026, A
108	27	84.4	1181	1	US-07-951-715A-13	Sequence 13, Appl	181	25	78.1	223	2	US-09-252-991A-17251	Sequence 17251, A
109	27	84.4	1181	1	US-07-951-715A-15	Sequence 15, Appl	182	25	78.1	254	2	US-09-252-991A-23311	Sequence 23311, A
110	27	84.4	1181	1	US-07-951-715A-17	Sequence 17, Appl	183	25	78.1	313	2	US-09-270-767-42356	Sequence 42356, A
111	27	84.4	1181	1	US-07-951-715A-17	Sequence 17, Appl	184	25	78.1	315	2	US-09-904-615-124	Sequence 124, App
112	27	84.4	1181	1	US-07-951-715A-17	Sequence 17, Appl	185	25	78.1	315	2	US-10-054-998-124	Sequence 1659, App
113	27	84.4	1181	1	US-08-459-448A-13	Sequence 13, Appl	186	25	78.1	338	2	US-09-902-540-16259	Sequence 8184, Ap
114	27	84.4	1181	1	US-08-459-448A-15	Sequence 15, Appl	187	25	78.1	344	2	US-09-328-352-81824	Sequence 16337, A
115	27	84.4	1181	1	US-08-459-448A-17	Sequence 17, Appl	188	25	78.1	350	1	US-09-428-796A-16337	Sequence 14, Appl
116	27	84.4	1181	1	US-08-459-448A-28	Sequence 28, Appl	189	25	78.1	350	1	US-07-868-353A-11	Sequence 23, Appl
117	27	84.4	1181	2	US-08-459-595A-11	Sequence 11, Appl	190	25	78.1	350	2	US-08-407-804-23	Sequence 23, Appl
118	27	84.4	1181	2	US-08-459-595A-13	Sequence 13, Appl	191	25	78.1	350	2	US-09-124-807-23	Sequence 23, Appl
119	27	84.4	1181	2	US-08-459-595A-15	Sequence 15, Appl	192	25	78.1	354	1	US-07-868-353A-15	Sequence 15, Appl
120	27	84.4	1181	2	US-08-459-595A-17	Sequence 17, Appl	193	25	78.1	354	1	US-08-407-804-24	Sequence 24, Appl
121	27	84.4	1181	2	US-08-459-595A-28	Sequence 28, Appl	194	25	78.1	354	2	US-09-124-807-24	Sequence 11, Appl
122	27	84.4	1181	2	US-08-459-504B-11	Sequence 11, Appl	195	25	78.1	358	1	US-08-604-913B-11	Sequence 1, Appl
123	27	84.4	1181	2	US-08-459-504B-13	Sequence 13, Appl	196	25	78.1	375	1	US-07-817-917-1	Sequence 27, Appl
124	27	84.4	1181	2	US-08-459-504B-15	Sequence 15, Appl	197	25	78.1	403	2	US-08-861-774E-27	Sequence 4028, Ap
125	27	84.4	1181	2	US-08-459-504B-17	Sequence 17, Appl	198	25	78.1	461	2	US-09-107-433-4028	Sequence 590, App
126	27	84.4	1181	2	US-08-459-504B-28	Sequence 28, Appl	199	25	78.1	461	2	US-09-303-518D-590	Sequence 592, App
127	27	84.4	1181	2	US-08-459-444-11	Sequence 11, Appl	200	25	78.1	461	2	US-09-303-518D-592	Sequence 4206, Ap
128	27	84.4	1181	2	US-08-459-444-13	Sequence 13, Appl	201	25	78.1	476	2	US-09-543-681A-4206	Sequence 8095, Ap
129	27	84.4	1181	2	US-08-459-444-15	Sequence 15, Appl	202	25	78.1	517	2	US-09-949-016-8095	Sequence 3, Appl
130	27	84.4	1181	2	US-08-459-444-17	Sequence 17, Appl	203	25	78.1	521	1	US-08-276-213-3	Sequence 18787, A
131	27	84.4	1181	2	US-08-459-444-17	Sequence 17, Appl	204	25	78.1	528	2	US-09-248-796A-18787	Sequence 673, App
132	27	84.4	1181	2	US-08-459-444-28	Sequence 28, Appl	205	25	78.1	534	2	US-09-538-092-673	Sequence 124, Appl
133	27	84.4	1181	2	US-09-547-422-11	Sequence 11, Appl	206	25	78.1	534	2	US-09-487-558B-124	Sequence 51, Appl
134	27	84.4	1181	2	US-09-547-422-13	Sequence 13, Appl	207	25	78.1	539	2	US-08-851-567B-51	Sequence 15, Appl
135	27	84.4	1181	2	US-09-547-422-15	Sequence 15, Appl	208	25	78.1	589	2	US-09-643-657-14	Sequence 15, Appl
136	27	84.4	1181	2	US-09-547-422-17	Sequence 17, Appl	209	25	78.1	591	2	US-09-643-657-15	Sequence 6, Appl
137	27	84.4	1181	2	US-09-547-422-28	Sequence 28, Appl	210	25	78.1	592	1	US-08-736-770-6	Sequence 169, App
138	27	84.4	1181	2	US-09-988-462-11	Sequence 11, Appl	211	25	78.1	592	2	US-09-643-657-169	Sequence 169, App
139	27	84.4	1181	2	US-09-988-462-13	Sequence 13, Appl	212	25	78.1	592	2	US-09-480-884A-169	Sequence 1809, Ap
140	27	84.4	1181	2	US-09-988-462-15	Sequence 15, Appl	213	25	78.1	592	2	US-09-702-705-1809	Sequence 1809, Ap
141	27	84.4	1181	2	US-09-988-462-17	Sequence 17, Appl	214	25	78.1	592	2	US-09-736-457-1809	Sequence 169, App
142	27	84.4	1181	6	US-09-988-462-28	Sequence 28, Appl	215	25	78.1	592	2	US-09-542-615A-169	Sequence 169, App
143	27	84.4	1188	6	5254799-6	Patent No. 5254799	216	25	78.1	592	2	US-09-606-421B-169	Sequence 4, Appl
144	26	81.2	65	2	US-09-949-016-9281	Sequence 9281, Ap	217	25	78.1	592	2	US-09-643-657-4	Sequence 169, App
145	26	81.2	250	2	US-09-270-767-40335	Sequence 40335, A	218	25	78.1	592	2	US-09-671-32E-1809	Sequence 1809, Ap
146	26	81.2	250	2	US-09-270-767-55551	Sequence 55551, A	219	25	78.1	592	2	US-09-466-396A-169	Sequence 169, App
147	26	81.2	251	2	US-09-252-991A-22652	Sequence 22652, A	220	25	78.1	592	2	US-09-476-496A-169	Sequence 169, App
148	26	81.2	372	2	US-09-480-921B-2	Sequence 2, Appl	221	25	78.1	592	2	US-09-630-946B-169	Sequence 169, App
149	26	81.2	552	1	US-08-588-821-2	Sequence 2, Appl	222	25	78.1	592	2	US-09-285-479-169	Sequence 1809, Ap
150	26	81.2	552	1	US-08-915-214-2	Sequence 2, Appl	223	25	78.1	592	2	US-10-017-754-1609	Sequence 169, App
151	26	81.2	552	1	US-09-005-532-2	Sequence 2, Appl	224	25	78.1	592	2	US-10-007-700-169	Sequence 8823, Ap
152	26	81.2	552	2	US-08-701-582D-14	Sequence 14, Appl	225	25	78.1	605	2	US-09-949-016-8823	Sequence 2, Appl
153	26	81.2	552	2	US-09-096-776B-9	Sequence 9, Appl	226	25	78.1	619	2	US-09-800-065-2	Sequence 13, Appl
154	26	81.2	552	2	US-09-312-748-4	Sequence 4, Appl	227	25	78.1	620	2	US-09-643-657-13	Sequence 14, Appl
155	26	81.2	552	2	US-09-923-922-9	Sequence 9, Appl	228	25	78.1	685	2	US-08-937-067-14	Sequence 36547, A
156	26	81.2	765	2	US-09-252-991A-17416	Sequence 17416, A	229	25	78.1	686	2	US-09-270-767-36547	Sequence 51764, A
157	26	81.2	798	2	US-09-417-197-77	Sequence 77, Appl	230	25	78.1	700	2	US-09-408-647E-2	Sequence 2, Appl
158	26	81.2	806	2	US-09-417-197-53	Sequence 53, Appl	231	25	78.1	723	2	US-09-976-59A-503	Sequence 503, App
159	26	81.2	814	2	US-09-248-796A-20405	Sequence 20405, A	232	25	78.1	750	2	US-09-583-110-4010	Sequence 4010, Ap
160	26	81.2	819	2	US-09-976-59A-369	Sequence 369, App	233	25	78.1	752	2	US-09-724-653-7	Sequence 7, Appl
161	26	81.2	827	2	US-09-949-016-7807	Sequence 7807, App	234	25	78.1	766	2	US-09-724-653-14	Sequence 2, Appl
162	26	81.2	1497	2	US-09-902-540-14734	Sequence 14734, A	235	25	78.1	766	2	US-09-724-653-14	Sequence 14, Appl
163	26	81.2	2283	2	US-10-172-502-4	Sequence 4, Appl	236	25	78.1	766	2	US-09-643-653-15	Sequence 15, Appl
164	26	81.2	3079	4	US-09-949-016-7896	Sequence 4, Appl	237	25	78.1	768	2	US-09-489-039A-12897	Sequence 12897, A
165	26	81.2	3854	6	5219837-4	Patent No. 5219837	238	25	78.1	791	2	US-09-643-597-170	Sequence 170, App
166	25	78.1	18	6	5219837-4	Patent No. 5219837	239	25	78.1	791	2	US-09-480-884A-170	Sequence 170, App
167	25	78.1	60	2	US-09-117-952-785	Sequence 785, App	240	25	78.1	791	2	US-09-542-616A-170	Sequence 170, App
168	25	78.1	68	2	US-09-270-767-57643	Sequence 57643, A	241	25	78.1	791	2	US-09-606-421B-170	Sequence 170, App
169	25	78.1	84	2	US-08-905-223-341	Sequence 441, App	242	25	78.1	791	2	US-09-466-396A-170	Sequence 170, App
170	25	78.1	96	2	US-09-270-767-60448	Sequence 60448, A	243	25	78.1	791	2	US-09-476-496A-170	Sequence 170, App
171	25	78.1	96	2	US-09-513-999C-5037	Sequence 5037, Ap	244	25	78.1	791	2	US-09-630-946B-170	Sequence 170, App
172	25	78.1	137	2	US-10-104-047-3241	Sequence 3241, Ap	245	25	78.1	791	2	US-09-285-479-170	Sequence 170, App
173	25	78.1	140	2	US-09-949-016-6789	Sequence 6789, Ap	246	25	78.1	791	2		

247	25	78.1	791	2	US-10-007-700-170	Sequence 170, App	320	24	75.0	143	2	US-09-248-796A-18180	Sequence 18180, A
248	25	78.1	861	2	US-09-902-540-12877	Sequence 12877, A	321	24	75.0	150	2	US-08-946-322A-48	Sequence 48, Appl
249	25	78.1	864	2	US-09-902-540-11770	Sequence 11770, A	322	24	75.0	150	2	US-09-562-912A-48	Sequence 48, Appl
250	25	78.1	881	2	US-10-007-700-430	Sequence 430, App	323	24	75.0	152	2	US-09-621-976-4700	Sequence 4700, Ap
251	25	78.1	910	2	US-09-949-016-7055	Sequence 7055, Ap	324	24	75.0	153	2	US-09-902-540-11126	Sequence 13126, A
252	25	78.1	920	2	US-09-643-597-357	Sequence 357, App	325	24	75.0	154	2	US-09-732-210-859	Sequence 859, App
253	25	78.1	920	2	US-09-630-940B-357	Sequence 357, App	326	24	75.0	158	2	US-09-248-796A-23151	Sequence 23151, A
254	25	78.1	920	2	US-10-007-700-357	Sequence 357, App	327	24	75.0	160	2	US-09-270-767-57547	Sequence 57547, A
255	25	78.1	933	2	US-08-764-870-14	Sequence 14, Appl	328	24	75.0	162	2	US-09-765-815-14	Sequence 14, Appl
256	25	78.1	933	2	US-08-980-115-14	Sequence 14, Appl	329	24	75.0	165	2	US-09-252-991A-20304	Sequence 20304, A
257	25	78.1	938	2	US-08-897-843A-1	Sequence 1, Appl1	330	24	75.0	170	2	US-09-252-991A-17871	Sequence 17871, A
258	25	78.1	942	2	US-09-919-172-87	Sequence 87, Appl	331	24	75.0	170	2	US-09-252-991A-29047	Sequence 29047, A
259	25	78.1	943	2	US-09-193-562D-32	Sequence 32, Appl	332	24	75.0	171	2	US-09-270-767-41920	Sequence 41920, A
260	25	78.1	943	2	US-09-643-597-161	Sequence 161, App	333	24	75.0	175	2	US-09-248-796A-14341	Sequence 14341, A
261	25	78.1	943	2	US-09-480-884A-161	Sequence 161, App	334	24	75.0	193	2	US-09-107-533A-7122	Sequence 7122, Ap
262	25	78.1	943	2	US-09-542-615A-161	Sequence 161, App	335	24	75.0	198	2	US-09-325-932A-15131	Sequence 151, App
263	25	78.1	943	2	US-09-606-421B-161	Sequence 161, App	336	24	75.0	199	2	US-09-252-991A-17323	Sequence 17323, A
264	25	78.1	943	2	US-09-623-624-4	Sequence 4, Appl1	337	24	75.0	199	2	US-09-452-846E-3	Sequence 3, Appl1
265	25	78.1	943	2	US-09-221-107-161	Sequence 4, Appl	338	24	75.0	214	2	US-09-538-092-204	Sequence 204, Appl
266	25	78.1	943	2	US-10-055-412B-32	Sequence 32, Appl	339	24	75.0	219	2	US-09-484-577A-32	Sequence 32, Appl
267	25	78.1	943	2	US-09-466-396A-161	Sequence 161, App	340	24	75.0	222	2	US-09-248-796A-24928	Sequence 24928, A
268	25	78.1	943	2	US-09-476-496A-161	Sequence 161, App	341	24	75.0	226	2	US-09-148-545-145	Sequence 145, App
269	25	78.1	943	2	US-10-270-595-4	Sequence 4, Appl	342	24	75.0	226	2	US-09-621-011-145	Sequence 145, App
270	25	78.1	943	2	US-09-630-940B-161	Sequence 161, App	343	24	75.0	230	2	US-09-230-196-18	Sequence 18, Appl
271	25	78.1	943	2	US-09-285-479-161	Sequence 161, App	344	24	75.0	230	2	US-09-230-196-23	Sequence 23, Appl
272	25	78.1	943	2	US-10-007-700-161	Sequence 161, App	345	24	75.0	236	2	US-09-489-039A-9119	Sequence 9119, Ap
273	25	78.1	990	2	US-09-949-016-10562	Sequence 10562, A	346	24	75.0	236	2	US-09-489-039A-9984	Sequence 9984, Ap
274	25	78.1	1113	2	US-09-959-392-4	Sequence 4, Appl1	347	24	75.0	249	1	US-08-680-726A-88	Sequence 88, Appl
275	25	78.1	1203	2	US-09-799-875-5	Sequence 5, Appl1	348	24	75.0	249	2	US-09-092-409-88	Sequence 2131, Ap
276	25	78.1	1367	1	US-07-813-593-4	Sequence 4, Appl1	349	24	75.0	256	2	US-09-540-236-2131	Sequence 2131, Ap
277	25	78.1	1367	1	US-07-977-451-6	Sequence 6, Appl1	350	24	75.0	261	2	US-09-252-929A-33140	Sequence 33140, A
278	25	78.1	1367	1	US-07-946-507-4	Sequence 4, Appl1	351	24	75.0	272	2	US-09-710-279-588	Sequence 588, App
279	25	78.1	1367	1	US-08-252-517-6	Sequence 6, Appl1	352	24	75.0	273	2	US-09-248-796A-18140	Sequence 18140, A
280	25	78.1	1367	1	US-07-906-397A-6	Sequence 6, Appl1	353	24	75.0	275	2	US-09-147-915-4	Sequence 4, Appl1
281	25	78.1	1367	1	US-08-601-891-6	Sequence 6, Appl1	354	24	75.0	281	2	US-09-134-001C-3491	Sequence 3491, Ap
282	25	78.1	1367	1	US-08-443-861-2	Sequence 2, Appl1	355	24	75.0	291	2	US-09-543-681A-6290	Sequence 6290, Ap
283	25	78.1	1367	1	US-09-021-324-6	Sequence 6, Appl1	356	24	75.0	292	1	US-08-737-526-4	Sequence 4, Appl1
284	25	78.1	1367	2	US-08-193-829B-2	Sequence 2, Appl1	357	24	75.0	298	2	US-09-098-580-4	Sequence 4, Appl1
285	25	78.1	1367	2	US-09-872-136B-6	Sequence 6, Appl1	358	24	75.0	298	2	US-09-270-767-38427	Sequence 38427, A
286	25	78.1	1367	2	US-09-766-678-2	Sequence 2, Appl1	359	24	75.0	298	2	US-09-270-767-53644	Sequence 53644, A
287	25	78.1	1367	2	US-09-919-408A-6	Sequence 6, Appl1	360	24	75.0	300	2	US-09-248-796A-16245	Sequence 16245, A
288	25	78.1	1367	4	PCT-US92-02750-8	Sequence 8, Appl1	361	24	75.0	303	2	US-09-543-681A-7924	Sequence 7924, Ap
289	25	78.1	1367	4	PCT-US92-05401-6	Sequence 6, Appl1	362	24	75.0	313	2	US-09-071-035-180	Sequence 180, App
290	25	78.1	1367	4	PCT-US92-09893-6	Sequence 6, Appl1	363	24	75.0	313	2	US-09-071-035-180	Sequence 180, App
291	25	78.1	1442	2	US-09-902-540-9797	Sequence 9777, Ap	364	24	75.0	318	1	US-08-220-955-4	Sequence 4, Appl1
292	25	78.1	1442	2	US-08-851-567B-47	Sequence 47, Appl.	365	24	75.0	318	2	US-09-489-039A-8369	Sequence 8369, Ap
293	25	78.1	2516	2	US-09-817-514A-2	Sequence 2, Appl1	366	24	75.0	321	2	US-09-134-000C-3783	Sequence 3783, Ap
294	25	78.1	2516	2	US-09-251-645-13	Sequence 13, Appl1	367	24	75.0	327	1	US-08-238-163-4	Sequence 4, Appl1
295	25	75.0	7	1	US-08-182-067-6	Sequence 6, Appl1	368	24	75.0	330	2	US-09-270-767-39773	Sequence 39773, A
296	24	75.0	7	1	US-08-465-313-6	Sequence 6, Appl1	369	24	75.0	330	2	US-09-270-767-54990	Sequence 54990, A
297	24	75.0	7	2	US-09-809-739-3	Sequence 3, Appl1	370	24	75.0	335	2	US-09-071-035-178	Sequence 178, App
298	24	75.0	7	2	US-09-378-967-6	Sequence 6, Appl1	371	24	75.0	335	2	US-10-206-576-178	Sequence 33924, A
299	24	75.0	8	2	US-09-160-483-3	Sequence 3, Appl1	372	24	75.0	336	2	US-09-270-767-33924	Sequence 33924, A
300	24	75.0	29	2	US-09-471-276-1502	Sequence 1502, Ap	373	24	75.0	336	2	US-09-270-767-49141	Sequence 49141, A
301	24	75.0	53	2	US-09-270-767-60589	Sequence 60589, A	374	24	75.0	347	2	US-09-270-767-42381	Sequence 42381, A
302	24	75.0	57	2	US-09-621-976-6395	Sequence 6395, Ap	375	24	75.0	348	2	US-09-248-796A-18141	Sequence 18141, A
303	24	75.0	64	2	US-09-471-276-966	Sequence 966, App	376	24	75.0	350	2	US-09-270-767-42267	Sequence 42267, A
304	24	75.0	76	1	US-08-848-252-4	Sequence 4, Appl1	377	24	75.0	365	2	US-09-489-847-322	Sequence 322, App
305	24	75.0	80	2	US-09-270-767-57169	Sequence 57169, A	378	24	75.0	372	2	US-08-311-731A-379	Sequence 379, App
306	24	75.0	80	2	US-08-253-155A-29	Sequence 29, Appl	379	24	75.0	385	2	US-09-270-767-42866	Sequence 42866, A
307	24	75.0	94	1	US-09-252-991A-20541	Sequence 20541, A	380	24	75.0	387	2	US-09-436-522A-8	Sequence 8, Appl1
308	24	75.0	119	2	US-08-722-126A-9	Sequence 9, Appl1	381	24	75.0	394	2	US-09-328-352-5409	Sequence 5409, Ap
309	24	75.0	122	4	PCT-US95-04258-9	Sequence 9, Appl1	382	24	75.0	395	2	US-09-328-352-5819	Sequence 5819, Ap
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312	24	75.0	125	1	US-08-465-313-2	Sequence 2, Appl1	385	24	75.0	409	2	US-09-248-796A-15850	Sequence 15850, A
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314	24	75.0	125	2	US-09-378-967-2	Sequence 2, Appl1	387	24	75.0	416	2	US-09-287-558B-54	Sequence 54, Appl
315	24	75.0	127	2	US-09-809-739-10	Sequence 10, Appl	388	24	75.0	420	2	US-09-252-991A-29353	Sequence 29353, A
316	24	75.0	127	2	US-09-270-767-45094	Sequence 45094, A	389	24	75.0	428	2	US-08-403-797-2	Sequence 2, Appl1
317	24	75.0	128	2	US-09-134-000C-3953	Sequence 3953, Ap	390	24	75.0	428	2	US-09-949-016-10965	Sequence 10965, A
318	24	75.0	137	2	US-09-270-767-57667	Sequence 57667, A	391	24	75.0	428	2	US-09-949-016-10965	Sequence 57667, A
319	24	75.0	140	2	US-09-471-276-850	Sequence 850, App	392	24	75.0	430	2	US-09-949-016-6234	Sequence 6234, Ap

393	24	75.0	439	1	US-08-959-638-9	Sequence 9, Appl1	466	24	75.0	908	2	US-08-867-921-4	Sequence 4, Appl1
394	24	75.0	440	2	US-09-252-991A-18824	Sequence 18824, A	467	24	75.0	908	2	US-08-637-654-94	Sequence 94, Appl1
395	24	75.0	444	2	US-09-328-352-6744	Sequence 6744, Ap	468	24	75.0	908	2	US-08-649-518-94	Sequence 94, Appl1
396	24	75.0	449	2	US-09-976-594-379	Sequence 379, App	469	24	75.0	908	2	US-08-778-570B-22	Sequence 22, Appl1
397	24	75.0	449	2	US-10-183-770A-2	Sequence 2, Appl1	470	24	75.0	908	2	US-09-059-584-22	Sequence 12, Appl1
398	24	75.0	452	2	US-09-489-039A-7220	Sequence 7220, Ap	471	24	75.0	908	2	US-08-753-750B-12	Sequence 12, Appl1
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402	24	75.0	491	2	US-09-270-767-44430	Sequence 44430, A	475	24	75.0	1031	2	US-09-902-540-12805	Sequence 12805, A
403	24	75.0	504	2	US-09-902-540-13356	Sequence 13356, A	476	24	75.0	1035	2	US-10-781-294-24	Sequence 24, Appl1
404	24	75.0	518	2	US-09-248-796A-18238	Sequence 18238, A	477	24	75.0	1066	2	US-09-817-762-5	Sequence 5, Appl1
405	24	75.0	521	2	US-09-949-016-7570	Sequence 7570, Ap	478	24	75.0	1083	2	US-09-394-272-11	Sequence 11, Appl1
406	24	75.0	521	2	US-09-902-540-11865	Sequence 11865, A	479	24	75.0	1258	2	US-10-200-012-16	Sequence 16, Appl1
407	24	75.0	523	2	US-09-107-532A-4149	Sequence 4149, Ap	480	24	75.0	1279	2	US-09-538-092-976	Sequence 976, App
408	24	75.0	529	2	US-09-381-656-1	Sequence 1, Appl1	481	24	75.0	1325	2	US-09-270-767-43789	Sequence 43789, A
409	24	75.0	529	2	US-10-164-230-61	Sequence 1, Appl1	482	24	75.0	1341	2	US-09-252-991A-6785	Sequence 26785, A
410	24	75.0	533	2	US-10-038-972A-15	Sequence 15, Appl1	483	24	75.0	1356	2	US-09-098-707A-2	Sequence 2, Appl1
411	24	75.0	542	2	US-09-489-847-323	Sequence 323, App	484	24	75.0	1356	2	US-09-483-533-2	Sequence 2, Appl1
412	24	75.0	550	2	US-09-107-532A-5564	Sequence 5564, Ap	485	24	75.0	1356	2	US-09-949-016-6198	Sequence 6198, Ap
413	24	75.0	552	2	US-08-557-006C-40	Sequence 40, Appl1	486	24	75.0	1356	2	US-10-100-405A-2	Sequence 2, Appl1
414	24	75.0	552	2	US-09-538-092-1212	Sequence 1212, Ap	487	24	75.0	1356	2	US-10-022-939-2	Sequence 2, Appl1
415	24	75.0	555	1	US-09-824-735-4	Sequence 4, Appl1	488	24	75.0	1456	2	US-09-949-016-9853	Sequence 9853, Ap
416	24	75.0	555	1	US-08-982-232-7	Sequence 7, Appl1	489	24	75.0	1588	1	US-08-698-551-16	Sequence 16, Appl1
417	24	75.0	555	1	US-08-982-232-14	Sequence 14, Appl1	490	24	75.0	1588	1	US-08-602-228-16	Sequence 16, Appl1
418	24	75.0	558	2	US-09-252-991A-25673	Sequence 25673, A	491	24	75.0	1588	1	US-08-839-032A-16	Sequence 16, Appl1
419	24	75.0	577	2	US-09-489-039A-13973	Sequence 13973, A	492	24	75.0	1588	2	US-09-185-258C-16	Sequence 16, Appl1
420	24	75.0	584	2	US-09-160-483-1	Sequence 1, Appl1	493	24	75.0	1588	2	US-09-976-594-965	Sequence 965, App
421	24	75.0	594	2	US-09-949-016-9261	Sequence 9261, Ap	494	24	75.0	2004	2	US-09-538-092-1371	Sequence 1371, Ap
422	24	75.0	596	2	US-09-252-991A-18934	Sequence 18934, A	495	24	75.0	2004	2	US-09-949-016-6756	Sequence 6756, Ap
423	24	75.0	598	2	US-10-038-972A-14	Sequence 14, Appl1	496	24	75.0	2409	6	5180808-2	Patent No. 5180808
424	24	75.0	603	2	US-10-781-294-64	Sequence 64, Appl1	497	24	75.0	2954	7	US-09-150-867-1	Sequence 1, Appl1
425	24	75.0	604	2	US-09-339-947A-8	Sequence 8, Appl1	498	24	75.0	7	2	US-08-599-228-5	Sequence 5, Appl1
426	24	75.0	608	2	US-09-369-247-68	Sequence 68, Appl1	499	23	71.9	7	2	US-09-125-098-5	Sequence 5, Appl1
427	24	75.0	608	2	US-10-062-548-68	Sequence 68, Appl1	500	23	71.9	7	2	US-09-540-018-5	Sequence 5, Appl1
428	24	75.0	615	2	US-09-949-002-433	Sequence 433, App	501	23	71.9	7	2	US-09-192-854-159	Sequence 159, App
429	24	75.0	619	2	US-10-104-047-3680	Sequence 3680, Ap	502	23	71.9	7	2	US-09-511-933-281	Sequence 281, App
430	24	75.0	634	2	US-09-614-912-88	Sequence 88, Appl1	503	23	71.9	12	1	US-08-419-903A-7	Sequence 7, Appl1
431	24	75.0	634	2	US-09-614-912-100	Sequence 100, App	504	23	71.9	14	1	US-08-419-903A-5	Sequence 5, Appl1
432	24	75.0	634	2	US-09-614-912-100	Sequence 100, App	505	23	71.9	15	1	US-08-419-903A-8	Sequence 8, Appl1
433	24	75.0	672	2	US-09-083-587-2	Sequence 2, Appl1	506	23	71.9	15	1	US-08-257-783-10	Sequence 10, Appl1
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435	24	75.0	675	2	US-09-248-796A-20699	Sequence 20699, A	508	23	71.9	15	4	PCT-US95-07157-10	Sequence 28, Appl1
436	24	75.0	713	2	US-09-714-865-4	Sequence 4, Appl1	509	23	71.9	30	2	US-09-627-165B-28	Sequence 28, Appl1
437	24	75.0	735	2	US-09-321-589-1	Sequence 1, Appl1	510	23	71.9	36	6	5248606-7	Patent No. 5248606
438	24	75.0	735	2	US-09-302-540-13533	Sequence 13533, A	511	23	71.9	36	2	US-09-962-756-1314	Sequence 1314, Ap
439	24	75.0	735	2	US-10-038-972A-13	Sequence 13, Appl1	512	23	71.9	38	1	US-08-324-301-9	Sequence 9, Appl1
440	24	75.0	742	2	US-10-104-047-2476	Sequence 2476, Ap	513	23	71.9	40	2	US-08-812-586A-40	Sequence 40, Appl1
441	24	75.0	765	2	US-09-107-532A-3750	Sequence 3750, Ap	514	23	71.9	40	2	US-09-535-832A-37	Sequence 37, Appl1
442	24	75.0	765	2	US-09-949-016-9252	Sequence 9252, Ap	515	23	71.9	43	2	US-10-318-675-132	Sequence 132, App
443	24	75.0	780	2	US-09-949-016-10205	Sequence 10205, A	516	23	71.9	44	1	US-07-749-541A-8	Sequence 8, Appl1
444	24	75.0	809	2	US-09-543-681A-6686	Sequence 6686, Ap	517	23	71.9	44	2	US-08-905-223-397	Sequence 397, App
445	24	75.0	811	2	US-10-104-047-3559	Sequence 3559, Ap	518	23	71.9	52	2	US-09-513-999C-4456	Sequence 4456, Ap
446	24	75.0	820	2	US-09-248-796A-17231	Sequence 17231, A	519	23	71.9	62	2	US-09-134-001C-3788	Sequence 3788, Ap
447	24	75.0	832	2	US-08-591-502B-60	Sequence 60, Appl1	520	23	71.9	63	2	US-09-397-243D-8	Sequence 8, Appl1
448	24	75.0	832	2	US-08-591-502B-61	Sequence 61, Appl1	521	23	71.9	63	2	US-09-397-243D-10	Sequence 10, Appl1
449	24	75.0	832	2	US-08-591-502B-62	Sequence 62, Appl1	522	23	71.9	63	2	US-10-037-417-128	Sequence 128, App
450	24	75.0	832	2	US-08-591-502B-63	Sequence 63, Appl1	523	23	71.9	66	1	US-07-938-188-2	Sequence 2, Appl1
451	24	75.0	845	2	US-08-591-502B-64	Sequence 64, Appl1	524	23	71.9	66	1	US-08-306-062-2	Sequence 2, Appl1
452	24	75.0	845	2	US-09-248-796A-17962	Sequence 17962, A	525	23	71.9	66	1	US-09-306-062-2	Sequence 2, Appl1
453	24	75.0	856	2	US-09-902-540-11879	Sequence 11879, A	526	23	71.9	76	2	US-10-241-602B-15	Sequence 15, Appl1
454	24	75.0	885	1	US-08-066-167-2	Sequence 2, Appl1	527	23	71.9	77	2	US-09-590-759-88	Sequence 88, Appl1
455	24	75.0	885	2	US-09-543-681A-4596	Sequence 4596, Ap	528	23	71.9	77	2	US-09-590-759-89	Sequence 89, Appl1
456	24	75.0	904	2	US-09-252-991A-29119	Sequence 29119, A	529	23	71.9	77	2	US-09-590-759-90	Sequence 90, Appl1
457	24	75.0	908	1	US-08-487-890A-94	Sequence 94, Appl1	530	23	71.9	77	2	US-09-590-759-92	Sequence 92, Appl1
458	24	75.0	908	1	US-08-487-890A-94	Sequence 94, Appl1	531	23	71.9	77	2	US-09-590-759-92	Sequence 92, Appl1
459	24	75.0	908	1	US-08-337-483-94	Sequence 94, Appl1	532	23	71.9	82	2	US-09-661-322A-34	Sequence 34, Appl1
460	24	75.0	908	1	US-08-478-373-94	Sequence 94, Appl1	533	23	71.9	84	2	US-09-134-001C-3377	Sequence 3377, Ap
461	24	75.0	908	2	US-08-474-571-94	Sequence 94, Appl1	534	23	71.9	84	2	US-09-621-976-4739	Sequence 4739, Ap
462	24	75.0	908	2	US-08-463-577A-94	Sequence 94, Appl1	535	23	71.9	84	2	US-09-248-796A-17256	Sequence 17256, A
463	24	75.0	908	2	US-08-448-194-4	Sequence 4, Appl1	536	23	71.9	89	2	US-09-107-532A-5415	Sequence 5415, Ap
464	24	75.0	908	2	US-08-613-009A-16	Sequence 16, Appl1	537	23	71.9	89	2	US-09-543-681A-5724	Sequence 5724, Ap
465	24	75.0	908	2	US-08-897-438-94	Sequence 94, Appl1	538	23	71.9	90	2	US-09-543-681A-5364	Sequence 5364, Ap

539	23	71.9	91	2	US-10-330-613A-64	Sequence 64, Appl	612	23	71.9	160	2	US-09-198-452A-1244	Sequence 1244, Ap
540	23	71.9	93	2	US-09-248-796A-28179	Sequence 28179, A	613	23	71.9	166	2	US-09-270-767-55981	Sequence 55981, A
541	23	71.9	95	2	US-09-627-896B-27	Sequence 27, Appl	614	23	71.9	168	2	US-09-252-991A-27900	Sequence 27900, A
542	23	71.9	95	2	US-10-194-975-58	Sequence 58, Appl	615	23	71.9	171	2	US-09-489-039A-13551	Sequence 13551, A
543	23	71.9	95	2	US-10-194-975-67	Sequence 67, Appl	616	23	71.9	173	2	US-09-302-626B-18	Sequence 18, Appl
544	23	71.9	95	2	US-10-194-975-69	Sequence 69, Appl	617	23	71.9	176	2	US-09-252-991A-16997	Sequence 16997, A
545	23	71.9	95	2	US-10-194-975-70	Sequence 70, Appl	618	23	71.9	179	2	US-10-083-336A-2	Sequence 2, Appl
546	23	71.9	95	2	US-09-339-596A-42	Sequence 42, Appl	619	23	71.9	183	2	US-09-270-767-33627	Sequence 32627, A
547	23	71.9	95	2	US-10-330-613A-63	Sequence 63, Appl	620	23	71.9	185	2	US-09-270-767-47844	Sequence 47844, A
548	23	71.9	97	2	US-09-134-000C-4809	Sequence 4809, Ap	621	23	71.9	188	2	US-10-083-336A-9	Sequence 9, Appl
549	23	71.9	97	2	US-09-270-767-57053	Sequence 57053, A	622	23	71.9	188	2	US-10-083-336A-4	Sequence 4, Appl
550	23	71.9	100	2	US-09-899-896-8	Sequence 8, Appl	623	23	71.9	188	2	US-10-083-336A-8	Sequence 8, Appl
551	23	71.9	101	2	US-09-328-352-7947	Sequence 7947, Ap	624	23	71.9	188	2	US-10-083-336A-6	Sequence 6, Appl
552	23	71.9	102	2	US-09-726-219A-173	Sequence 173, App	625	23	71.9	189	2	US-10-083-336A-6	Sequence 11, Appl
553	23	71.9	102	2	US-09-196-522-173	Sequence 173, App	626	23	71.9	190	2	US-10-083-336A-11	Sequence 31, Appl
554	23	71.9	105	2	US-09-252-991A-20873	Sequence 20873, A	627	23	71.9	193	2	US-08-896-933-31	Sequence 31, Appl
555	23	71.9	105	2	US-09-543-681A-3528	Sequence 5328, Ap	628	23	71.9	193	2	US-09-314-235-31	Sequence 31, Appl
556	23	71.9	106	1	US-08-376-852-83	Sequence 83, Appl	629	23	71.9	193	2	US-09-708-008B-31	Sequence 31, Appl
557	23	71.9	106	1	US-08-376-852-85	Sequence 85, Appl	630	23	71.9	194	1	US-08-446-918A-6	Sequence 6, Appl
558	23	71.9	106	1	US-08-899-575-83	Sequence 85, Appl	631	23	71.9	194	1	US-08-580-806-6	Sequence 6, Appl
559	23	71.9	106	1	US-08-899-575-85	Sequence 85, Appl	632	23	71.9	194	2	US-08-311-731A-306	Sequence 306, App
560	23	71.9	106	1	US-08-899-575-83	Sequence 85, Appl	633	23	71.9	196	2	US-09-107-433-4096	Sequence 4096, Ap
561	23	71.9	106	1	US-08-899-575-85	Sequence 85, Appl	634	23	71.9	198	2	US-10-083-336A-3	Sequence 3, Appl
562	23	71.9	106	2	US-09-471-276-1316	Sequence 1316, Ap	635	23	71.9	198	2	US-10-083-336A-7	Sequence 7, Appl
563	23	71.9	106	4	PCT-US95-08743-83	Sequence 83, Appl	636	23	71.9	199	2	US-08-478-316-32	Sequence 32, Appl
564	23	71.9	106	4	PCT-US95-08743-85	Sequence 85, Appl	637	23	71.9	199	2	US-09-019-739A-32	Sequence 32, Appl
565	23	71.9	107	1	US-08-300-386A-66	Sequence 66, Appl	638	23	71.9	199	2	US-10-083-336A-5	Sequence 5, Appl
566	23	71.9	107	1	US-08-300-386A-66	Sequence 66, Appl	639	23	71.9	200	1	US-08-131-625B-11	Sequence 11, Appl
567	23	71.9	107	1	US-08-899-575-84	Sequence 84, Appl	640	23	71.9	200	2	US-08-301-435-15	Sequence 15, Appl
568	23	71.9	107	1	US-08-899-575-84	Sequence 84, Appl	641	23	71.9	200	2	US-09-601-326-32	Sequence 32, Appl
569	23	71.9	107	2	US-08-599-226-9	Sequence 9, Appl	642	23	71.9	200	4	US-10-083-336A-10	Sequence 10, Appl
570	23	71.9	107	2	US-08-599-226-9	Sequence 9, Appl	643	23	71.9	200	4	PCT-US95-10904-15	Sequence 15, Appl
571	23	71.9	107	2	US-08-931-645-66	Sequence 66, Appl	644	23	71.9	203	2	US-09-489-039A-13649	Sequence 13649, A
572	23	71.9	107	2	US-09-240-274-157	Sequence 157, App	645	23	71.9	212	2	US-09-270-767-32729	Sequence 32729, A
573	23	71.9	107	2	US-09-240-274-170	Sequence 170, App	646	23	71.9	212	2	US-09-543-681A-6322	Sequence 47946, A
574	23	71.9	107	2	US-09-125-098-1	Sequence 9, Appl	647	23	71.9	219	2	US-09-504-358-4	Sequence 4, Appl
575	23	71.9	107	2	US-09-125-098-9	Sequence 9, Appl	648	23	71.9	226	2	US-09-954-314-4	Sequence 4, Appl
576	23	71.9	107	2	US-09-540-018-1	Sequence 9, Appl	649	23	71.9	226	2	US-10-230-562-A	Sequence 4, Appl
577	23	71.9	107	2	US-09-540-018-9	Sequence 9, Appl	650	23	71.9	228	2	US-09-540-236-3252	Sequence 3252, Ap
578	23	71.9	107	2	US-09-848-798-157	Sequence 157, App	651	23	71.9	229	2	US-08-350-841A-1597	Sequence 1597, Ap
579	23	71.9	107	4	US-09-848-798-170	Sequence 170, Appl	652	23	71.9	234	1	US-08-152-456A-2	Sequence 2, Appl
580	23	71.9	107	4	PCT-US95-08743-84	Sequence 84, Appl	653	23	71.9	234	1	US-08-440-221-2	Sequence 11, App
581	23	71.9	107	4	PCT-US95-11235-66	Sequence 66, Appl	654	23	71.9	234	1	US-08-486-099-111	Sequence 11, App
582	23	71.9	108	2	US-09-240-274-31	Sequence 31, Appl	655	23	71.9	234	2	US-08-484-1203A-121	Sequence 121, App
583	23	71.9	108	2	US-09-240-274-161	Sequence 161, App	656	23	71.9	234	2	US-08-360-1203A-111	Sequence 111, App
584	23	71.9	108	2	US-09-240-274-177	Sequence 177, App	657	23	71.9	234	2	US-08-919-597-111	Sequence 111, App
585	23	71.9	108	2	US-09-848-798-31	Sequence 31, Appl	658	23	71.9	234	2	US-08-475-668A-111	Sequence 111, App
586	23	71.9	108	2	US-09-848-798-161	Sequence 161, App	659	23	71.9	234	2	US-08-485-551A-111	Sequence 111, App
587	23	71.9	108	2	US-09-848-798-177	Sequence 177, App	660	23	71.9	234	2	US-08-471-912A-111	Sequence 111, App
588	23	71.9	109	1	US-08-300-386A-68	Sequence 68, Appl	661	23	71.9	234	2	US-08-485-264A-111	Sequence 111, App
589	23	71.9	109	1	US-08-300-386A-69	Sequence 68, Appl	662	23	71.9	234	2	US-08-474-349A-111	Sequence 111, App
590	23	71.9	109	2	US-08-931-645-68	Sequence 68, Appl	663	23	71.9	234	2	US-09-144-776B-12	Sequence 12, Appl
591	23	71.9	109	2	US-08-931-645-69	Sequence 68, Appl	664	23	71.9	234	2	US-08-470-896-111	Sequence 111, App
592	23	71.9	109	4	PCT-US95-11235-68	Sequence 69, Appl	665	23	71.9	234	2	US-08-485-546A-111	Sequence 111, App
593	23	71.9	109	4	PCT-US95-11235-69	Sequence 69, Appl	666	23	71.9	234	2	US-08-882-431B-12	Sequence 12, Appl
594	23	71.9	117	2	US-09-513-999C-6272	Sequence 6272, Ap	667	23	71.9	234	2	US-08-487-266A-111	Sequence 111, App
595	23	71.9	117	2	US-09-438-185A-114	Sequence 114, App	668	23	71.9	234	2	US-08-484-741-111	Sequence 111, App
596	23	71.9	124	2	US-09-640-211A-724	Sequence 724, App	669	23	71.9	237	2	US-09-216-001-1	Sequence 1, Appl
597	23	71.9	128	2	US-09-252-991A-29019	Sequence 29019, A	670	23	71.9	237	2	US-08-878-862-1	Sequence 1, Appl
598	23	71.9	129	2	US-09-489-039A-10738	Sequence 10738, A	671	23	71.9	253	2	US-09-489-039A-13739	Sequence 13739, A
599	23	71.9	131	2	US-09-270-767-35750	Sequence 35750, A	672	23	71.9	255	2	US-09-328-352-4719	Sequence 4719, Ap
600	23	71.9	131	2	US-09-270-767-50967	Sequence 50967, A	673	23	71.9	256	2	US-09-248-796A-20626	Sequence 20626, A
601	23	71.9	137	2	US-09-456-830-41	Sequence 41, Appl	674	23	71.9	258	2	US-10-101-466A-723	Sequence 723, App
602	23	71.9	137	2	US-09-002-285-41	Sequence 41, Appl	675	23	71.9	259	2	US-09-248-796A-28192	Sequence 28192, A
603	23	71.9	137	2	US-09-589-477-41	Sequence 41, Appl	676	23	71.9	266	2	US-09-198-452A-927	Sequence 927, App
604	23	71.9	137	2	US-10-099-285A-41	Sequence 41, Appl	677	23	71.9	266	2	US-09-489-039A-13381	Sequence 13381, A
605	23	71.9	139	2	US-08-454-899G-15	Sequence 15, Appl	678	23	71.9	267	1	US-07-901-707-1	Sequence 1, Appl
606	23	71.9	140	2	US-09-252-991A-25759	Sequence 25759, A	679	23	71.9	267	1	US-07-988-430-1	Sequence 16, Appl
607	23	71.9	144	2	US-09-902-540-12977	Sequence 12977, A	680	23	71.9	267	1	US-08-218-303-16	Sequence 1, Appl
608	23	71.9	146	2	US-09-543-681A-7523	Sequence 7523, Ap	681	23	71.9	267	1	US-08-425-335-1	Sequence 1, Appl
609	23	71.9	148	2	US-09-252-991A-16276	Sequence 16276, A	682	23	71.9	267	1	US-08-488-118B-1	Sequence 1, Appl
610	23	71.9	148	2	US-09-252-991A-28538	Sequence 28538, A	683	23	71.9	267	1	US-08-477-484B-1	Sequence 1, Appl
611	23	71.9	157	1	US-08-257-999-4	Sequence 4, Appl	684	23	71.9	267	1		

685	23	71.9	267	1	US-08-646-360-1	Sequence 1, Appl.	758	23	71.9	412	2	US-09-902-540-11795	Sequence 11795, A
686	23	71.9	267	1	US-08-338-793D-61	Sequence 61, Appl	759	23	71.9	413	2	US-09-540-236-3208	Sequence 3208, Ap
687	23	71.9	267	2	US-08-839-765-1	Sequence 1, Appl	760	23	71.9	431	2	US-09-479-614-14	Sequence 14, Appl
688	23	71.9	267	2	US-09-136-389-1	Sequence 1, Appl	761	23	71.9	431	2	US-09-583-110-4734	Sequence 4734, Ap
689	23	71.9	267	2	US-09-610-838-1	Sequence 1, Appl	762	23	71.9	432	2	US-09-949-016-9706	Sequence 9706, Ap
690	23	71.9	267	2	US-09-538-873-1	Sequence 1, Appl	763	23	71.9	433	2	US-09-489-039A-7721	Sequence 7721, Ap
691	23	71.9	267	2	US-09-711-485-1	Sequence 1, Appl	764	23	71.9	439	2	US-09-252-991A-17127	Sequence 17127, A
692	23	71.9	267	2	US-10-282-935-1	Sequence 1, Appl	765	23	71.9	439	2	US-09-107-433-4351	Sequence 4351, Ap
693	23	71.9	267	2	US-09-282-935-1	Sequence 1, Appl	766	23	71.9	439	2	US-09-902-540-12672	Sequence 12672, A
694	23	71.9	267	4	PCT-US92-09487-1	Sequence 8, Appl	767	23	71.9	442	2	US-09-328-352-6877	Sequence 6877, Ap
695	23	71.9	268	1	US-08-356-786-8	Sequence 8, Appl	768	23	71.9	443	2	US-09-088-435-2	Sequence 2, Appl
696	23	71.9	269	1	US-09-079-030-120	Sequence 120, App	769	23	71.9	447	2	US-09-639-378A-2	Sequence 2, Appl
697	23	71.9	276	2	US-09-107-433-4424	Sequence 4424, Ap	770	23	71.9	455	2	US-09-248-796A-23277	Sequence 23277, A
698	23	71.9	276	2	US-09-438-185A-863	Sequence 863, App	771	23	71.9	459	1	US-08-630-592-2	Sequence 2, Appl
699	23	71.9	280	2	US-09-792-024-66	Sequence 66, Appl	772	23	71.9	459	1	US-08-714-991-2	Sequence 2, Appl
700	23	71.9	281	2	US-09-270-767-48377	Sequence 48377, A	773	23	71.9	459	2	US-09-032-365A-2	Sequence 2, Appl
701	23	71.9	282	2	US-09-252-991A-26037	Sequence 26037, A	774	23	71.9	460	1	US-08-630-592-7	Sequence 7, Appl
702	23	71.9	287	2	US-09-543-681A-5639	Sequence 5639, Ap	775	23	71.9	460	1	US-08-714-991-7	Sequence 7, Appl
703	23	71.9	290	1	US-08-378-761A-27	Sequence 27, Appl	776	23	71.9	460	2	US-09-032-365A-8	Sequence 8, Appl
704	23	71.9	290	6	US-08-485-286-27	Sequence 27, Appl	777	23	71.9	464	2	US-09-252-991A-27559	Sequence 27559, A
705	23	71.9	291	2	US-09-270-767-37022	Sequence 37022, A	778	23	71.9	473	2	US-09-049-672A-4	Sequence 4, Appl
706	23	71.9	291	2	US-09-270-767-52239	Sequence 52239, A	779	23	71.9	480	1	US-07-752-428E-2	Sequence 2, Appl
707	23	71.9	292	2	US-09-489-039A-12623	Sequence 12623, A	780	23	71.9	480	1	US-07-752-428C-2	Sequence 2, Appl
708	23	71.9	299	2	US-09-743-237-5	Sequence 5, Appl	781	23	71.9	480	1	US-07-752-428C-4	Sequence 4, Appl
709	23	71.9	299	2	US-10-876-841A-5	Sequence 5, Appl	782	23	71.9	481	2	US-09-252-991A-17797	Sequence 17797, A
710	23	71.9	300	2	US-09-270-767-46716	Sequence 46716, A	783	23	71.9	485	2	US-08-243-542-1	Sequence 1, Appl
711	23	71.9	310	2	US-09-270-767-41808	Sequence 41808, A	784	23	71.9	488	1	US-08-477-407-1	Sequence 1, Appl
712	23	71.9	313	2	US-09-270-767-41808	Sequence 41808, A	785	23	71.9	488	1	US-08-484-355-1	Sequence 1, Appl
713	23	71.9	320	2	US-09-489-039A-13804	Sequence 13804, A	786	23	71.9	488	1	US-08-484-355-1	Sequence 1, Appl
714	23	71.9	320	2	US-09-489-039A-14175	Sequence 14175, A	787	23	71.9	496	2	US-09-489-039A-6319	Sequence 6319, Ap
715	23	71.9	331	1	US-08-134-570-12	Sequence 12, Appl	788	23	71.9	496	2	US-09-479-614-29	Sequence 29, Appl
716	23	71.9	334	1	US-09-252-991A-20599	Sequence 20599, A	789	23	71.9	496	2	US-10-104-047-3456	Sequence 3456, Ap
717	23	71.9	339	1	US-08-892-880-3	Sequence 3, Appl	790	23	71.9	500	2	US-09-489-039A-12315	Sequence 12315, A
718	23	71.9	340	2	US-09-252-991A-29871	Sequence 29871, A	791	23	71.9	502	2	US-07-946-497-2	Sequence 2, Appl
719	23	71.9	340	2	US-10-104-047-3319	Sequence 3319, Ap	792	23	71.9	503	1	US-08-483-322-2	Sequence 2, Appl
720	23	71.9	344	2	US-09-543-681A-4795	Sequence 4795, Ap	793	23	71.9	503	1	US-08-478-882-2	Sequence 2, Appl
721	23	71.9	347	2	US-09-543-681A-6024	Sequence 6024, Ap	794	23	71.9	504	2	US-08-955-918C-7	Sequence 7, Appl
722	23	71.9	353	2	US-09-466-778-11	Sequence 11, Appl	795	23	71.9	504	2	US-08-697-766A-7	Sequence 7, Appl
723	23	71.9	359	2	US-09-098-219B-2	Sequence 2, Appl	796	23	71.9	505	1	US-08-631-200-2	Sequence 2, Appl
724	23	71.9	359	2	US-10-164-204-2	Sequence 2, Appl	797	23	71.9	505	1	US-08-630-592-4	Sequence 4, Appl
725	23	71.9	359	2	US-09-923-109-2	Sequence 2, Appl	798	23	71.9	505	1	US-08-829-553-8	Sequence 8, Appl
726	23	71.9	363	1	US-07-946-497-7	Sequence 7, Appl	799	23	71.9	505	1	US-08-714-991-4	Sequence 4, Appl
727	23	71.9	363	1	US-08-483-322-7	Sequence 7, Appl	800	23	71.9	505	1	US-08-829-553-2	Sequence 2, Appl
728	23	71.9	363	1	US-08-478-882-7	Sequence 7, Appl	801	23	71.9	505	1	US-08-922-267A-2	Sequence 2, Appl
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732	23	71.9	364	2	US-09-072-596-74	Sequence 74, Appl	805	23	71.9	505	2	US-08-812-824-3	Sequence 3, Appl
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734	23	71.9	364	2	US-10-193-002-74	Sequence 74, Appl	807	23	71.9	505	2	US-09-814-986-2	Sequence 8, Appl
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736	23	71.9	367	2	US-09-902-540-15316	Sequence 15316, A	809	23	71.9	506	1	US-08-829-553-8	Sequence 8, Appl
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747	23	71.9	397	1	US-08-371-377-19	Sequence 19, Appl	820	23	71.9	510	2	US-10-104-047-3594	Sequence 3594, Ap
748	23	71.9	397	1	US-09-086-662-2	Sequence 2, Appl	821	23	71.9	512	2	US-09-032-365A-6	Sequence 6, Appl
749	23	71.9	397	2	US-08-875-5530-25	Sequence 25, Appl	822	23	71.9	512	2	US-08-676-166A-5	Sequence 5, Appl
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753	23	71.9	408	2	US-09-540-236-3813	Sequence 3813, Ap	826	23	71.9	524	1	US-08-477-407-2	Sequence 2, Appl
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833	23	71.9	534	2	US-09-543-681A-6817	Sequence 6817, Ap	906	23	71.9	879	1	US-08-413-118-106	Sequence 106, App
834	23	71.9	534	2	US-09-344-882-24	Sequence 24, Appl1	907	23	71.9	879	2	US-08-473-446-2	Sequence 2, Appl1
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836	23	71.9	535	2	US-10-104-047-1971	Sequence 1971, Ap	909	23	71.9	879	2	US-08-473-446-106	Sequence 106, App
837	23	71.9	536	2	US-09-449-632-2	Sequence 2, Appl1	910	23	71.9	883	2	US-09-489-038A-12755	Sequence 12755, A
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839	23	71.9	539	2	US-09-258-031C-76	Sequence 76, Appl1	912	23	71.9	901	2	US-09-270-767-45367	Sequence 45367, A
840	23	71.9	540	2	US-09-302-626B-168	Sequence 168, App	913	23	71.9	901	2	US-09-949-016-7207	Sequence 7207, Ap
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842	23	71.9	558	1	US-08-663-694-12	Sequence 12, Appl1	915	23	71.9	955	2	US-09-252-991A-18882	Sequence 18882, A
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845	23	71.9	561	1	US-08-714-921-27	Sequence 27, Appl1	918	23	71.9	1003	1	US-08-107-755A-6	Sequence 6, Appl1
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847	23	71.9	565	2	US-08-937-067-8	Sequence 8, Appl1	920	23	71.9	1003	1	US-08-370-861A-6	Sequence 6, Appl1
848	23	71.9	573	2	US-09-134-001C-4656	Sequence 4656, Ap	921	23	71.9	1003	2	US-10-197-220-95	Sequence 95, Appl1
849	23	71.9	576	2	US-10-083-336A-1	Sequence 1, Appl1	922	23	71.9	1016	2	US-08-194-220-7	Sequence 7, Appl1
850	23	71.9	589	2	US-09-252-991A-31105	Sequence 31105, A	923	23	71.9	1026	1	US-08-614-377A-7	Sequence 7, Appl1
851	23	71.9	592	2	US-09-614-912-90	Sequence 90, Appl1	924	23	71.9	1026	1	US-09-142-648B-7	Sequence 7, Appl1
852	23	71.9	594	2	US-09-857-556A-34	Sequence 34, Appl1	925	23	71.9	1026	2	US-08-323-477-2	Sequence 2, Appl1
853	23	71.9	600	2	US-09-438-185A-1013	Sequence 1013, Ap	926	23	71.9	1115	2	US-10-193-950A-2	Sequence 2, Appl1
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863	23	71.9	670	1	US-08-477-407-3	Sequence 3, Appl1	936	23	71.9	1176	1	US-07-828-798A-12	Sequence 12, Appl1
864	23	71.9	670	1	US-08-484-355-13	Sequence 3, Appl1	937	23	71.9	1176	1	US-08-257-999-2	Sequence 2, Appl1
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873	23	71.9	719	2	US-09-857-556A-33	Sequence 33, Appl1	946	23	71.9	1180	1	US-08-486-270-8	Sequence 8, Appl1
874	23	71.9	720	2	US-09-857-556A-26	Sequence 26, Appl1	947	23	71.9	1180	2	US-08-367-264-8	Sequence 8, Appl1
875	23	71.9	721	2	US-09-857-556A-10	Sequence 10, Appl1	948	23	71.9	1180	2	US-08-660-148-2	Sequence 2, Appl1
876	23	71.9	726	2	US-09-538-092-498	Sequence 498, App	949	23	71.9	1180	2	US-09-153-757-8	Sequence 8, Appl1
877	23	71.9	728	2	US-09-712-363-167	Sequence 167, App	950	23	71.9	1180	2	US-09-459-715-8	Sequence 8, Appl1
878	23	71.9	746	2	US-09-134-001C-3214	Sequence 3214, Ap	951	23	71.9	1191	2	US-09-248-796A-16243	Sequence 16243, A
879	23	71.9	753	2	US-09-270-767-46781	Sequence 46781, A	952	23	71.9	1195	2	US-09-540-236-3165	Sequence 3165, Ap
880	23	71.9	766	2	US-09-538-092-216	Sequence 216, App	953	23	71.9	1209	2	US-09-949-002-494	Sequence 494, App
881	23	71.9	769	1	US-08-243-542-4	Sequence 4, Appl1	954	23	71.9	1209	2	US-09-949-002-494	Sequence 24, Appl1
882	23	71.9	769	1	US-08-477-407-4	Sequence 4, Appl1	955	23	71.9	1214	2	US-10-164-595-24	Sequence 24, Appl1
883	23	71.9	769	1	US-08-484-355-4	Sequence 4, Appl1	956	23	71.9	1261	2	US-09-949-016-9651	Sequence 9651, App
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887	23	71.9	772	2	US-09-949-016-7315	Sequence 7315, Ap	960	23	71.9	1376	2	US-09-294-298A-4	Sequence 4, Appl1
888	23	71.9	772	2	US-09-949-016-7316	Sequence 7316, Ap	961	23	71.9	1381	2	US-09-808-701A-25	Sequence 25, Appl1
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891	23	71.9	778	4	PCT-US93-03076-3	Sequence 3, Appl1	964	23	71.9	1513	4	PCT-US93-03076-2	Sequence 2, Appl1
892	23	71.9	778	4	PCT-US93-03076-4	Sequence 4, Appl1	965	23	71.9	1624	2	US-09-607-510-2	Sequence 2, Appl1
893	23	71.9	779	4	PCT-US93-03076-31	Sequence 31, Appl1	966	23	71.9	1803	2	US-09-902-540-15978	Sequence 15978, A
894	23	71.9	784	2	US-08-817-832B-31	Sequence 31, Appl1	967	23	71.9	1919	2	US-10-152-886-13	Sequence 13, Appl1
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896	23	71.9	789	2	US-09-949-016-10170	Sequence 10170, A	969	23	71.9	2321	2	US-09-230-652-2	Sequence 2, Appl1
897	23	71.9	789	2	US-09-252-991A-27011	Sequence 27011, A	970	23	71.9	2415	2	US-09-943-681A-38124	Sequence 38124, Ap
898	23	71.9	793	2	US-09-523-849-32	Sequence 32, Appl1	971	23	71.9	2717	2	US-09-543-681A-6124	Sequence 6124, Ap
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901	23	71.9	804	2	US-09-328-352-5545	Sequence 5545, Ap	974	23	68.8	7	2	US-09-192-854-31	Sequence 31, Appl1
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ALIGNMENTS

Sequence 47, Appl
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RESULT 1
US-08-974-899-14
Sequence 14, Application US/08974899

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-14

Query Match 100.0%; Score 32; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 1 SGGTLOS 7

RESULT 2
US-09-795-798-14
Sequence 14, Application US/09795798

GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-795-798-14

Query Match 100.0%; Score 32; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 1 SGGTLOS 7

RESULT 3
US-08-974-899-1
Sequence 1, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-1

Query Match 100.0%; Score 32; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 50 SGGTLOS 56

RESULT 4
US-08-974-899-2
Sequence 2, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-795-798-1

SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-974-899-2

Query Match 100.0%; Score 32; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 50 SGGTLOS 56

RESULT 5
US-09-795-798-1
Sequence 1, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-795-798-1

Query Match 100.0%; Score 32; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 50 SGGTLOS 56

RESULT 6
US-09-795-798-2
Sequence 2, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.

OY 1 SGSTLOS 7
|||||:
Db 51 SGSTLES 57

RESULT 9

US-09-026-985-47
; Sequence 47, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPacIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-47

Query Match 90.6%; Score 29; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
|||||:
Db 51 SGSTLES 57

RESULT 10
US-09-121-952A-47
; Sequence 47, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Kouments, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-47

Query Match 90.6%; Score 29; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTLOS 7
|||||:
Db 51 SGSTLES 57

RESULT 11
US-09-234-340A-47
; Sequence 47, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Kouments, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPacIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,340A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952

FILING DATE: 24-JUL-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-47

Query Match 90.6%; Score 29; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||:
Db 51 SGSTLES 57

RESULT 12
US-09-355-014-47

; Sequence 47; Application US/09355014
; Patent No. 6870033
; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc., Hsei, Vanessa
; Koumenis, Iphigenia
; Leong, Steven R.
; Presta, Leonard G.
; Shahrokhi, Zahra
; Zapata, Gerardo A.

; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; Humanized Anti-IL-8 Monoclonal Antibodies

; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/355,014
; FILING DATE: 21-JUL-1999
; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3PCT

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-355-014-47

Query Match 90.6%; Score 29; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||:
Db 51 SGSTLES 57

RESULT 13

US-09-252-991A-22821
; Sequence 22821; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22821
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22821

Query Match 90.6%; Score 29; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 1,8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||:
Db 148 SGSTVS 154

RESULT 14

5219837-1

; Patent No. 5219837

; APPLICANT: COHEN, JEFFREY A.; GREENE, MARK I.; WILLIAMS,
; WILLIAM V.

; TITLE OF INVENTION: METHOD OF STIMULATING MYELINATION
; OF CELLS

; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/541,779
; FILING DATE: 21-JUN-1990
; SEQ ID NO: 1
; LENGTH: 16
5219837-1

Query Match 87.5%; Score 28; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLO 6
|||||:
Db 11 SGSTLO 16

RESULT 15

5219837-7

; Patent No. 5219837

; APPLICANT: COHEN, JEFFREY A.; GREENE, MARK I.; WILLIAMS,
; WILLIAM V.

; TITLE OF INVENTION: METHOD OF STIMULATING MYELINATION
; OF CELLS
; NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/541,779
FILING DATE: 21-JUN-1990
SEQ ID NO:7:
LENGTH: 17
5219837-7

Query Match 87.5%; Score 28; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||
Db 12 SGGSTLQ 17

RESULT 16
5219837-9
; Patent No. 5219837
; APPLICANT: COHEN, JEFFREY A.; GREENE, MARK I.; WILLIAMS,
; WILLIAM V.
; TITLE OF INVENTION: METHOD OF STIMULATING MYELINATION
; OF CELLS
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/541,779
; FILING DATE: 21-JUN-1990
; SEQ ID NO:9:
; LENGTH: 17
5219837-9

Query Match 87.5%; Score 28; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||
Db 12 SGGSTLQ 17

RESULT 17
5219837-2
; Patent No. 5219837
; APPLICANT: COHEN, JEFFREY A.; GREENE, MARK I.; WILLIAMS,
; WILLIAM V.
; TITLE OF INVENTION: METHOD OF STIMULATING MYELINATION
; OF CELLS
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/541,779
; FILING DATE: 21-JUN-1990
; SEQ ID NO:2:
; LENGTH: 18
5219837-2

Query Match 87.5%; Score 28; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||
Db 13 SGGSTLQ 18

RESULT 18
5219837-3
; Patent No. 5219837
; APPLICANT: COHEN, JEFFREY A.; GREENE, MARK I.; WILLIAMS,
; WILLIAM V.
; TITLE OF INVENTION: METHOD OF STIMULATING MYELINATION
; OF CELLS
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/541,779
FILING DATE: 21-JUN-1990
SEQ ID NO:3:
LENGTH: 18
5219837-3

Query Match 87.5%; Score 28; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||
Db 13 SGGSTLQ 18

RESULT 19
US-09-270-767-39590
; Sequence 39590, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 39590
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-39590

Query Match 87.5%; Score 28; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||
Db 19 SGGSTLQ 24

RESULT 20
US-09-270-767-54807
; Sequence 54807, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 54807
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-54807

Query Match 87.5%; Score 28; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
|||
Db 19 SGGSTLQ 24

RESULT 21
US-09-910-430-18
; Sequence 18, Application US/09910430
; Patent No. 6794166

GENERAL INFORMATION:
APPLICANT: Godfroi, Edmond
APPLICANT: Bollen, Alex
APPLICANT: Lebouille, Gerard
TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
TITLE OF INVENTION: GLANDS
FILE REFERENCE: VANM229.001CPI
CURRENT APPLICATION NUMBER: US/09/910,430
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: PCT/BE00/00061
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: GB 9913425.6
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 488
TYPE: PRT
ORGANISM: Ixodes ricinus
US-09-910-430-18

Query Match 87.5%; Score 28; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGTLOS 7
|||||
DB 291 SGTLOS 296

RESULT 22
US-08-937-067-13
Sequence 13, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umansky, Samuil
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-13

Query Match 87.5%; Score 28; DB 2; Length 572;
Best Local Similarity 85.7%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGTLOS 7
|||||
DB 548 SGTLOS 554

RESULT 23
US-09-809-665A-16
Sequence 16, Application US/09809665A
Patent No. 6790950
GENERAL INFORMATION:
APPLICANT: Lowery E., David, et al.
TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
FILE REFERENCE: 28341/00435
CURRENT APPLICATION NUMBER: US/09/809,665A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 60/153,453
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/128,689
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 09/545,199
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 210
TYPE: PRT
ORGANISM: Pasteurella multocida
US-09-809-665A-16

Query Match 87.5%; Score 28; DB 2; Length 2110;
Best Local Similarity 85.7%; Pred. No. 1.8e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGTLOS 7
|||||
DB 1630 SGTLOS 1636

RESULT 24
US-09-270-767-33995
Sequence 33995, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33995
LENGTH: 75
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-33995

Query Match 84.4%; Score 27; DB 2; Length 75;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGTLOS 7
|||||
DB 38 SGTLOS 44

RESULT 25
US-09-270-767-49212
Sequence 49212, Application US/09270767


```
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ NUMBER OF SEQ ID NOS: 1999-03-17
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 49212
/ LENGTH: 75
/ TYPE: PRM
/ ORGANISM: Drosophila melanogaster
US-09-270-767-49212

Query Match      84.4%; Score 27; DB 2; Length 75;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SCSSTLOS 7
DB      38 SCSSTLOS 44

RESULT 26
US-09-661-322A-14
/ Sequence 14, Application US/09661322A
/ Patent No. 6593293
/ GENERAL INFORMATION:
/ APPLICANT: Baum, James A.
/ APPLICANT: Chu, Chih-Rei
/ APPLICANT: Donovan, William P.
/ APPLICANT: Gilmer, Amy J.
/ APPLICANT: Rupert, Mark J.
/ TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin Compos
/ FILE REFERENCE: MECO201
/ CURRENT APPLICATION NUMBER: US/09/661,322A
/ CURRENT FILING DATE: 2000-09-13
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: Patentln version 3.0
/ SEQ ID NO 14
/ LENGTH: 93
/ TYPE: PRM
/ ORGANISM: Bacillus thuringiensis
US-09-661-322A-14

Query Match      84.4%; Score 27; DB 2; Length 93;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SCSSTLOS 7
DB      22 SCSSTLOS 28

RESULT 27
US-09-456-830-7
/ Sequence 7, Application US/09456830
/ Patent No. 6274721
/ GENERAL INFORMATION:
/ APPLICANT: Schnepf, H. Ernest
/ APPLICANT: Wicker, Carol
/ APPLICANT: Narva, Kenneth E.
/ APPLICANT: Walz, Michelle
/ APPLICANT: Stockhoff
/ TITLE OF INVENTION: Toxins Active Against Pests
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
```

```
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/456,830
/ FILING DATE: 07-DEC-1999
/ CLASSIFICATION: 534
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: MA701
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 375-8100
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 137 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-456-830-7

Query Match      84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 SCSSTLOS 7
DB      66 SCSSTLOS 72

RESULT 28
US-09-456-830-15
/ Sequence 15, Application US/09456830
/ Patent No. 6274721
/ GENERAL INFORMATION:
/ APPLICANT: Schnepf, H. Ernest
/ APPLICANT: Wicker, Carol
/ APPLICANT: Narva, Kenneth E.
/ APPLICANT: Walz, Michelle
/ APPLICANT: Stockhoff
/ TITLE OF INVENTION: Toxins Active Against Pests
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: Florida
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/456,830
/ FILING DATE: 07-DEC-1999
/ CLASSIFICATION: 534
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: MA701
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (352) 372-5800
/ TELEFAX: (352) 372-5800
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
```

LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-456-830-15

Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSGSTLOS 7
|||
Db 66 SSGSNIQS 72

RESULT 29
US-09-456-830-19
Sequence 19, Application US/09456830
Patent No. 6274721

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/456,830
FILING DATE: 07-DEC-1999
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA701
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-456-830-19

Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSGSTLOS 7
|||
Db 66 SSGSNIQS 72

RESULT 30
US-09-456-830-37
Sequence 37, Application US/09456830
Patent No. 6274721

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/456,830
FILING DATE: 07-DEC-1999
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA701
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-456-830-37

Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSGSTLOS 7
|||
Db 66 SSGSNIQS 72

RESULT 31
US-09-002-285-7
Sequence 7, Application US/09002285
Patent No. 6368213
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-002-285-7

Query Match 84.4%; Score 27; DB 2; Length 137;
Best local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
Db 66 SGGNLOS 72

RESULT 32
US-09-002-285-15
Sequence 15, Application US/09002285
Patent No. 6369213
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-002-285-15

Query Match 84.4%; Score 27; DB 2; Length 137;
Best local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
Db 66 SGGNLOS 72

RESULT 33
US-09-002-285-19
Sequence 19, Application US/09002285
Patent No. 6369213
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-002-285-19

Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
DB 66 SCSNLOS 72

RESULT 34
US-09-002-285-37
; Sequence 37, Application US/09002285
; Patent No. 6369213
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; APPLICANT: Muller-Cohn, Judy
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/002,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-002-285-37

Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
DB 66 SCSNLOS 72

RESULT 35
US-09-589-477-7
; Sequence 7, Application US/09589477

; Patent No. 6570005
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/589,477
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/886,615
; FILING DATE: 1-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/674,002
; FILING DATE: 1-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanders, Jay M.
; REGISTRATION NUMBER: 39,355
; REFERENCE/DOCKET NUMBER: MA-701C1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (352) 375-8100
; TELEFAX: (352) 372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-589-477-7

Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
DB 66 SCSNLOS 72

RESULT 36
US-09-589-477-15
; Sequence 15, Application US/09589477
; Patent No. 6570005
; GENERAL INFORMATION:
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Wicker, Carol
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Walz, Michelle
; APPLICANT: Stockhoff, Brian
; TITLE OF INVENTION: Toxins Active Against Pests
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-589-477-15

Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCSSTLOS 7
DB 66 SCSNLOS 72

RESULT 37
US-09-589-477-19
Sequence 19, Application US/09589477
Patent No. 6570005
GENERAL INFORMATION:
APPLICANT: Schmepl, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-589-477-19

Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCSSTLOS 7
DB 66 SCSNLOS 72

RESULT 38
US-09-589-477-37
Sequence 37, Application US/09589477
Patent No. 6570005
GENERAL INFORMATION:
APPLICANT: Schmepl, H. Ernest
APPLICANT: Wicker, Carol
APPLICANT: Narva, Kenneth E.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-589-477-37

Query Match
Best Local Similarity 84.4%; Score 27; DB 2; Length 137;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 66 SGSNLOS 72

RESULT 39
US-10-099-285A-7
Sequence 7, Application US/10099285A
Patent No. 6752992
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7;

US-10-099-285A-7

Query Match
Best Local Similarity 84.4%; Score 27; DB 2; Length 137;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 66 SGSNLOS 72

RESULT 40
US-10-099-285A-15
Sequence 15, Application US/10099285A
Patent No. 6752992
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15;

US-10-099-285A-15

Query Match
Best Local Similarity 84.4%; Score 27; DB 2; Length 137;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 66 SGSNLOS 72

RESULT 41
US-10-099-285A-19
Sequence 19, Application US/10099285A
Patent No. 6752992
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-JUL-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-099-285A-19
Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGSTLOS 7
Db 66 SGSNLOS 72
RESULT 42
US-10-099-285A-37
Sequence 37, Application US/10099285A
Patent No. 6752992
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
Wicker, Carol
Narva, Kenneth E.
Stockhoff, Brian
Muller-Cohn, Judy

TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285A
FILING DATE: 02-JUL-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 09/002,285
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-099-285A-37
Query Match 84.4%; Score 27; DB 2; Length 137;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 SGSTLOS 7
Db 66 SGSNLOS 72
RESULT 43
US-08-433-783-43
Sequence 43, Application US/08433783
Patent No. 5770431
GENERAL INFORMATION:
APPLICANT: Liu, Chi-Li
APPLICANT: Adams, Lee F.
APPLICANT: Luitburrow, Patricia A.
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS STRAINS
TITLE OF INVENTION: ACTIVE AGAINST LEPIDOPTERAN AND COLEOPTERAN PESTS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5770431 of No. 5770431th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,783
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,358
FILING DATE: 10-NOV-1994
APPLICATION NUMBER: US 08/264,100
FILING DATE: 22-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,651
FILING DATE: 09-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/166,391
FILING DATE: 13-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,073
FILING DATE: 15-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agtis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3778.230-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-783-43

Query Match 84.4%; Score 27; DB 1; Length 358;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
DB 348 SGGSNLOS 354

RESULT 44
US-08-337-358-43
Sequence 43, Application US/08337358
Patent No. 5879676
GENERAL INFORMATION:
APPLICANT: Liu, Chi-Li
APPLICANT: Adams, Lee F.
APPLICANT: Lutburrow, Patricia A.
APPLICANT: Thomas, Michael D.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS STRAINS
TITLE OF INVENTION: ACTIVE AGAINST LEPIDOPTERAN AND COLEOPTERAN PESTS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 58796760 No. 5879676disk of No. 5879676th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,358
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Agtis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3778.230-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-337-358-43

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/264,100
FILING DATE: 22-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,651
FILING DATE: 09-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/166,391
FILING DATE: 13-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,073
FILING DATE: 15-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agtis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3778.230-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-337-358-43

Query Match 84.4%; Score 27; DB 1; Length 358;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
DB 348 SGGSNLOS 354

RESULT 45
PCT-US95-07537A-43
Sequence 43, Application PC/TUS9507537A
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS STRAINS
TITLE OF INVENTION: ACTIVE AGAINST LEPIDOPTERAN AND COLEOPTERAN PESTS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07537A
FILING DATE: 15-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,073
FILING DATE: 15-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/264,100
FILING DATE: 22-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/194,651
FILING DATE: 09-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,073
FILING DATE: 15-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agtis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3778.230-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-337-358-43

REFERENCE/DOCKET NUMBER: 3778.404-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-07537A-43

Query Match 84.4%; Score 27; DB 4; Length 358;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 348 SGGSTLOS 354

RESULT 46
PCT-US95-07537-43
Sequence 43, Application PC/TUS9507537
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS STRAINS
TITLE OF INVENTION: ACTIVE AGAINST LEPIDOPTERAN AND COLEOPTERAN PESTS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07537
FILING DATE: 15-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/264,100
FILING DATE: 22-JUN-1994
PRIOR APPLICATION DATA: US 08/337,358
FILING DATE: 10-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Agria Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3778.404-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-07537-43

Query Match 84.4%; Score 27; DB 4; Length 358;
Best Local Similarity 85.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7

Db 348 SGGSTLOS 354

RESULT 47
US-09-902-540-10181
Sequence 10181, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10181
LENGTH: 569
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-10181

Query Match 84.4%; Score 27; DB 2; Length 569;
Best Local Similarity 85.7%; Pred. No. 7.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 550 SGGSTLOS 556

RESULT 48
5523211-1
Patent No. 5523211
APPLICANT: PUSZTAI-CAREY, MARIANNE; CAREY, PAUL R.; LESSARD,
TIMOTHY; YAGUCHI, MAKOTO
TITLE OF INVENTION: IDENTIFICATION, QUANTITATION AND
PURIFICATION OF INSECTICIDAL PROTEINS FROM BACILLUS THURINGIENSIS
NUMBER OF SEQUENCES: 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,076
FILING DATE: 19-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 102,491
FILING DATE: 05-AUG-1993
APPLICATION NUMBER: 836,967
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: 493,453
FILING DATE: 14-MAR-1990
SEQ ID NO: 1
LENGTH: 593
5523211-1

Query Match 84.4%; Score 27; DB 6; Length 593;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 528 SGGSTLOS 534

RESULT 49
5523211-2
Patent No. 5523211
APPLICANT: PUSZTAI-CAREY, MARIANNE; CAREY, PAUL R.; LESSARD,
TIMOTHY; YAGUCHI, MAKOTO
TITLE OF INVENTION: IDENTIFICATION, QUANTITATION AND
PURIFICATION OF INSECTICIDAL PROTEINS FROM BACILLUS THURINGIENSIS

Db 557 SSSNLOS 563
 Search completed: January 17, 2006, 12:07:49
 UOB time : 19.0909 secs

NUMBER OF SEQUENCES: 3
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/277,076
 FILING DATE: 19-JUL-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 102,491
 FILING DATE: 05-AUG-1993
 APPLICATION NUMBER: 836,967
 FILING DATE: 19-FEB-1992
 APPLICATION NUMBER: 493,453
 FILING DATE: 14-MAR-1990
 SEQ ID NO: 2
 LENGTH: 593
 5523211-2

Query Match 84.4%; Score 27; DB 6; Length 593;
 Best Local Similarity 85.7%; Pred. No. 7.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
 Db 528 SSSNLOS 534

RESULT 50
 US-08-622-740-8
 Sequence 8, Application US/08622740
 Patent No. 5990390
 GENERAL INFORMATION:
 APPLICANT: Lundquist, Ronald C.
 APPLICANT: Walters, David A.
 APPLICANT: Kirihara, Julie A.
 TITLE OF INVENTION: Methods and Compositions for the
 TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
 STREET: 3500 IDS Center
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/622,740
 FILING DATE: 27-MARCH-1996
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Woessner, Warren D.
 REGISTRATION NUMBER: 30,440
 REFERENCE/DOCKET NUMBER: 950.013US4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-339-0331
 TELEFAX: 612-339-3061
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 614 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-622-740-8

Query Match 84.4%; Score 27; DB 1; Length 614;
 Best Local Similarity 85.7%; Pred. No. 8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
 ||| |||

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OW protein - protein search, using sw model

Run on: January 17, 2006, 11:50:44 ; Search time 34.0455 Seconds
(without alignments)
85.909 Million cell updates/sec

Title: US-10-665-658-14
Perfect score: 32
Sequence: 1 SCSTLQS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	7	US-09-795-798-14	Sequence 14, Appl
2	32	100.0	7	US-10-727-737-55	Sequence 55, Appl
3	32	100.0	100	US-10-425-115-214302	Sequence 214302,
4	32	100.0	101	US-10-010-729-23	Sequence 23, Appl
5	32	100.0	107	US-11-003-819-10	Sequence 10, Appl
6	32	100.0	108	US-09-795-798-1	Sequence 1, Appl
7	32	100.0	108	US-09-795-798-2	Sequence 2, Appl
8	32	100.0	108	US-10-010-729-43	Sequence 43, Appl
9	32	100.0	108	US-10-727-737-1	Sequence 1, Appl
10	32	100.0	108	US-10-727-737-2	Sequence 2, Appl
11	32	100.0	108	US-10-877-832-5	Sequence 5, Appl
12	32	100.0	214	US-10-424-599-249629	Sequence 3, Appl
13	30	93.8	242	US-10-424-599-249629	Sequence 249629,
14	29	90.6	7	US-10-727-737-57	Sequence 57, Appl
15	29	90.6	7	US-10-727-737-58	Sequence 58, Appl
16	29	90.6	48	US-10-425-115-212123	Sequence 212123,
17	29	90.6	109	US-09-726-258-47	Sequence 47, Appl
18	29	90.6	347	US-10-282-122A-66553	Sequence 66553, A
19	29	90.6	428	US-11-097-143-16788	Sequence 16788, A
20	29	90.6	665	US-09-864-761-43276	Sequence 43276, A
21	29	90.6	1377	US-10-205-342-25	Sequence 25, Appl
22	29	90.6	1387	US-10-450-763-39403	Sequence 39403, A
23	29	90.6	2228	US-10-450-763-39401	Sequence 39401, A
24	28	87.5	17	US-10-105-545-1	Sequence 1, Appl
25	28	87.5	17	US-10-105-545-6	Sequence 6, Appl
26	28	87.5	18	US-10-105-545-2	Sequence 2, Appl
27	28	87.5	18	US-10-105-545-19	Sequence 19, Appl

28	28	87.5	42	US-10-424-599-154913	Sequence 154913,
29	28	87.5	43	US-10-425-115-237614	Sequence 237614,
30	28	87.5	60	US-10-425-115-354064	Sequence 354064,
31	28	87.5	67	US-09-764-891-3607	Sequence 3607, Ap
32	28	87.5	80	US-10-242-355-401	Sequence 401, Ap
33	28	87.5	108	US-10-891-972-26	Sequence 26, Appl
34	28	87.5	110	US-10-106-698-6352	Sequence 6352, Ap
35	28	87.5	114	US-10-732-923-12398	Sequence 12398, A
36	28	87.5	147	US-10-424-599-174967	Sequence 174967,
37	28	87.5	186	US-11-097-143-38067	Sequence 38067, A
38	28	87.5	191	US-10-425-114-68883	Sequence 68883, A
39	28	87.5	202	US-10-767-701-40334	Sequence 40334, A
40	28	87.5	202	US-10-425-115-349367	Sequence 349367,
41	28	87.5	218	US-10-425-115-296478	Sequence 296478,
42	28	87.5	221	US-10-424-599-266598	Sequence 266598,
43	28	87.5	223	US-10-450-763-36778	Sequence 36778, A
44	28	87.5	241	US-10-767-701-46400	Sequence 46400, A
45	28	87.5	248	US-10-425-115-185877	Sequence 185877,
46	28	87.5	252	US-10-767-701-41192	Sequence 41192, A
47	28	87.5	255	US-10-425-114-55860	Sequence 55860, A
48	28	87.5	273	US-10-425-115-238055	Sequence 238055,
49	28	87.5	283	US-10-437-963-141800	Sequence 141800,
50	28	87.5	285	US-10-767-701-40250	Sequence 40250, A
51	28	87.5	294	US-10-087-192-1068	Sequence 1068, Ap
52	28	87.5	318	US-10-774-355A-1774	Sequence 1774, Ap
53	28	87.5	350	US-10-425-114-39736	Sequence 39736, A
54	28	87.5	354	US-10-425-115-295928	Sequence 295928,
55	28	87.5	357	US-10-425-115-185875	Sequence 185875,
56	28	87.5	361	US-10-425-114-55862	Sequence 55862, A
57	28	87.5	384	US-10-437-963-167254	Sequence 167254,
58	28	87.5	416	US-10-425-114-48456	Sequence 48456, A
59	28	87.5	435	US-10-369-493-6907	Sequence 6907, Ap
60	28	87.5	444	US-10-437-963-178298	Sequence 178298,
61	28	87.5	454	US-10-032-585-7816	Sequence 7816, Ap
62	28	87.5	472	US-10-425-114-61203	Sequence 61203, A
63	28	87.5	488	US-09-910-430-18	Sequence 18, Appl
64	28	87.5	488	US-10-165-605A-18	Sequence 18, Appl
65	28	87.5	499	US-10-425-115-324540	Sequence 324540,
66	28	87.5	560	US-10-437-963-187287	Sequence 187287,
67	28	87.5	566	US-10-425-115-186251	Sequence 186251,
68	28	87.5	572	US-09-847-102A-55	Sequence 55, Appl
69	28	87.5	572	US-10-146-474-13	Sequence 13, Appl
70	28	87.5	572	US-10-301-764-13	Sequence 13, Appl
71	28	87.5	573	US-10-152-548-14	Sequence 14, Appl
72	28	87.5	574	US-09-847-102A-54	Sequence 54, Appl
73	28	87.5	574	US-10-285-976-51	Sequence 51, Appl
74	28	87.5	574	US-10-723-860-1079	Sequence 1079, Ap
75	28	87.5	651	US-10-425-115-285705	Sequence 285705,
76	28	87.5	654	US-10-369-493-22744	Sequence 22744, A
77	28	87.5	655	US-10-425-114-60893	Sequence 60893, A
78	28	87.5	693	US-10-087-192-1065	Sequence 1065, Ap
79	28	87.5	713	US-11-097-143-24642	Sequence 24642, A
80	28	87.5	732	US-11-097-143-24639	Sequence 24639, A
81	28	87.5	834	US-10-739-930-6117	Sequence 6117, Ap
82	28	87.5	911	US-10-732-923-7111	Sequence 7111, Ap
83	28	87.5	963	US-10-369-493-18428	Sequence 18428, A
84	28	87.5	1046	US-11-097-143-15102	Sequence 15102, A
85	28	87.5	1366	US-11-097-143-8397	Sequence 8397, Ap
86	28	87.5	1398	US-09-809-665A-16	Sequence 16, Appl
87	28	87.5	2110	US-10-854-299-16	Sequence 16, Appl
88	28	87.5	7	US-10-727-737-59	Sequence 59, Appl
89	27	84.4	12	US-10-286-457-343	Sequence 343, App
90	27	84.4	12	US-10-282-122A-65512	Sequence 65512, A
91	27	84.4	71	US-10-428-961-14	Sequence 14, Appl
92	27	84.4	93	US-09-764-869-663	Sequence 663, App
93	27	84.4	129	US-10-091-504-633	Sequence 633, App
94	27	84.4	129	US-10-227-577-633	Sequence 633, App
95	27	84.4	137	US-10-099-285-7	Sequence 7, Appl
96	27	84.4	137	US-10-099-285-15	Sequence 15, Appl
97	27	84.4	137	US-10-099-285-19	Sequence 19, Appl
98	27	84.4	137	US-10-099-285-37	Sequence 37, Appl
99	27	84.4	170	US-10-767-701-61799	Sequence 61799, A
100	27	84.4	4		

101	27	84.4	172	4	US-10-424-599-256035	Sequence 256035,	174	26	81.2	212	5	US-10-513-725-8	Sequence 8, Appl1
102	27	84.4	216	4	US-10-437-963-127148	Sequence 127148,	175	26	81.2	219	4	US-10-319-799-37	Sequence 37, Appl1
103	27	84.4	224	4	US-10-396-115-1426	Sequence 1426, Ap	176	26	81.2	219	4	US-10-424-599-244323	Sequence 244323,
104	27	84.4	280	4	US-10-382-122A-77738	Sequence 77738, A	177	26	81.2	221	4	US-10-425-115-331067	Sequence 331067,
105	27	84.4	358	2	US-08-964-116-43	Sequence 43, Appl	178	26	81.2	221	5	US-10-732-922-5579	Sequence 5579, Ap
106	27	84.4	390	4	US-10-156-761-9707	Sequence 9707, Ap	179	26	81.2	233	4	US-10-282-122A-66805	Sequence 66805, A
107	27	84.4	438	6	US-11-097-143-30795	Sequence 30795, A	180	26	81.2	239	4	US-10-262-833-114	Sequence 174, Appl
108	27	84.4	581	4	US-10-102-469-2	Sequence 2, Appl1	181	26	81.2	239	4	US-10-336-603A-58	Sequence 174, Appl
109	27	84.4	596	4	US-10-424-599-274985	Sequence 274985,	182	26	81.2	245	4	US-10-425-114-48915	Sequence 40580, A
110	27	84.4	609	4	US-10-107-581-3	Sequence 3, Appl1	183	26	81.2	248	4	US-10-424-599-202362	Sequence 48915, A
111	27	84.4	609	4	US-10-107-581-4	Sequence 4, Appl1	184	26	81.2	273	4	US-10-369-499-18979	Sequence 202362,
112	27	84.4	609	4	US-10-107-581-5	Sequence 5, Appl1	185	26	81.2	276	4	US-10-369-499-18979	Sequence 18979, A
113	27	84.4	609	4	US-10-107-581-6	Sequence 6, Appl1	186	26	81.2	299	4	US-10-282-122A-54624	Sequence 54624, A
114	27	84.4	609	4	US-10-107-581-7	Sequence 7, Appl1	187	26	81.2	305	3	US-09-925-302-567	Sequence 567, App
115	27	84.4	609	4	US-10-107-581-8	Sequence 8, Appl1	188	26	81.2	305	3	US-09-925-302-567	Sequence 567, App
116	27	84.4	610	6	US-11-018-615-23	Sequence 23, Appl	189	26	81.2	319	4	US-10-258-662-16	Sequence 16, Appl1
117	27	84.4	614	5	US-10-919-228-8	Sequence 8, Appl1	190	26	81.2	335	5	US-10-450-763-33372	Sequence 32372, A
118	27	84.4	615	4	US-10-102-469-8	Sequence 8, Appl1	191	26	81.2	335	5	US-10-450-763-58403	Sequence 58403, A
119	27	84.4	617	4	US-10-137-682A-1	Sequence 1, Appl1	192	26	81.2	345	4	US-10-437-963-139763	Sequence 139763,
120	27	84.4	617	4	US-10-429-096-1	Sequence 1, Appl1	193	26	81.2	345	4	US-10-425-115-315828	Sequence 315828,
121	27	84.4	619	6	US-11-097-143-36861	Sequence 36861, A	194	26	81.2	354	3	US-09-095-478-6	Sequence 6, Appl1
122	27	84.4	653	3	US-09-826-660-27	Sequence 27, Appl	195	26	81.2	354	4	US-10-276-774-2258	Sequence 2258, Ap
123	27	84.4	958	4	US-10-408-765A-1768	Sequence 1768, Ap	196	26	81.2	372	4	US-10-047-412A-2	Sequence 2, Appl1
124	27	84.4	1150	4	US-10-099-285-74	Sequence 74, Appl	197	26	81.2	379	3	US-09-095-478-8	Sequence 8, Appl1
125	27	84.4	1150	6	US-11-018-615-18	Sequence 18, Appl	198	26	81.2	412	3	US-09-095-478-3	Sequence 3, Appl1
126	27	84.4	1150	6	US-11-018-615-19	Sequence 19, Appl	199	26	81.2	426	3	US-09-095-478-1	Sequence 1, Appl1
127	27	84.4	1152	4	US-10-614-524-6	Sequence 6, Appl1	200	26	81.2	430	4	US-10-437-963-200942	Sequence 200942,
128	27	84.4	1152	6	US-11-018-615-17	Sequence 17, Appl	201	26	81.2	438	6	US-11-097-143-37854	Sequence 37854, A
129	27	84.4	1155	3	US-09-756-643-2	Sequence 2, Appl1	202	26	81.2	458	4	US-10-424-599-261452	Sequence 261452,
130	27	84.4	1155	3	US-09-988-462-9	Sequence 9, Appl1	203	26	81.2	463	3	US-09-095-478-2	Sequence 2, Appl1
131	27	84.4	1155	4	US-10-136-998A-2	Sequence 2, Appl1	204	26	81.2	482	5	US-10-739-930-5916	Sequence 5916, Ap
132	27	84.4	1155	5	US-10-926-819-6	Sequence 6, Appl1	205	26	81.2	515	4	US-10-424-599-259997	Sequence 259997,
133	27	84.4	1176	4	US-10-782-141-6	Sequence 7, Appl1	206	26	81.2	552	3	US-09-923-923-9	Sequence 9, Appl1
134	27	84.4	1176	4	US-10-782-096-7	Sequence 7, Appl1	207	26	81.2	552	4	US-10-390-553-9	Sequence 9, Appl1
135	27	84.4	1176	4	US-10-782-570-5	Sequence 5, Appl1	208	26	81.2	587	6	US-11-097-143-29616	Sequence 29616, A
136	27	84.4	1176	5	US-10-783-817-3	Sequence 3, Appl1	209	26	81.2	609	5	US-10-450-763-34439	Sequence 34439, A
137	27	84.4	1176	5	US-10-781-979-8	Sequence 8, Appl1	210	26	81.2	641	4	US-10-437-963-181519	Sequence 181519,
138	27	84.4	1176	5	US-10-926-819-5	Sequence 5, Appl1	211	26	81.2	730	4	US-10-369-499-237619	Sequence 237619,
139	27	84.4	1177	4	US-10-035-060-2	Sequence 2, Appl1	212	26	81.2	744	4	US-10-282-122A-45361	Sequence 45361, A
140	27	84.4	1177	4	US-10-035-060-6	Sequence 6, Appl1	213	26	81.2	756	5	US-10-732-922-7393	Sequence 7393, Ap
141	27	84.4	1177	4	US-10-035-060-8	Sequence 8, Appl1	214	26	81.2	756	5	US-10-732-922-22109	Sequence 22109, A
142	27	84.4	1177	4	US-10-102-469-24	Sequence 24, Appl	215	26	81.2	777	5	US-10-072-036-77	Sequence 77, Appl
143	27	84.4	1181	3	US-09-988-462-11	Sequence 11, Appl	216	26	81.2	798	4	US-10-072-036-77	Sequence 77, Appl
144	27	84.4	1181	3	US-09-988-462-12	Sequence 12, Appl	217	26	81.2	801	4	US-10-437-963-200946	Sequence 200946,
145	27	84.4	1181	3	US-09-988-462-15	Sequence 15, Appl	218	26	81.2	806	4	US-10-072-036-53	Sequence 53, Appl
146	27	84.4	1181	3	US-09-988-462-17	Sequence 17, Appl	219	26	81.2	819	4	US-10-303-683-18	Sequence 18, Appl
147	27	84.4	1181	3	US-09-988-462-28	Sequence 28, Appl	220	26	81.2	820	4	US-10-303-683-19	Sequence 19, Appl
148	27	84.4	1181	4	US-10-136-998A-8	Sequence 8, Appl1	221	26	81.2	859	4	US-10-092-900A-154	Sequence 154, App
149	27	84.4	1181	4	US-10-136-998A-10	Sequence 10, Appl	222	26	81.2	1009	4	US-10-741-601-507	Sequence 507, App
150	27	84.4	1181	4	US-10-136-998A-12	Sequence 12, Appl	223	26	81.2	1057	4	US-10-424-599-161909	Sequence 161909,
151	27	84.4	1181	4	US-10-136-998A-12	Sequence 12, Appl	224	26	81.2	1057	4	US-10-424-599-161909	Sequence 161909,
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153	26	81.2	55	4	US-10-425-115-318358	Sequence 318358,	226	26	81.2	1445	4	US-10-450-763-46026	Sequence 46026, A
154	26	81.2	60	4	US-10-424-599-257475	Sequence 257475,	227	26	81.2	1453	4	US-10-282-122A-45027	Sequence 45027, A
155	26	81.2	87	4	US-10-425-115-274658	Sequence 274658,	228	26	81.2	1703	6	US-11-097-143-18582	Sequence 18582, A
156	26	81.2	89	4	US-10-424-599-243191	Sequence 243191,	229	26	81.2	2261	5	US-10-470-048B-60	Sequence 60, Appl1
157	26	81.2	95	4	US-10-425-115-197594	Sequence 197594,	230	26	81.2	2271	4	US-10-282-122A-43924	Sequence 43924, A
158	26	81.2	96	4	US-10-437-963-144626	Sequence 144626,	231	26	81.2	2283	4	US-10-172-502-4	Sequence 4, Appl1
159	26	81.2	115	5	US-10-916-758-30	Sequence 30, Appl1	232	26	81.2	2283	4	US-11-020-509-4	Sequence 4, Appl1
160	26	81.2	130	5	US-10-450-763-44759	Sequence 44759, A	233	26	81.2	2283	6	US-10-815-242-12713	Sequence 12713, A
161	26	81.2	136	4	US-10-424-599-253784	Sequence 253784,	234	26	81.2	2283	3	US-09-815-242-12713	Sequence 2024, Ap
162	26	81.2	139	4	US-10-424-599-261776	Sequence 261776,	235	26	81.2	3079	4	US-10-105-545-7	Sequence 7, Appl1
163	26	81.2	148	5	US-10-660-811A-265	Sequence 265, App	236	25	78.1	17	4	US-10-105-545-7	Sequence 20, Appl
164	26	81.2	155	4	US-10-424-599-282955	Sequence 282955,	237	25	78.1	18	4	US-10-105-545-20	Sequence 52, Appl
165	26	81.2	156	4	US-10-425-115-274656	Sequence 274656,	238	25	78.1	32	5	US-10-875-133-52	Sequence 20, Appl
166	26	81.2	158	3	US-09-847-208-117	Sequence 117, App	239	25	78.1	32	4	US-10-029-386-31920	Sequence 31920, A
167	26	81.2	162	4	US-10-425-115-317461	Sequence 317461,	240	25	78.1	43	3	US-09-978-360A-508	Sequence 508, Appl
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171	26	81.2	181	4	US-10-425-115-304923	Sequence 304923,	244	25	78.1	52	4	US-10-424-599-282099	Sequence 282099,
172	26	81.2	197	4	US-10-425-115-315829	Sequence 315829,	245	25	78.1	53	4	US-10-424-599-222761	Sequence 222761,
173	26	81.2	207	5	US-10-732-923-3889	Sequence 3889, Ap	246	25	78.1	57	4	US-10-767-701-53577	Sequence 53577, A

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249	25	78.1	59	4	US-10-425-115-359459	Sequence 359459,	322	25	78.1	191	5	US-10-732-923-12705	Sequence 12705, A
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251	25	78.1	61	4	US-10-372-876-335	Sequence 335, App	324	25	78.1	194	4	US-10-424-599-244402	Sequence 244402, A
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255	25	78.1	80	3	US-09-664-408A-1870	Sequence 1870, Ap	328	25	78.1	206	3	US-09-272-809-12	Sequence 12,
256	25	78.1	82	4	US-10-424-599-232720	Sequence 232720,	329	25	78.1	211	4	US-10-425-115-261338	Sequence 261338
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258	25	78.1	85	4	US-10-282-122A-77169	Sequence 77169, A	331	25	78.1	213	4	US-10-425-115-251274	Sequence 251274,
259	25	78.1	86	4	US-10-767-701-37668	Sequence 37668, A	332	25	78.1	214	4	US-10-437-963-129859	Sequence 129859,
260	25	78.1	87	5	US-10-450-763-47164	Sequence 47164, A	333	25	78.1	216	4	US-10-425-115-343634	Sequence 343634,
261	25	78.1	89	4	US-10-425-115-366753	Sequence 366753,	334	25	78.1	216	4	US-10-424-599-217324	Sequence 217324,
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263	25	78.1	94	4	US-10-437-963-130164	Sequence 130164,	336	25	78.1	221	5	US-10-450-763-40295	Sequence 40295, A
264	25	78.1	94	4	US-10-450-763-53829	Sequence 53829, A	337	25	78.1	223	5	US-10-693-623-66	Sequence 66, Appl1
265	25	78.1	99	5	US-10-450-763-55632	Sequence 55632, A	338	25	78.1	234	4	US-10-767-701-33427	Sequence 33427, A
266	25	78.1	100	4	US-10-058-820-7	Sequence 7, Appl1	339	25	78.1	235	4	US-10-424-599-243719	Sequence 243719,
267	25	78.1	102	4	US-10-437-963-191328	Sequence 191328,	340	25	78.1	236	4	US-10-296-115-798	Sequence 798, App
268	25	78.1	104	4	US-10-437-963-204622	Sequence 204622,	341	25	78.1	240	4	US-10-767-701-37189	Sequence 37189, A
269	25	78.1	106	4	US-10-040-244-17	Sequence 17, Appl1	342	25	78.1	243	4	US-10-424-599-221898	Sequence 221898,
270	25	78.1	106	5	US-10-450-763-57191	Sequence 57191, A	343	25	78.1	247	4	US-10-335-977-8664	Sequence 8664, App
271	25	78.1	109	4	US-10-156-761-8423	Sequence 8423, A	344	25	78.1	250	4	US-10-424-599-216099	Sequence 216099,
272	25	78.1	110	4	US-10-425-115-315769	Sequence 315769,	345	25	78.1	252	4	US-10-437-963-109142	Sequence 109142,
273	25	78.1	112	5	US-10-450-763-39637	Sequence 39637, A	346	25	78.1	252	4	US-10-425-115-343639	Sequence 343639,
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275	25	78.1	114	4	US-10-205-841-8	Sequence 8, Appl1	348	25	78.1	257	4	US-10-767-701-38484	Sequence 38484, A
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279	25	78.1	125	4	US-10-437-963-160561	Sequence 160561,	352	25	78.1	267	4	US-10-425-115-279765	Sequence 279765,
280	25	78.1	126	4	US-10-767-701-36256	Sequence 36256, A	353	25	78.1	272	4	US-09-764-875-650	Sequence 650, App
281	25	78.1	126	4	US-10-424-599-255422	Sequence 255422,	354	25	78.1	272	4	US-10-425-115-229330	Sequence 229330,
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283	25	78.1	134	4	US-10-437-963-186499	Sequence 186499,	356	25	78.1	278	4	US-10-369-493-9985	Sequence 9985, App
284	25	78.1	135	4	US-10-264-237-1535	Sequence 1535, Ap	357	25	78.1	283	4	US-10-282-122A-48488	Sequence 48488, A
285	25	78.1	137	4	US-10-104-047-3241	Sequence 3241, Ap	358	25	78.1	287	4	US-10-369-430A-28	Sequence 28, Appl1
286	25	78.1	138	4	US-10-425-115-213281	Sequence 213281,	359	25	78.1	293	4	US-10-156-761-12937	Sequence 12937, A
287	25	78.1	140	4	US-10-264-237-2348	Sequence 2348, Ap	360	25	78.1	293	4	US-10-335-977-8665	Sequence 8665, App
288	25	78.1	140	4	US-10-842-740-27	Sequence 27, Appl1	361	25	78.1	296	4	US-10-296-115-750	Sequence 750, App
289	25	78.1	145	4	US-10-767-701-59415	Sequence 59415, A	362	25	78.1	303	4	US-10-425-115-69442	Sequence 69442, A
290	25	78.1	147	3	US-09-738-973-99	Sequence 99, Appl1	363	25	78.1	303	4	US-10-425-115-332789	Sequence 332789,
291	25	78.1	147	3	US-09-854-133-99	Sequence 99, Appl1	364	25	78.1	305	4	US-10-767-701-40762	Sequence 40762, A
292	25	78.1	147	4	US-10-144-649A-99	Sequence 99, Appl1	365	25	78.1	306	4	US-10-425-115-232513	Sequence 232513,
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294	25	78.1	152	4	US-10-291-172-650	Sequence 650, App	367	25	78.1	306	4	US-10-425-115-232516	Sequence 232516,
295	25	78.1	152	4	US-10-221-278-650	Sequence 650, App	368	25	78.1	308	5	US-10-508-309-36	Sequence 36, Appl1
296	25	78.1	154	4	US-10-425-115-217875	Sequence 217875,	369	25	78.1	311	4	US-10-437-963-185160	Sequence 185160,
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300	25	78.1	158	5	US-10-732-923-21762	Sequence 21762, A	373	25	78.1	315	3	US-09-904-615-124	Sequence 124, App
301	25	78.1	159	3	US-09-738-973-98	Sequence 98, Appl1	374	25	78.1	319	4	US-10-054-988-181	Sequence 181, App
302	25	78.1	159	3	US-09-854-133-98	Sequence 98, Appl1	375	25	78.1	319	4	US-10-425-114-64132	Sequence 64132, A
303	25	78.1	159	4	US-10-144-649A-98	Sequence 98, Appl1	376	25	78.1	322	4	US-10-425-115-65639	Sequence 65639, A
304	25	78.1	160	4	US-10-440-516-42	Sequence 42, Appl1	377	25	78.1	324	5	US-10-732-923-8046	Sequence 8046, App
305	25	78.1	160	4	US-10-106-698-4314	Sequence 4314, Ap	378	25	78.1	324	5	US-10-450-763-45436	Sequence 45436, A
306	25	78.1	162	5	US-10-424-599-159033	Sequence 159033,	379	25	78.1	325	5	US-10-425-115-254562	Sequence 254562,
307	25	78.1	162	5	US-10-450-763-58181	Sequence 58181, A	380	25	78.1	325	5	US-10-732-923-7715	Sequence 7715, App
308	25	78.1	163	4	US-10-437-963-150271	Sequence 150271,	381	25	78.1	326	4	US-10-437-963-120005	Sequence 120005,
309	25	78.1	165	4	US-10-424-599-213411	Sequence 213411,	382	25	78.1	331	5	US-10-450-763-339982	Sequence 339982,
310	25	78.1	165	4	US-10-437-963-167347	Sequence 167347,	383	25	78.1	336	4	US-10-282-122A-77794	Sequence 77794, A
311	25	78.1	172	5	US-10-450-763-58400	Sequence 58400, A	384	25	78.1	336	4	US-10-425-115-319947	Sequence 319947,
312	25	78.1	176	4	US-10-767-701-52638	Sequence 52638, A	385	25	78.1	338	4	US-10-424-599-162486	Sequence 162486,
313	25	78.1	181	5	US-10-732-923-12409	Sequence 12409, A	386	25	78.1	340	4	US-10-425-115-325880	Sequence 325880,
314	25	78.1	181	5	US-10-732-923-12412	Sequence 12412, A	387	25	78.1	340	5	US-10-282-122A-671195	Sequence 671195, A
315	25	78.1	183	4	US-10-767-701-33267	Sequence 33267, A	388	25	78.1	343	4	US-10-500-550-12	Sequence 12, Appl1
316	25	78.1	185	4	US-10-424-599-153319	Sequence 153319,	389	25	78.1	343	4	US-10-335-977-7208	Sequence 7208, App
317	25	78.1	186	5	US-10-722-045-50	Sequence 50, Appl1	390	25	78.1	346	4	US-10-425-115-305861	Sequence 305861,
318	25	78.1	187	4	US-10-437-963-140913	Sequence 140913,	391	25	78.1	346	4	US-10-335-977-7209	Sequence 7209, App
319	25	78.1	187	4	US-10-425-115-326956	Sequence 326956,	392	25	78.1	349	4	US-10-238-075-596	Sequence 596, App

393	25	78.1	350	3	US-09-789-996-23	Sequence 23, Appl	466	25	78.1	519	4	US-10-140-470-210	Sequence 210, App
394	25	78.1	350	3	US-09-952-680A-24	Sequence 24, Appl	467	25	78.1	519	4	US-10-175-746-210	Sequence 210, App
395	25	78.1	350	4	US-10-352-843-15	Sequence 15, Appl	468	25	78.1	519	4	US-10-176-918-210	Sequence 210, App
396	25	78.1	350	4	US-10-380-393B-11	Sequence 1, Appl1	469	25	78.1	519	4	US-10-176-921-210	Sequence 210, App
397	25	78.1	350	4	US-10-059-266B-8	Sequence 8, Appl1	470	25	78.1	519	4	US-10-137-865-210	Sequence 210, App
398	25	78.1	350	4	US-10-408-765A-428	Sequence 428, Appl	471	25	78.1	519	4	US-10-140-477-210	Sequence 210, App
399	25	78.1	350	5	US-10-215-982-24	Sequence 24, Appl1	472	25	78.1	519	4	US-10-142-431-210	Sequence 210, App
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403	25	78.1	350	5	US-10-732-923-7978	Sequence 7978, Ap	476	25	78.1	519	4	US-10-142-423-210	Sequence 210, App
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406	25	78.1	350	5	US-10-732-923-8034	Sequence 8044, Ap	479	25	78.1	519	4	US-10-143-031-210	Sequence 210, App
407	25	78.1	354	3	US-09-789-996-24	Sequence 24, Appl	480	25	78.1	519	4	US-10-123-108-210	Sequence 210, App
408	25	78.1	358	4	US-10-128-714-3466	Sequence 3466, Ap	481	25	78.1	519	4	US-10-123-261-210	Sequence 210, App
409	25	78.1	358	4	US-10-128-714-8466	Sequence 8466, Ap	482	25	78.1	519	4	US-10-140-922-210	Sequence 210, App
410	25	78.1	358	5	US-10-732-923-7693	Sequence 7693, Ap	483	25	78.1	519	4	US-10-140-928-210	Sequence 210, App
411	25	78.1	359	4	US-10-369-493-2254	Sequence 2254, A	484	25	78.1	519	4	US-10-121-043-210	Sequence 210, App
412	25	78.1	359	4	US-10-451-467A-240	Sequence 240, App	485	25	78.1	519	4	US-10-123-293-210	Sequence 210, App
413	25	78.1	359	5	US-10-987-548-1	Sequence 1, Appl1	486	25	78.1	519	4	US-10-123-903-210	Sequence 210, App
414	25	78.1	364	4	US-10-424-599-221340	Sequence 221340,	487	25	78.1	519	4	US-10-124-819-210	Sequence 210, App
415	25	78.1	370	4	US-10-282-122A-73291	Sequence 73291, A	488	25	78.1	519	4	US-10-124-822-210	Sequence 210, App
416	25	78.1	374	3	US-09-934-455-304	Sequence 304, App	489	25	78.1	519	4	US-10-140-928-210	Sequence 210, App
417	25	78.1	374	4	US-10-286-264-112	Sequence 112, App	490	25	78.1	519	4	US-10-140-928-210	Sequence 210, App
418	25	78.1	374	4	US-10-225-066A-736	Sequence 726, App	491	25	78.1	519	4	US-10-160-498-210	Sequence 210, App
419	25	78.1	374	4	US-10-374-780A-2396	Sequence 2396, Ap	492	25	78.1	519	4	US-10-124-824-210	Sequence 210, App
420	25	78.1	374	4	US-10-412-699B-448	Sequence 448, App	493	25	78.1	519	4	US-10-127-822A-210	Sequence 210, App
421	25	78.1	374	5	US-10-225-066A-726	Sequence 726, App	494	25	78.1	519	4	US-10-127-829A-210	Sequence 210, App
422	25	78.1	378	5	US-10-450-763-43869	Sequence 43869, A	495	25	78.1	519	4	US-10-127-833A-210	Sequence 210, App
423	25	78.1	383	4	US-10-437-963-135749	Sequence 135749,	496	25	78.1	519	4	US-10-127-833A-210	Sequence 210, App
424	25	78.1	383	4	US-10-425-115-325879	Sequence 325879,	497	25	78.1	519	4	US-10-127-901A-210	Sequence 210, App
425	25	78.1	383	4	US-10-425-115-354839	Sequence 354839,	498	25	78.1	519	4	US-10-128-699A-210	Sequence 210, App
426	25	78.1	385	5	US-10-858-367-15	Sequence 15, Appl	499	25	78.1	519	4	US-10-131-813A-210	Sequence 210, App
427	25	78.1	386	4	US-10-424-599-193060	Sequence 193060,	500	25	78.1	519	4	US-10-131-818A-210	Sequence 210, App
428	25	78.1	390	6	US-11-097-143-9888	Sequence 9888, Ap	501	25	78.1	519	4	US-10-131-822A-210	Sequence 210, App
429	25	78.1	396	4	US-10-424-599-214347	Sequence 214347,	502	25	78.1	519	4	US-10-131-828A-210	Sequence 210, App
430	25	78.1	398	4	US-10-425-114-55191	Sequence 55191, A	503	25	78.1	519	4	US-10-131-830A-210	Sequence 210, App
431	25	78.1	400	5	US-10-741-600-877	Sequence 877, App	504	25	78.1	519	4	US-10-131-833A-210	Sequence 210, App
432	25	78.1	401	5	US-10-367-057-22	Sequence 22, Appl	505	25	78.1	519	4	US-10-137-872A-210	Sequence 210, App
433	25	78.1	403	3	US-09-924-256A-27	Sequence 27, Appl1	506	25	78.1	519	4	US-10-147-500-210	Sequence 210, App
434	25	78.1	404	4	US-10-425-114-37714	Sequence 37714, A	507	25	78.1	519	4	US-10-147-502-210	Sequence 210, App
435	25	78.1	406	5	US-10-739-930-8259	Sequence 8259, Ap	508	25	78.1	519	4	US-10-147-515-210	Sequence 210, App
436	25	78.1	407	4	US-10-437-963-150403	Sequence 150403,	509	25	78.1	519	4	US-10-147-511-210	Sequence 210, App
437	25	78.1	423	4	US-10-767-701-44089	Sequence 44089, A	510	25	78.1	519	4	US-10-147-526-210	Sequence 210, App
438	25	78.1	425	5	US-10-739-930-10126	Sequence 10126, A	511	25	78.1	519	4	US-10-147-527-210	Sequence 210, App
439	25	78.1	431	4	US-10-437-963-183261	Sequence 183261,	512	25	78.1	519	4	US-10-121-041-210	Sequence 210, App
440	25	78.1	435	4	US-10-282-122A-47662	Sequence 47662, A	513	25	78.1	519	4	US-10-121-043-210	Sequence 210, App
441	25	78.1	444	4	US-10-270-333-132	Sequence 132, App	514	25	78.1	519	4	US-10-121-047-210	Sequence 210, App
442	25	78.1	444	6	US-11-097-143-25158	Sequence 25158, A	515	25	78.1	519	4	US-10-123-215-210	Sequence 210, App
443	25	78.1	448	4	US-10-425-115-263779	Sequence 263779,	516	25	78.1	519	4	US-10-123-902-210	Sequence 210, App
444	25	78.1	458	4	US-10-369-493-10042	Sequence 10042, A	517	25	78.1	519	4	US-10-123-908-210	Sequence 210, App
445	25	78.1	461	5	US-10-617-320-4028	Sequence 4028, Ap	518	25	78.1	519	4	US-10-123-909-210	Sequence 210, App
446	25	78.1	462	4	US-10-425-114-68617	Sequence 68617, A	519	25	78.1	519	4	US-10-123-910-210	Sequence 210, App
447	25	78.1	464	5	US-10-858-367-7	Sequence 7, Appl1	520	25	78.1	519	4	US-10-124-813-210	Sequence 210, App
448	25	78.1	474	4	US-10-282-122A-68950	Sequence 68950, A	521	25	78.1	519	4	US-10-124-813-210	Sequence 210, App
449	25	78.1	476	4	US-10-058-820-4	Sequence 4, Appl1	522	25	78.1	519	4	US-10-125-922-210	Sequence 210, App
450	25	78.1	477	3	US-09-994-288-2	Sequence 2, Appl1	523	25	78.1	519	4	US-10-125-924-210	Sequence 210, App
451	25	78.1	477	5	US-10-450-763-43695	Sequence 43695, A	524	25	78.1	519	4	US-10-140-860-210	Sequence 210, App
452	25	78.1	483	4	US-10-156-761-8763	Sequence 8763, Ap	525	25	78.1	519	4	US-10-142-417-210	Sequence 210, App
453	25	78.1	483	4	US-10-369-493-16123	Sequence 16123, A	526	25	78.1	519	4	US-10-147-519-210	Sequence 210, App
454	25	78.1	483	5	US-10-972-024-559	Sequence 559, App	527	25	78.1	519	4	US-10-157-782-210	Sequence 210, App
455	25	78.1	500	3	US-09-861-038-2	Sequence 2, Appl1	528	25	78.1	519	4	US-10-152-395-210	Sequence 210, App
456	25	78.1	503	4	US-10-282-122A-67299	Sequence 67299, A	529	25	78.1	519	4	US-10-125-926A-210	Sequence 210, App
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460	25	78.1	517	4	US-10-092-900A-1332	Sequence 1332, App	533	25	78.1	519	4	US-10-127-838B-210	Sequence 210, App
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463	25	78.1	519	4	US-10-140-808-210	Sequence 210, App	536	25	78.1	519	4	US-10-127-845A-210	Sequence 210, App
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465	25	78.1	519	4	US-10-123-904-210	Sequence 210, App	538	25	78.1	519	4	US-10-127-848A-210	Sequence 210, App

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686	25	78.1	519	4	US-10-145-755-210	Sequence 210, App	759	25	78.1	519	4	US-10-152-373-210	Sequence 210, App
687	25	78.1	519	4	US-10-145-818-210	Sequence 210, App	760	25	78.1	519	4	US-10-121-044-210	Sequence 210, App
688	25	78.1	519	4	US-10-145-820-210	Sequence 210, App	761	25	78.1	519	4	US-10-121-055-210	Sequence 210, App
689	25	78.1	519	4	US-10-145-872-210	Sequence 210, App	762	25	78.1	519	4	US-10-121-057-210	Sequence 210, App
690	25	78.1	519	4	US-10-145-873-210	Sequence 210, App	763	25	78.1	519	4	US-10-121-058-210	Sequence 210, App
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692	25	78.1	519	4	US-10-147-482-210	Sequence 210, App	765	25	78.1	519	4	US-10-121-060-210	Sequence 210, App
693	25	78.1	519	4	US-10-147-503-210	Sequence 210, App	766	25	78.1	519	4	US-10-123-109-210	Sequence 210, App
694	25	78.1	519	4	US-10-147-503-210	Sequence 210, App	767	25	78.1	519	4	US-10-123-154-210	Sequence 210, App
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696	25	78.1	519	4	US-10-152-401-210	Sequence 210, App	769	25	78.1	519	4	US-10-123-906-210	Sequence 210, App
697	25	78.1	519	4	US-10-157-783-210	Sequence 210, App	770	25	78.1	519	4	US-10-124-814-210	Sequence 210, App
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699	25	78.1	519	4	US-10-158-462-210	Sequence 210, App	772	25	78.1	519	4	US-10-124-820-210	Sequence 210, App
700	25	78.1	519	4	US-10-143-035-210	Sequence 210, App	773	25	78.1	519	4	US-10-125-704-210	Sequence 210, App
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703	25	78.1	519	4	US-10-145-824-210	Sequence 210, App	776	25	78.1	519	4	US-10-145-889-210	Sequence 210, App
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706	25	78.1	519	4	US-10-145-875-210	Sequence 210, App	779	25	78.1	519	4	US-10-152-371-210	Sequence 210, App
707	25	78.1	519	4	US-10-145-877-210	Sequence 210, App	780	25	78.1	519	4	US-10-152-374-210	Sequence 210, App
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709	25	78.1	519	4	US-10-146-787-210	Sequence 210, App	782	25	78.1	519	4	US-10-152-377-210	Sequence 210, App
710	25	78.1	519	4	US-10-146-790-210	Sequence 210, App	783	25	78.1	519	4	US-10-152-385-210	Sequence 210, App
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713	25	78.1	519	4	US-10-147-485-210	Sequence 210, App	786	25	78.1	519	4	US-10-157-785-210	Sequence 210, App
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715	25	78.1	519	4	US-10-147-487-210	Sequence 210, App	788	25	78.1	519	4	US-10-157-796-210	Sequence 210, App
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718	25	78.1	519	4	US-10-147-498-210	Sequence 210, App	791	25	78.1	519	4	US-10-123-156-210	Sequence 210, App
719	25	78.1	519	4	US-10-147-514-210	Sequence 210, App	792	25	78.1	519	4	US-10-123-214-210	Sequence 210, App
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722	25	78.1	519	4	US-10-152-384-210	Sequence 210, App	795	25	78.1	519	4	US-10-152-385-210	Sequence 210, App
723	25	78.1	519	4	US-10-152-406-210	Sequence 210, App	796	25	78.1	519	4	US-10-152-393-210	Sequence 210, App
724	25	78.1	519	4	US-10-156-847-210	Sequence 210, App	797	25	78.1	519	4	US-10-153-396-210	Sequence 210, App
725	25	78.1	519	4	US-10-157-778-210	Sequence 210, App	798	25	78.1	519	4	US-10-153-552-210	Sequence 210, App
726	25	78.1	519	4	US-10-157-799-210	Sequence 210, App	799	25	78.1	519	4	US-10-153-840-210	Sequence 210, App
727	25	78.1	519	4	US-10-160-504-210	Sequence 210, App	800	25	78.1	519	4	US-10-156-841-210	Sequence 210, App
728	25	78.1	519	4	US-10-145-634-210	Sequence 210, App	801	25	78.1	519	4	US-10-156-842-210	Sequence 210, App
729	25	78.1	519	4	US-10-147-520-210	Sequence 210, App	802	25	78.1	519	4	US-10-156-844-210	Sequence 210, App
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732	25	78.1	519	4	US-10-147-431-210	Sequence 210, App	805	25	78.1	519	4	US-10-121-052-210	Sequence 210, App
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735	25	78.1	519	4	US-10-152-383-210	Sequence 210, App	808	25	78.1	519	4	US-10-121-055-210	Sequence 210, App
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737	25	78.1	519	4	US-10-152-387-210	Sequence 210, App	810	25	78.1	519	4	US-10-123-212-210	Sequence 210, App
738	25	78.1	519	4	US-10-152-389-210	Sequence 210, App	811	25	78.1	519	4	US-10-123-213-210	Sequence 210, App
739	25	78.1	519	4	US-10-152-390-210	Sequence 210, App	812	25	78.1	519	4	US-10-123-291-210	Sequence 210, App
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741	25	78.1	519	4	US-10-153-756-210	Sequence 210, App	814	25	78.1	519	4	US-10-123-771-210	Sequence 210, App
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743	25	78.1	519	4	US-10-157-797-210	Sequence 210, App	816	25	78.1	519	4	US-10-123-911-210	Sequence 210, App
744	25	78.1	519	4	US-10-158-491-210	Sequence 210, App	817	25	78.1	519	4	US-10-124-823-210	Sequence 210, App
745	25	78.1	519	4	US-10-142-762-210	Sequence 210, App	818	25	78.1	519	4	US-10-125-931-210	Sequence 210, App
746	25	78.1	519	4	US-10-142-764-210	Sequence 210, App	819	25	78.1	519	4	US-10-125-932-210	Sequence 210, App
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750	25	78.1	519	4	US-10-145-962-210	Sequence 210, App	823	25	78.1	519	4	US-10-131-820A-210	Sequence 210, App
751	25	78.1	519	4	US-10-146-789-210	Sequence 210, App	824	25	78.1	519	4	US-10-142-886-210	Sequence 210, App
752	25	78.1	519	4	US-10-146-789-210	Sequence 210, App	825	25	78.1	519	4	US-10-146-786-210	Sequence 210, App
753	25	78.1	519	4	US-10-147-483-210	Sequence 210, App	826	25	78.1	519	4	US-10-146-786-210	Sequence 210, App
754	25	78.1	519	4	US-10-147-496-210	Sequence 210, App	827	25	78.1	519	4	US-10-147-499-210	Sequence 210, App
755	25	78.1	519	4	US-10-147-505-210	Sequence 210, App	828	25	78.1	519	4	US-10-157-798-210	Sequence 210, App
756	25	78.1	519	4	US-10-147-516-210	Sequence 210, App	829	25	78.1	519	4	US-10-123-913-210	Sequence 210, App
757	25	78.1	519	4	US-10-152-398-210	Sequence 210, App	830	25	78.1	519	4	US-10-140-473-210	Sequence 210, App
758	25	78.1	519	4	US-10-133-980-210	Sequence 210, App	831	25	78.1	519	4	US-10-140-806-210	Sequence 210, App

831	25	78.1	519	4	US-10-140-810-210	Sequence 210, App	904	25	78.1	519	5	US-10-145-961-210	Sequence 210, App
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833	25	78.1	519	4	US-10-141-699-210	Sequence 210, App	906	25	78.1	519	5	US-10-147-531-210	Sequence 210, App
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835	25	78.1	519	4	US-10-141-706-210	Sequence 210, App	908	25	78.1	519	5	US-10-158-788-210	Sequence 210, App
836	25	78.1	519	4	US-10-141-757-210	Sequence 210, App	909	25	78.1	519	5	US-10-955-952-210	Sequence 210, App
837	25	78.1	519	4	US-10-141-762-210	Sequence 210, App	910	25	78.1	519	6	US-11-005-609-133	Sequence 133, App
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839	25	78.1	519	4	US-10-142-429-210	Sequence 210, App	912	25	78.1	519	5	US-10-626-832-48	Sequence 48, App1
840	25	78.1	519	4	US-10-142-684-210	Sequence 210, App	913	25	78.1	519	4	US-09-801-368-124	Sequence 124, App
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842	25	78.1	519	4	US-10-143-115-210	Sequence 210, App	915	25	78.1	519	3	US-09-927-827-57	Sequence 328875, App1
843	25	78.1	519	4	US-10-143-956-210	Sequence 210, App	916	25	78.1	519	4	US-10-425-115-325875	Sequence 11387, A
844	25	78.1	519	4	US-10-144-958-210	Sequence 210, App	917	25	78.1	519	4	US-10-156-761-11187	Sequence 712, App
845	25	78.1	519	4	US-10-145-632-210	Sequence 210, App	918	25	78.1	519	4	US-10-112-944-712	Sequence 40380, A
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847	25	78.1	519	4	US-10-145-749-210	Sequence 210, App	920	25	78.1	519	4	US-10-369-493-10236	Sequence 10236, A
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849	25	78.1	519	4	US-10-145-871-210	Sequence 210, App	922	25	78.1	519	4	US-10-072-012-716	Sequence 716, App
850	25	78.1	519	4	US-10-146-794-210	Sequence 210, App	923	25	78.1	519	4	US-10-389-566-2342	Sequence 2322, App
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855	25	78.1	519	4	US-10-152-376-210	Sequence 210, App	928	25	78.1	519	5	US-10-450-763-56116	Sequence 14, App1
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858	25	78.1	519	4	US-10-153-585-210	Sequence 210, App	931	25	78.1	519	4	US-10-659-549-15	Sequence 15, App1
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863	25	78.1	519	4	US-10-158-784-210	Sequence 210, App	936	25	78.1	519	2	US-09-902-941-1809	Sequence 1809, App
864	25	78.1	519	4	US-10-158-789-210	Sequence 210, App	937	25	78.1	519	3	US-09-849-626-1809	Sequence 1809, App
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872	25	78.1	519	4	US-10-141-754-210	Sequence 210, App	945	25	78.1	519	2	US-10-283-017-1809	Sequence 1809, App
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874	25	78.1	519	4	US-10-142-425-210	Sequence 210, App	947	25	78.1	519	2	US-10-775-972-169	Sequence 169, App
875	25	78.1	519	4	US-10-143-113-210	Sequence 210, App	948	25	78.1	519	2	US-10-852-335A-178	Sequence 178, App
876	25	78.1	519	4	US-10-146-730-210	Sequence 210, App	949	25	78.1	519	2	US-10-922-124-169	Sequence 169, App
877	25	78.1	519	4	US-10-146-792-210	Sequence 210, App	950	25	78.1	519	2	US-10-450-763-45226	Sequence 45226, A
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879	25	78.1	519	4	US-10-158-791-210	Sequence 210, App	952	25	78.1	519	3	US-09-847-102A-37	Sequence 37, App1
880	25	78.1	519	4	US-10-156-843-210	Sequence 210, App	953	25	78.1	519	3	US-10-858-167-13	Sequence 13, App1
881	25	78.1	519	4	US-10-157-786-210	Sequence 210, App	954	25	78.1	519	5	US-10-450-763-35650	Sequence 35650, A
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883	25	78.1	519	4	US-10-147-528-210	Sequence 210, App	956	25	78.1	519	5	US-09-800-065-2	Sequence 2, App1
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887	25	78.1	519	4	US-10-145-127-210	Sequence 210, App	960	25	78.1	519	4	US-10-450-763-60494	Sequence 60494, A
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889	25	78.1	519	4	US-10-143-118-210	Sequence 210, App	962	25	78.1	519	4	US-10-144-649A-738	Sequence 738, App
890	25	78.1	519	4	US-10-144-993-210	Sequence 210, App	963	25	78.1	519	4	US-10-483-506-18	Sequence 6, App1
891	25	78.1	519	4	US-10-158-787-210	Sequence 210, App	964	25	78.1	519	3	US-10-467-434-6	Sequence 2483, App
892	25	78.1	519	4	US-10-092-900A-130	Sequence 210, App	965	25	78.1	519	4	US-10-425-115-343632	Sequence 18658, A
893	25	78.1	519	4	US-10-142-426-210	Sequence 210, App	966	25	78.1	519	4	US-10-732-923-18659	Sequence 65028, A
894	25	78.1	519	4	US-10-140-024-210	Sequence 210, App	967	25	78.1	519	4	US-10-094-749-3124	Sequence 3124, App
895	25	78.1	519	4	US-10-147-536-210	Sequence 210, App	968	25	78.1	519	4	US-10-450-763-52885	Sequence 52885, A
896	25	78.1	519	4	US-10-152-372-210	Sequence 210, App	969	25	78.1	519	4	US-10-144-649A-739	Sequence 739, App
897	25	78.1	519	4	US-10-475-446-16	Sequence 16, App1	970	25	78.1	519	4	US-10-437-963-190596	Sequence 190596, App
898	25	78.1	519	4	US-10-125-795-210	Sequence 210, App	971	25	78.1	519	4	US-10-437-963-190596	Sequence 39644, A
899	25	78.1	519	4	US-10-145-626-210	Sequence 210, App	972	25	78.1	519	4	US-10-437-963-190596	Sequence 39644, A
900	25	78.1	519	4	US-10-145-819-210	Sequence 210, App	973	25	78.1	519	4	US-10-437-963-190596	Sequence 39644, A
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978 25 78.1 675 4 US-10-779-949-48 Sequence 48, Appl
979 25 78.1 682 4 US-10-152-548-16 Sequence 16, Appl
980 25 78.1 685 3 US-09-847-102A-57 Sequence 57, Appl
981 25 78.1 685 4 US-10-146-474-14 Sequence 14, Appl
982 25 78.1 685 4 US-10-301-764-14 Sequence 14, Appl
983 25 78.1 685 4 US-10-882-586A-9 Sequence 9, Appl1
984 25 78.1 694 3 US-09-847-102A-56 Sequence 2, Appl1
985 25 78.1 694 4 US-10-152-548-2 Sequence 144, App
986 25 78.1 694 4 US-10-205-823-144 Sequence 53, Appl
987 25 78.1 694 4 US-10-285-976-53 Sequence 1344, Ap
988 25 78.1 694 4 US-10-295-027-1344 Sequence 6, Appl1
989 25 78.1 694 4 US-10-311-623-6 Sequence 250, App
990 25 78.1 694 4 US-10-112-944-250 Sequence 106, App
991 25 78.1 694 5 US-10-882-586A-7 Sequence 7, Appl1
992 25 78.1 694 5 US-10-882-586A-7 Sequence 7, Appl1
993 25 78.1 694 6 US-11-051-454-144 Sequence 144, App
994 25 78.1 694 6 US-11-097-143-42183 Sequence 42183, A
995 25 78.1 697 4 US-10-437-963-157210 Sequence 157210,
996 25 78.1 698 5 US-10-450-763-54978 Sequence 54978, A
997 25 78.1 716 4 US-10-437-963-140947 Sequence 140947,
998 25 78.1 723 4 US-10-257-022-4 Sequence 4, Appl1
999 25 78.1 726 4 US-10-369-493-16817 Sequence 16817, A
1000 25 78.1 731 4 US-10-282-122A-60220 Sequence 60220, A

ALIGNMENTS

RESULT 1
US-09-795-798-14
; Sequence 14, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-795-798-14
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGTLOS 7
Db 1 SGGTLOS 7

RESULT 2
US-10-727-737-55
; Sequence 35, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-727-737-55
Query Match 100.0%; Score 32; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGTLOS 7
Db 1 SGGTLOS 7
RESULT 3
US-10-425-115-214302
; Sequence 214302, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 214302
LENGTH: 100
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1).(100)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_127041C.1.pep
US-10-425-115-214302

Query Match 100.0%; Score 32; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 31 SGGSTLOS 37

RESULT 4
US-10-010-729-23
Sequence 23, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: System
FILE REFERENCE: 1199-1-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/332,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 101
TYPE: PRT
ORGANISM: Mus musculus
US-10-010-729-23

Query Match 100.0%; Score 32; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 50 SGGSTLOS 56

RESULT 5
US-11-003-819-10
Sequence 10, Application US/11003819
Publication No. US20050158323A1
GENERAL INFORMATION:

APPLICANT: Evans, Elizabeth E.
APPLICANT: Paris, Mark J.
APPLICANT: Sahasrabudhe, Deepak M.
APPLICANT: Zauderer, Maurice
APPLICANT: Smith, Ernest S.
TITLE OF INVENTION: Methods of Killing Tumor Cells by Targeting Internal Antigens
TITLE OF INVENTION: Exposed on Apoptotic Tumor Cells
FILE REFERENCE: 1843.0190002
CURRENT APPLICATION NUMBER: US/11/003,819
CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: US 60/256,572
PRIOR FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US 60/531,688
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
LENGTH: 107
TYPE: PRT
ORGANISM: Mus sp.
US-11-003-819-10

Query Match 100.0%; Score 32; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 50 SGGSTLOS 56

RESULT 6
US-09-795-798-1
Sequence 1, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-795-798-1

Query Match 100.0%; Score 32; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||
Db 50 SGSTLOS 56

RESULT 7
US-09-795-798-2
; Sequence 2, Application US/09795798
; Publication No. US20030207336A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-795-798-2

Query Match 100.0%; Score 32; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||
Db 50 SGSTLOS 56

RESULT 8
US-10-010-729-43
; Sequence 43, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human 10M Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System

FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-43

Query Match 100.0%; Score 32; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||||
Db 50 SGSTLOS 56

RESULT 9
US-10-727-737-1
; Sequence 1, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid

```

;
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-727-737-1
Query Match      100.0%; Score 32; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLOS 7
        |||||
        50 SGGSTLOS 56

RESULT 10
US-10-727-737-2
; Sequence 2, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardiou, Paula M.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpacin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-727-737-2
Query Match      100.0%; Score 32; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLOS 7
        |||||
        50 SGGSTLOS 56

RESULT 11
US-10-877-532-5
; Sequence 5, Application US/10877532
; Publication No. US20050038231A1
; GENERAL INFORMATION:
; APPLICANT: FAHRNER, ROBERT L.
; APPLICANT: LAVEDIERE, AMY
; APPLICANT: McDONALD, PAUL J.
; APPLICANT: O'LEARY, RHONA M.
; TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAPHY
; FILE REFERENCE: P2015R1
; CURRENT APPLICATION NUMBER: US/10/877,532
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: US 60/490,500
; PRIOR FILING DATE: 2003-07-28
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 5
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-10-877-532-5
Query Match      100.0%; Score 32; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLOS 7
        |||||
        50 SGGSTLOS 56

RESULT 12
US-10-423-299-3
; Sequence 3, Application US/10423299
; Publication No. US20030229212A1
; GENERAL INFORMATION:
; APPLICANT: FAHRNER, ROBERT
; APPLICANT: FOLTMAN, DEBORAH
; APPLICANT: LEBRETTON, BENEDICTE
; APPLICANT: VAN REIS, ROBERT
; TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
; FILE REFERENCE: 39766-0121A
; CURRENT APPLICATION NUMBER: US/10/423,299
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/375,953
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-423-299-3
Query Match      100.0%; Score 32; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLOS 7
        |||||
        50 SGGSTLOS 56

RESULT 13
US-10-424-599-249629
; Sequence 249629, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
```

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 249629
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(242)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_67444C.1.pep
US-10-424-599-249629

Query Match          93.8%; Score 30; DB 4; Length 242;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGSTLOS 7
Db      101  SGSTLOS 107

RESULT 14
US-10-727-737-57
; Sequence 57, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-727-737-57

Query Match          90.6%; Score 29; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGSTLOS 7
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Db      1  AGSTLOS 7

RESULT 15
US-10-727-737-58
; Sequence 58, Application US/10727737
; Publication No. US20040146507A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Mutants
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/727,737
; FILING DATE: 03-Dec-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,329B
; FILING DATE: 20-Nov-1997
; APPLICATION NUMBER: 60/031945
; FILING DATE: 27-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1064R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-727-737-58

Query Match          90.6%; Score 29; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGSTLOS 7
Db      1  SCASTLOS 7

RESULT 16
US-10-425-115-212123
; Sequence 59, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
```

SEQ ID NO 212123
LENGTH: 48
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_125059C.1.pep
US-10-425-115-212123

Query Match 90.6%; Score 29; DB 4; Length 48;
Best Local Similarity 85.7%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTLOS 7
|:|:|:|:
Db 34 SGGTLOS 40

RESULT 17
US-09-726-258-47
Sequence 47, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumets, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-09-726-258-47

Query Match 90.6%; Score 29; DB 3; Length 109;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGGSTLOS 7
|:|:|:|:

Db 51 SGGSTLES 57

RESULT 18
US-10-282-122A-66553
Sequence 66553, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: BLITRA 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66553
LENGTH: 347
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-66553

Query Match 90.6%; Score 29; DB 4; Length 347;
Best Local Similarity 85.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTLOS 7
|:|:|:|:
Db 95 SGGSTLOS 101

RESULT 19
US-11-097-143-16788
Sequence 16788, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
US-11-097-143-16788

```

; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 4308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16788
; LENGTH: 428
; TYPE: PRT
; ORGANISM: DROSOPHILA
; US-11-097-143-16788

Query Match      90.6%; Score 29; DB 6; Length 428;
Best Local Similarity 85.7%; Pred. No. 6.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLOS 7
Db      420 SGGSTLOS 426

RESULT 20
; US-09-864-761-43276
; Sequence 43276, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
```

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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43276
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL121716.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EST HUMAN HIT: AA603882.1 EVALU 3.00e-71
; OTHER INFORMATION: SWISSPROT HIT: Q9Y3R5, EVALU 1.00e-64
; US-09-864-761-43276

Query Match      90.6%; Score 29; DB 3; Length 665;
Best Local Similarity 85.7%; Pred. No. 9.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLOS 7
Db      533 SGGSTLOS 539

RESULT 21
; US-10-205-342-25
; Sequence 25, Application US/10205342
; Publication No. US20030108906A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alister
; APPLICANT: Brooksbank, Robert
; APPLICANT: Plimock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: Wt-A-018198
; CURRENT APPLICATION NUMBER: US/10/205,342
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354,0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 1377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Protein HMGI/2
; US-10-205-342-25

Query Match      90.6%; Score 29; DB 4; Length 1377;
Best Local Similarity 85.7%; Pred. No. 2.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLOS 7
Db      486 SGGSTLOS 492

RESULT 22
; US-10-450-763-39403
; Sequence 39403, Application US/10450763
; Publication No. US20050196754A1
```



```

; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39403
; LENGTH: 1387
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(1387)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-39403

Query Match          90.6%; Score 29; DB 5; Length 1387;
Best Local Similarity 85.7%; Pred. No. 2,1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQS 7
   :|||||
Db 486 NGSSTLQS 492

RESULT 23
US-10-450-763-39401
; Sequence 39401, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39401
; LENGTH: 2228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-39401

Query Match          90.6%; Score 29; DB 5; Length 2228;
Best Local Similarity 85.7%; Pred. No. 3,5e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

; APPLICANT: Weiner, David B.
; APPLICANT: Cohen, Jeffrey A.
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Williams, Robert M.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND US
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 4040/114920S2
; CURRENT APPLICATION NUMBER: US/10/105,545
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 08/752,816
; PRIOR FILING DATE: 1996-11-21
; PRIOR APPLICATION NUMBER: US 07/940,654
; PRIOR FILING DATE: 1992-09-03
; PRIOR APPLICATION NUMBER: US 07/702,833
; PRIOR FILING DATE: 1991-05-20
; PRIOR APPLICATION NUMBER: US 07/326,328
; PRIOR FILING DATE: 1989-03-21
; PRIOR APPLICATION NUMBER: US 07/074,264
; PRIOR FILING DATE: 1987-07-16
; PRIOR APPLICATION NUMBER: US 07/462,542
; PRIOR FILING DATE: 1990-01-09
; PRIOR APPLICATION NUMBER: US 07/648,303
; PRIOR FILING DATE: 1991-01-25
; PRIOR APPLICATION NUMBER: US 07/685,881
; PRIOR FILING DATE: 1991-04-15
; PRIOR APPLICATION NUMBER: US 07/574,391
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: US 07/194,026
; PRIOR FILING DATE: 1988-05-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-105-545-1

Query Match          87.5%; Score 28; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLQ 6
   :|||||
Db 12 SGGSTLQ 17

RESULT 25
US-10-105-545-6
; Sequence 6, Application US/10105545
; Publication No. US20030144479A1
; GENERAL INFORMATION:
; APPLICANT: Mark, Greene I.
; APPLICANT: Williams, William V.
; APPLICANT: Weiner, David B.
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Cohen, Jeffrey A.
; APPLICANT: Williams, Robert M.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND US
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 4040/114920S2
; CURRENT APPLICATION NUMBER: US/10/105,545
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 08/752,816
; PRIOR FILING DATE: 1996-11-21
; PRIOR APPLICATION NUMBER: US 07/940,654
; PRIOR FILING DATE: 1992-09-03
; PRIOR APPLICATION NUMBER: US 07/702,833
; PRIOR FILING DATE: 1991-05-20
; PRIOR APPLICATION NUMBER: US 07/326,328
; PRIOR FILING DATE: 1989-03-21
```

```

; PRIOR APPLICATION NUMBER: US 07/074,264
; PRIOR FILING DATE: 1987-07-16
; PRIOR APPLICATION NUMBER: US 07/462,542
; PRIOR FILING DATE: 1990-01-09
; PRIOR APPLICATION NUMBER: US 07/648,303
; PRIOR FILING DATE: 1991-01-25
; PRIOR APPLICATION NUMBER: US 07/685,881
; PRIOR FILING DATE: 1991-04-15
; PRIOR APPLICATION NUMBER: US 07/574,391
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: US 07/194,026
; PRIOR FILING DATE: 1988-05-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-545-6

Query Match      87.5%; Score 28; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLQ 6
Db      12 SGGSTLQ 17

RESULT 26
US-10-545-2
; Sequence 2, Application US/10105545
; Publication No. US20030144479A1
; GENERAL INFORMATION:
; APPLICANT: Mark, Greene I.
; APPLICANT: Williams, William V.
; APPLICANT: Weiner, David B.
; APPLICANT: Cohen, Jeffrey A.
; APPLICANT: Kleber-Emmons, Thomas
; APPLICANT: Williams, Robert M.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND USING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 4040/11492US2
; CURRENT APPLICATION NUMBER: US/10/105,545
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 08/752,816
; PRIOR FILING DATE: 1996-11-21
; PRIOR APPLICATION NUMBER: US 07/940,654
; PRIOR FILING DATE: 1992-09-03
; PRIOR APPLICATION NUMBER: US 07/702,833
; PRIOR FILING DATE: 1991-05-20
; PRIOR APPLICATION NUMBER: US 07/326,328
; PRIOR FILING DATE: 1989-03-21
; PRIOR APPLICATION NUMBER: US 07/074,264
; PRIOR FILING DATE: 1987-07-16
; PRIOR APPLICATION NUMBER: US 07/462,542
; PRIOR FILING DATE: 1990-01-09
; PRIOR APPLICATION NUMBER: US 07/648,303
; PRIOR FILING DATE: 1991-01-25
; PRIOR APPLICATION NUMBER: US 07/685,881
; PRIOR FILING DATE: 1991-04-15
; PRIOR APPLICATION NUMBER: US 07/574,391
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: US 07/194,026
; PRIOR FILING DATE: 1988-05-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 18
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-545-2

Query Match      87.5%; Score 28; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLQ 6
Db      13 SGGSTLQ 18

RESULT 27
US-10-545-19
; Sequence 19, Application US/10105545
; Publication No. US20030144479A1
; GENERAL INFORMATION:
; APPLICANT: Mark, Greene I.
; APPLICANT: Williams, William V.
; APPLICANT: Weiner, David B.
; APPLICANT: Cohen, Jeffrey A.
; APPLICANT: Kleber-Emmons, Thomas
; APPLICANT: Williams, Robert M.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE COMPOUNDS AND METHODS OF CONSTRUCTING AND USING
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 4040/11492US2
; CURRENT APPLICATION NUMBER: US/10/105,545
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 08/752,816
; PRIOR FILING DATE: 1996-11-21
; PRIOR APPLICATION NUMBER: US 07/940,654
; PRIOR FILING DATE: 1992-09-03
; PRIOR APPLICATION NUMBER: US 07/702,833
; PRIOR FILING DATE: 1991-05-20
; PRIOR APPLICATION NUMBER: US 07/326,328
; PRIOR FILING DATE: 1989-03-21
; PRIOR APPLICATION NUMBER: US 07/074,264
; PRIOR FILING DATE: 1987-07-16
; PRIOR APPLICATION NUMBER: US 07/462,542
; PRIOR FILING DATE: 1990-01-09
; PRIOR APPLICATION NUMBER: US 07/648,303
; PRIOR FILING DATE: 1991-01-25
; PRIOR APPLICATION NUMBER: US 07/685,881
; PRIOR FILING DATE: 1991-04-15
; PRIOR APPLICATION NUMBER: US 07/574,391
; PRIOR FILING DATE: 1990-08-27
; PRIOR APPLICATION NUMBER: US 07/194,026
; PRIOR FILING DATE: 1988-05-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-545-19

Query Match      87.5%; Score 28; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLQ 6
Db      13 SGGSTLQ 18

RESULT 28
US-10-424-599-154913
```

```
; Sequence 154913, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 154913
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110908C.1.pep
US-10-424-599-154913
```

```
Query Match      87.5%; Score 28; DB 4; Length 42;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 SGGSTLQ 7
        |||||
Db      22 SGGSTFQS 28
```

```
RESULT 29
US-10-425-115-237614
; Sequence 237614, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 237614
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_14828C.1.pep
US-10-425-115-237614
```

```
Query Match      87.5%; Score 28; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SGGSTLQ 6
        |||||
Db      7 SGGSTLQ 12
```

```
RESULT 30
US-10-425-115-354064
; Sequence 354064, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
```

```
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 354064
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_8607C.1.pep
US-10-425-115-354064
```

```
Query Match      87.5%; Score 28; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SGGSTLQ 6
        |||||
Db      53 SGGSTLQ 58
```

```
RESULT 31
US-09-764-891-3607
; Sequence 3607, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3607
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-3607
```

```
Query Match      87.5%; Score 28; DB 3; Length 67;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 SGGSTLQ 7
        |||||
Db      20 SGGSTFQS 26
```

```
RESULT 32
US-10-242-355-401
; Sequence 401, Application US/10242355
; Publication No. US20030235831A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC003C1
; CURRENT APPLICATION NUMBER: US/10/242,355
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,897
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
```

PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 401
LENGTH: 80
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (41)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: misc_feature
LOCATION: (60)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-355-401

Query Match 87.5%; Score 28; DB 4; Length 80;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSTLOS 7
|||||:
Db 51 GSSTLRS 57

RESULT 33
US-10-891-972-26
Sequence 26, Application US/10891972
Publication No. US2005065327A1
GENERAL INFORMATION:
APPLICANT: Monk, Phillip David
APPLICANT: Dermatus, Ltdz
APPLICANT: Shorrock, Celia Patricia
APPLICANT: Winter, Ralph Raymond
TITLE OF INVENTION: HUMAN ANTIBODY MOLECULES FOR IL-13
FILE REFERENCE: 05569.0008.NPUS03
CURRENT APPLICATION NUMBER: US/10/891,972
CURRENT FILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: US 60/487,512
PRIOR FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: US 60/558,216
PRIOR FILING DATE: 2004-03-31
PRIOR APPLICATION NUMBER: US 60/573,791
PRIOR FILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: GB 0407315.1
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PatentIn version 3.3
SEQ ID NO 26
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: LIGHT CHAIN DOMAIN OF BAK209B11
US-10-891-972-26

Query Match 87.5%; Score 28; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSSTLOS 7
|||||

Db 51 GSSTLOS 56

RESULT 34
US-10-106-698-6352
Sequence 6352, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Co1on and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 6352
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (58)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6352

Query Match 87.5%; Score 28; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSTLOS 7
|||||:
Db 20 GSSTLRS 26

RESULT 35
US-10-732-923-12398
Sequence 12398, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 12398
LENGTH: 114
TYPE: PRT
ORGANISM: Ginkgo biloba
US-10-732-923-12398

Query Match 87.5%; Score 28; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSSTLOS 7
|||||:
Db 47 GSSTLRS 52

RESULT 36
US-10-424-599-174967
Sequence 174967, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 174967
LENGTH: 147
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_129013C.1.pep
US-10-424-599-174967

Query Match 87.5%; Score 28; DB 4; Length 147;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGGSTLQ 7
Db 76 SGGSTLQ 82

RESULT 37
US-11-097-143-38067
Sequence 38067, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38067
LENGTH: 186
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-38067

Query Match 87.5%; Score 28; DB 6; Length 186;
Best Local Similarity 85.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTLQ 7
Db 36 SGGSTLQ 42

RESULT 38
US-10-425-114-68883
Sequence 68883, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 68883
LENGTH: 191
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700089425_FLI.pep
US-10-425-114-68883

Query Match 87.5%; Score 28; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTLQ 6
Db 125 SGGSTLQ 130

RESULT 39
US-10-767-701-40334
Sequence 40334, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 40334
LENGTH: 202
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAV03-C55305_1.pep
US-10-767-701-40334

Query Match 87.5%; Score 28; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGGSTLQ 6
Db 136 SGGSTLQ 141

RESULT 40
US-10-425-115-349967
Sequence 349967, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua

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; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 349967
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_82344C.1.pep
US-10-425-115-349967

Query Match      87.5%; Score 28; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGGTLOS 6
        |||||
Db      125  SGGTLOS 130

RESULT 41
US-10-425-115-296478
; Sequence 296478, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 296478
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(218)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_33461C.1.pep
US-10-425-115-296478

Query Match      87.5%; Score 28; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  SGGTLOS 7
        |||||
Db      120  SGGTLOS 125

RESULT 42
US-10-424-599-266598
; Sequence 266598, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 266598
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(221)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8275C.1.pep
US-10-424-599-266598

Query Match      87.5%; Score 28; DB 4; Length 221;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGGTLOS 6
        |||||
Db      180  SGGTLOS 185

RESULT 43
US-10-450-763-36778
; Sequence 36778, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36778
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(223)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-36778

Query Match      87.5%; Score 28; DB 5; Length 223;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1  SGGTLOS 7
        |||||
Db      60  SGGTLOS 66

RESULT 44
US-10-767-701-46400
; Sequence 46400, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701

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; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46400
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(241)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C6090_1.pep
; US-10-767-701-46400

Query Match      87.5%; Score 28; DB 4; Length 241;
Best local Similarity 85.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTLQS 7
Db 84 GSGSTLQS 90

RESULT 45
US-10-425-115-185877
; Sequence 185877, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 185877
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(248)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_101105C.1.pep
; US-10-425-115-185877

Query Match      87.5%; Score 28; DB 4; Length 248;
Best local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSTLQS 7
Db 228 GSTLQS 233

RESULT 46
US-10-767-701-41192
; Sequence 41192, Application US/10767701
; Publication No. US2004012668A1
; GENERAL INFORMATION:
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 41192

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; LENGTH: 252
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C25865_1.pep
; US-10-767-701-41192

Query Match      87.5%; Score 28; DB 4; Length 252;
Best local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSTLQS 7
Db 124 GSTLQS 129

RESULT 47
US-10-425-114-55860
; Sequence 55860, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 55860
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3591-097-H8_F1.1.pep
; US-10-425-114-55860

Query Match      87.5%; Score 28; DB 4; Length 255;
Best local Similarity 100.0%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSTLQS 7
Db 63 GSTLQS 68

RESULT 48
US-10-425-115-238055
; Sequence 238055, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 238055
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_148695C.1.pep
; US-10-425-115-238055

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Query Match 87.5%; Score 28; DB 4; Length 273;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 172 GSTLOS 177

Search completed: January 17, 2006, 12:13:13
 Job time : 39.0455 secs

QY 2 GSTLOS 7
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 Db 81 GSTLOS 86

RESULT 49
 US-10-437-963-141800
 ; Sequence 141800, Application US/10437963
 ; Publication NO. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 141800
 ; LENGTH: 283
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_4286C.1.pep
 US-10-437-963-141800

Query Match 87.5%; Score 28; DB 4; Length 283;
 Best Local Similarity 85.7%; Pred. No. 6.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTLOS 7
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 Db 264 SGSSLOS 270

RESULT 50
 US-10-767-701-40250
 ; Sequence 40250, Application US/10767701
 ; Publication NO. US20040172684A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Zhou, Yihua
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53535)B
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; CURRENT FILING DATE: 2004-01-29
 ; NUMBER OF SEQ ID NOS: 63128
 ; SEQ ID NO 40250
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49987_1.pep
 US-10-767-701-40250

Query Match 87.5%; Score 28; DB 4; Length 285;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSTLOS 7
 |||||

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:59:34 : Search time 2.3333 Seconds
(without alignments)
28.363 Million cell updates/sec

Title: US-10-665-658-14

Perfect score: 32

Sequence: 1 SGSTRQS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

Published Applications AA.New:*
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep:*
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7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	32	100.0	7	US-10-665-658-14	Sequence 14, App1
2	32	100.0	7	US-10-665-658-61	Sequence 61, App1
3	32	100.0	107	US-11-107-028-49	Sequence 49, App1
4	32	100.0	107	US-11-107-028-51	Sequence 51, App1
5	32	100.0	108	US-10-665-658-1	Sequence 1, App1
6	32	100.0	108	US-10-665-658-2	Sequence 2, App1
7	29	90.6	7	US-10-665-658-63	Sequence 63, App1
8	29	90.6	7	US-10-665-658-64	Sequence 64, App1
9	27	84.4	7	US-10-665-658-65	Sequence 65, App1
10	27	84.4	275	US-10-467-657-1544	Sequence 1544, App1
11	27	84.4	609	US-11-062-225-3	Sequence 3, App1
12	27	84.4	609	US-11-062-225-4	Sequence 4, App1
13	27	84.4	609	US-11-062-225-5	Sequence 5, App1
14	27	84.4	609	US-11-062-225-6	Sequence 6, App1
15	27	84.4	609	US-11-062-225-7	Sequence 7, App1
16	27	84.4	609	US-11-062-225-8	Sequence 8, App1
17	26	81.2	552	US-11-219-995-9	Sequence 9, App1
18	25	78.1	154	US-10-467-657-102	Sequence 102, App1
19	25	78.1	154	US-10-467-657-7744	Sequence 7744, App1
20	25	78.1	519	US-10-467-657-946	Sequence 946, App1
21	25	78.1	519	US-10-520-655-1	Sequence 1, App1
22	25	78.1	519	US-10-520-655-1	Sequence 1, App1
23	25	78.1	597	US-10-623-155-169	Sequence 169, App1
24	25	78.1	597	US-10-623-155-169	Sequence 169, App1
25	25	78.1	791	US-10-623-155-170	Sequence 170, App1

26	25	78.1	881	6	US-10-623-155-430	Sequence 430, App1
27	25	78.1	920	6	US-10-623-155-357	Sequence 357, App1
28	25	78.1	943	6	US-10-623-155-161	Sequence 161, App1
29	25	78.1	966	7	US-11-057-058-67	Sequence 67, App1
30	25	78.1	1113	7	US-11-067-811-4	Sequence 4, App1
31	25	78.1	2516	6	US-10-647-956A-2	Sequence 2, App1
32	24	75.0	108	6	US-10-925-366A-158	Sequence 158, App1
33	24	75.0	108	6	US-10-925-366A-160	Sequence 160, App1
34	24	75.0	108	6	US-10-925-366A-169	Sequence 169, App1
35	24	75.0	263	6	US-10-689-742-2	Sequence 2, App1
36	24	75.0	272	6	US-10-793-626-588	Sequence 588, App1
37	24	75.0	312	6	US-10-858-730-122	Sequence 122, App1
38	24	75.0	343	7	US-11-016-564-15	Sequence 15, App1
39	24	75.0	365	7	US-11-052-554A-194	Sequence 194, App1
40	24	75.0	495	7	US-11-052-554A-258	Sequence 258, App1
41	24	75.0	533	7	US-11-145-035-15	Sequence 15, App1
42	24	75.0	592	7	US-11-104-110-9	Sequence 9, App1
43	24	75.0	598	7	US-11-145-035-14	Sequence 14, App1
44	24	75.0	607	6	US-10-131-826A-102	Sequence 102, App1
45	24	75.0	735	7	US-11-184-380-24	Sequence 24, App1
46	24	75.0	735	7	US-11-145-035-13	Sequence 13, App1
47	24	75.0	773	7	US-11-052-554A-341	Sequence 341, App1
48	24	75.0	959	6	US-10-467-962B-4	Sequence 4, App1
49	24	75.0	1306	6	US-10-995-561-905	Sequence 905, App1
50	24	75.0	1356	6	US-10-995-561-904	Sequence 904, App1
51	24	75.0	1356	6	US-10-995-561-906	Sequence 906, App1
52	24	75.0	1450	6	US-10-485-517-152	Sequence 152, App1
53	23	71.9	43	6	US-10-957-887B-171	Sequence 171, App1
54	23	71.9	43	6	US-10-957-887B-175	Sequence 175, App1
55	23	71.9	95	7	US-11-054-668-58	Sequence 58, App1
56	23	71.9	95	7	US-11-054-669-67	Sequence 67, App1
57	23	71.9	95	7	US-11-054-669-69	Sequence 69, App1
58	23	71.9	95	7	US-11-054-669-71	Sequence 71, App1
59	23	71.9	95	7	US-11-084-554-111	Sequence 111, App1
60	23	71.9	95	7	US-11-084-554-134	Sequence 134, App1
61	23	71.9	95	7	US-11-084-554-135	Sequence 135, App1
62	23	71.9	95	7	US-11-084-554-140	Sequence 140, App1
63	23	71.9	95	7	US-11-061-848-44	Sequence 44, App1
64	23	71.9	95	7	US-11-061-848-46	Sequence 46, App1
65	23	71.9	95	7	US-11-061-848-47	Sequence 47, App1
66	23	71.9	95	7	US-11-061-848-56	Sequence 56, App1
67	23	71.9	95	7	US-11-061-848-57	Sequence 57, App1
68	23	71.9	95	7	US-11-061-848-71	Sequence 71, App1
69	23	71.9	95	7	US-11-061-848-73	Sequence 73, App1
70	23	71.9	102	6	US-10-771-257-108	Sequence 108, App1
71	23	71.9	103	6	US-10-771-257-102	Sequence 102, App1
72	23	71.9	103	6	US-10-771-257-114	Sequence 114, App1
73	23	71.9	105	7	US-11-084-554-12	Sequence 12, App1
74	23	71.9	106	7	US-11-155-775-32	Sequence 32, App1
75	23	71.9	107	6	US-10-771-257-65	Sequence 65, App1
76	23	71.9	107	7	US-11-084-554-1	Sequence 1, App1
77	23	71.9	107	7	US-11-084-554-6	Sequence 6, App1
78	23	71.9	107	7	US-11-127-677-63	Sequence 63, App1
79	23	71.9	107	7	US-11-064-174-157	Sequence 157, App1
80	23	71.9	107	7	US-11-064-174-170	Sequence 170, App1
81	23	71.9	107	7	US-11-051-453-31	Sequence 31, App1
82	23	71.9	108	6	US-10-925-366A-97	Sequence 97, App1
83	23	71.9	108	6	US-10-925-366A-141	Sequence 141, App1
84	23	71.9	108	6	US-10-925-366A-147	Sequence 147, App1
85	23	71.9	108	6	US-10-925-366A-171	Sequence 171, App1
86	23	71.9	108	6	US-10-925-366A-177	Sequence 177, App1
87	23	71.9	108	6	US-10-925-366A-179	Sequence 179, App1
88	23	71.9	108	6	US-10-925-366A-181	Sequence 181, App1
89	23	71.9	108	6	US-10-925-366A-184	Sequence 184, App1
90	23	71.9	108	6	US-10-925-366A-193	Sequence 193, App1
91	23	71.9	108	6	US-10-771-257-4	Sequence 4, App1
92	23	71.9	108	6	US-10-771-257-25	Sequence 25, App1
93	23	71.9	108	6	US-10-771-257-78	Sequence 78, App1
94	23	71.9	108	6	US-10-771-257-77	Sequence 77, App1
95	23	71.9	108	6	US-10-771-257-78	Sequence 78, App1
96	23	71.9	108	7	US-11-127-677-4	Sequence 4, App1
97	23	71.9	108	7	US-11-127-677-25	Sequence 25, App1
98	23	71.9	108	7	US-11-127-677-28	Sequence 28, App1

99	23	71.9	108	7	US-11-127-677-75	Sequence 75, Appl	172	22	68.8	106	7	US-11-155-775-4	Sequence 4, Appl
100	23	71.9	108	7	US-11-127-677-76	Sequence 76, Appl	173	22	68.8	106	7	US-11-155-775-8	Sequence 8, Appl
101	23	71.9	108	7	US-11-127-932-11	Sequence 11, Appl	174	22	68.8	106	7	US-11-064-174-159	Sequence 159, Appl
102	23	71.9	108	7	US-11-064-174-31	Sequence 31, Appl	175	22	68.8	108	6	US-10-925-366A-150	Sequence 150, Appl
103	23	71.9	108	7	US-11-064-174-161	Sequence 161, Appl	176	22	68.8	108	6	US-10-925-366A-159	Sequence 159, Appl
104	23	71.9	108	7	US-11-064-174-177	Sequence 177, Appl	177	22	68.8	108	6	US-10-925-366A-161	Sequence 161, Appl
105	23	71.9	108	7	US-11-127-903-11	Sequence 11, Appl	178	22	68.8	108	6	US-10-925-366A-162	Sequence 162, Appl
106	23	71.9	109	6	US-10-771-257-29	Sequence 29, Appl	179	22	68.8	108	6	US-10-925-366A-163	Sequence 163, Appl
107	23	71.9	109	6	US-11-127-677-29	Sequence 29, Appl	180	22	68.8	108	6	US-10-925-366A-175	Sequence 175, Appl
108	23	71.9	106	6	US-10-925-366A-231	Sequence 231, Appl	181	22	68.8	108	6	US-10-925-366A-182	Sequence 182, Appl
109	23	71.9	129	7	US-11-051-453-45	Sequence 45, Appl	182	22	68.8	108	6	US-10-925-366A-189	Sequence 189, Appl
110	23	71.9	173	7	US-11-212-443-18	Sequence 18, Appl	183	22	68.8	108	6	US-10-925-366A-192	Sequence 192, Appl
111	23	71.9	195	7	US-11-052-554A-287	Sequence 287, Appl	184	22	68.8	108	6	US-10-925-366A-198	Sequence 198, Appl
112	23	71.9	236	7	US-11-086-289-4	Sequence 4, Appl	185	22	68.8	108	6	US-10-925-366A-200	Sequence 200, Appl
113	23	71.9	236	7	US-11-086-289-20	Sequence 20, Appl	186	22	68.8	108	6	US-10-925-366A-202	Sequence 202, Appl
114	23	71.9	241	7	US-11-054-515-1932	Sequence 1932, Ap	187	22	68.8	108	6	US-10-925-366A-206	Sequence 206, Appl
115	23	71.9	241	7	US-11-054-515-2054	Sequence 2054, Ap	188	22	68.8	108	6	US-10-925-366A-239	Sequence 239, Appl
116	23	71.9	244	7	US-11-054-515-82	Sequence 82, Appl	189	22	68.8	120	6	US-10-793-628-2404	Sequence 2404, Ap
117	23	71.9	244	7	US-11-054-515-164	Sequence 164, App	190	22	68.8	125	7	US-11-071-2	Sequence 2, Appl
118	23	71.9	244	7	US-11-054-515-261	Sequence 261, App	191	22	68.8	125	7	US-11-155-775-10	Sequence 10, Appl
119	23	71.9	244	7	US-11-054-515-280	Sequence 280, App	192	22	68.8	125	7	US-11-155-775-22	Sequence 22, Appl
120	23	71.9	249	7	US-11-054-515-1635	Sequence 1635, Ap	193	22	68.8	125	7	US-11-155-775-26	Sequence 26, Appl
121	23	71.9	249	7	US-11-128-059-56	Sequence 56, Appl	194	22	68.8	125	7	US-11-155-775-38	Sequence 38, Appl
122	23	71.9	250	7	US-11-128-059-62	Sequence 62, Appl	195	22	68.8	126	7	US-11-155-775-34	Sequence 34, Appl
123	23	71.9	251	7	US-11-054-515-1310	Sequence 1310, Ap	196	22	68.8	126	7	US-11-195-459-14	Sequence 14, Appl
124	23	71.9	253	7	US-11-054-515-936	Sequence 936, App	197	22	68.8	128	7	US-11-173-071-12	Sequence 12, Appl
125	23	71.9	253	7	US-11-054-515-994	Sequence 994, App	198	22	68.8	128	7	US-11-173-071-14	Sequence 14, Appl
126	23	71.9	268	7	US-11-010-795-24	Sequence 24, Appl	199	22	68.8	149	7	US-11-055-822-406	Sequence 406, App
127	23	71.9	276	6	US-10-467-657-2200	Sequence 2200, Ap	200	22	68.8	160	7	US-11-044-285-4	Sequence 4, Appl
128	23	71.9	299	7	US-11-192-374-5	Sequence 5, Appl	201	22	68.8	178	6	US-10-467-657-2220	Sequence 2220, Ap
129	23	71.9	345	6	US-10-888-962-7	Sequence 7, Appl	202	22	68.8	227	6	US-10-793-626-2642	Sequence 2642, Ap
130	23	71.9	348	6	US-10-517-939-300	Sequence 300, App	203	22	68.8	253	7	US-11-054-515-1829	Sequence 1829, Ap
131	23	71.9	353	7	US-11-128-059-90	Sequence 90, Appl	204	22	68.8	257	7	US-11-067-121-18	Sequence 18, Appl
132	23	71.9	360	6	US-10-517-939-218	Sequence 218, App	205	22	68.8	261	6	US-10-793-626-262	Sequence 262, App
133	23	71.9	397	6	US-10-828-033-25	Sequence 25, Appl	206	22	68.8	261	6	US-10-793-626-2442	Sequence 2442, Ap
134	23	71.9	424	7	US-11-055-822-1036	Sequence 1036, Ap	207	22	68.8	273	6	US-10-995-561-917	Sequence 917, App
135	23	71.9	445	6	US-10-517-939-368	Sequence 368, App	208	22	68.8	303	6	US-10-517-939-214	Sequence 214, App
136	23	71.9	463	6	US-10-641-678-71	Sequence 71, Appl	209	22	68.8	306	6	US-10-518-341-2	Sequence 2, Appl
137	23	71.9	481	6	US-10-467-657-4396	Sequence 4396, Ap	210	22	68.8	323	6	US-10-467-657-7180	Sequence 7180, Ap
138	23	71.9	513	6	US-10-641-678-66	Sequence 66, Appl	211	22	68.8	334	6	US-10-467-657-1034	Sequence 1034, Ap
139	23	71.9	514	6	US-10-641-678-67	Sequence 67, Appl	212	22	68.8	336	6	US-10-499-715-8	Sequence 8, Appl
140	23	71.9	534	7	US-11-167-856-24	Sequence 24, Appl	213	22	68.8	336	6	US-10-793-626-1868	Sequence 1868, Ap
141	23	71.9	540	7	US-11-212-443-168	Sequence 168, App	214	22	68.8	337	6	US-11-012-762-54	Sequence 54, Appl
142	23	71.9	544	7	US-11-052-554A-358	Sequence 358, App	215	22	68.8	361	7	US-11-012-762-54	Sequence 54, Appl
143	23	71.9	547	7	US-11-052-554A-285	Sequence 285, App	216	22	68.8	362	7	US-11-052-554A-77	Sequence 77, Appl
144	23	71.9	630	6	US-10-893-584-274	Sequence 274, App	217	22	68.8	362	7	US-11-052-554A-204	Sequence 204, App
145	23	71.9	640	7	US-11-212-443-20	Sequence 20, Appl	218	22	68.8	374	6	US-10-793-626-1356	Sequence 1356, Ap
146	23	71.9	719	6	US-10-524-647-116	Sequence 116, Appl	219	22	68.8	376	7	US-11-035-822-422	Sequence 422, App
147	23	71.9	721	7	US-11-128-059-88	Sequence 88, Appl	220	22	68.8	391	7	US-11-037-243-83	Sequence 83, Appl
148	23	71.9	761	6	US-10-485-517-252	Sequence 252, App	221	22	68.8	402	7	US-11-212-443-188	Sequence 188, Appl
149	23	71.9	897	6	US-10-453-372-208	Sequence 208, App	222	22	68.8	408	7	US-11-135-855-39	Sequence 39, Appl
150	23	71.9	931	7	US-11-128-059-86	Sequence 86, Appl	223	22	68.8	410	6	US-10-524-647-136	Sequence 136, App
151	23	71.9	955	7	US-11-052-554A-179	Sequence 179, Appl	224	22	68.8	431	6	US-10-467-657-2532	Sequence 2532, Ap
152	23	71.9	1016	7	US-11-103-957-41	Sequence 41, Appl	225	22	68.8	432	6	US-10-517-939-178	Sequence 178, App
153	23	71.9	1323	7	US-11-128-059-92	Sequence 92, Appl	226	22	68.8	434	6	US-10-821-234-1680	Sequence 1680, Ap
154	23	71.9	1327	7	US-11-128-059-84	Sequence 84, Appl	227	22	68.8	434	6	US-11-135-855-40	Sequence 40, Appl
155	23	71.9	1416	6	US-11-128-059-4	Sequence 4, Appl	228	22	68.8	441	7	US-11-174-150-48	Sequence 48, Appl
156	23	71.9	1502	6	US-10-453-372-252	Sequence 252, App	229	22	68.8	491	7	US-11-212-443-191	Sequence 191, App
157	23	71.9	1510	6	US-10-453-372-254	Sequence 254, App	230	22	68.8	512	6	US-10-821-234-1032	Sequence 1032, Ap
158	23	71.9	2439	7	US-11-128-059-76	Sequence 76, Appl	231	22	68.8	518	7	US-11-055-822-420	Sequence 420, App
159	23	71.9	2458	7	US-11-128-059-94	Sequence 94, Appl	232	22	68.8	519	6	US-10-523-477-8	Sequence 8, Appl
160	23	71.9	2551	6	US-10-453-372-256	Sequence 256, App	233	22	68.8	520	6	US-10-467-657-3948	Sequence 3948, Ap
161	23	71.9	2551	6	US-11-128-059-96	Sequence 96, Appl	234	22	68.8	550	7	US-11-120-308-158	Sequence 158, App
162	23	68.8	7	6	US-10-925-366A-29	Sequence 29, Appl	235	22	68.8	585	7	US-11-127-877-63	Sequence 63, Appl
163	23	68.8	7	6	US-10-925-366A-74	Sequence 74, Appl	236	22	68.8	589	7	US-10-821-234-1494	Sequence 1494, Ap
164	23	68.8	41	6	US-10-957-887B-203	Sequence 203, App	237	22	68.8	604	6	US-10-467-657-2280	Sequence 2280, Ap
165	22	68.8	42	6	US-10-957-887B-206	Sequence 206, App	238	22	68.8	657	7	US-11-110-082-37	Sequence 37, Appl
166	22	68.8	43	6	US-10-957-887B-202	Sequence 202, App	239	22	68.8	670	6	US-10-995-561-528	Sequence 528, App
167	22	68.8	43	6	US-10-957-887B-208	Sequence 208, App	240	22	68.8	687	7	US-11-117-169-6	Sequence 6, Appl
168	22	68.8	44	6	US-10-957-887B-138	Sequence 138, App	241	22	68.8	727	7	US-11-117-169-8	Sequence 8, Appl
169	22	68.8	64	6	US-10-467-657-5972	Sequence 5972, Ap	242	22	68.8	736	7	US-11-145-035-22	Sequence 22, Appl
170	22	68.8	76	6	US-10-925-366A-322	Sequence 322, App	243	22	68.8	753	7	US-11-037-243-68	Sequence 68, Appl
171	22	68.8	78	6	US-10-925-366A-314	Sequence 314, App	244	22	68.8	755	6	US-10-517-939-330	Sequence 330, App

245	22	68.8	774	7	US-11-000-463-459	Sequence 459, App	318	21	65.6	192	7	US-11-055-822-250	Sequence 250, App
246	22	68.8	783	7	US-11-192-219-7	Sequence 7, Appl1	319	21	65.6	199	7	US-11-053-185-47	Sequence 47, Appl1
247	22	68.8	795	7	US-11-052-554A-87	Sequence 87, Appl1	320	21	65.6	200	7	US-11-055-822-204	Sequence 204, Appl1
248	22	68.8	798	7	US-11-110-082-39	Sequence 39, Appl1	321	21	65.6	200	7	US-11-055-822-248	Sequence 248, App
249	22	68.8	813	6	US-10-661-866-19	Sequence 19, Appl1	322	21	65.6	201	7	US-11-124-368A-365	Sequence 265, App
250	22	68.8	837	7	US-11-094-519A-43	Sequence 43, Appl1	323	21	65.6	204	6	US-10-467-657-1954	Sequence 1954, Ap
251	22	68.8	845	7	US-11-094-519A-42	Sequence 42, Appl1	324	21	65.6	205	6	US-10-467-657-6222	Sequence 6222, Ap
252	22	68.8	896	7	US-11-192-219-3	Sequence 3, Appl1	325	21	65.6	205	7	US-11-127-622-3	Sequence 3, Appl1
253	22	68.8	898	7	US-11-166-730-3	Sequence 4, Appl1	326	21	65.6	218	6	US-10-980-388-99	Sequence 99, Appl1
254	22	68.8	923	7	US-11-192-219-4	Sequence 4, Appl1	327	21	65.6	218	6	US-11-143-980-33	Sequence 33, Appl1
255	22	68.8	934	7	US-11-108-864-19	Sequence 19, Appl1	328	21	65.6	222	6	US-10-467-657-5190	Sequence 5190, Ap
256	22	68.8	944	7	US-11-052-554A-10	Sequence 10, Appl1	329	21	65.6	223	6	US-10-467-657-3974	Sequence 3974, Ap
257	22	68.8	954	7	US-11-057-058-68	Sequence 68, Appl1	330	21	65.6	224	6	US-10-892-379-7	Sequence 7, Appl1
258	22	68.8	961	6	US-10-453-372-726	Sequence 726, App	331	21	65.6	229	7	US-11-170-653-54	Sequence 54, Appl1
259	22	68.8	961	6	US-10-453-372-728	Sequence 728, App	332	21	65.6	230	6	US-10-884-730-371	Sequence 370, App
260	22	68.8	967	6	US-10-453-372-712	Sequence 712, App	333	21	65.6	230	6	US-10-884-730-372	Sequence 371, App
261	22	68.8	967	6	US-10-453-372-714	Sequence 714, App	334	21	65.6	230	6	US-10-884-730-373	Sequence 372, App
262	22	68.8	1165	7	US-11-192-219-2	Sequence 2, Appl1	335	21	65.6	230	6	US-10-884-730-374	Sequence 373, App
263	22	68.8	1171	6	US-10-467-657-7842	Sequence 7842, Ap	336	21	65.6	230	6	US-10-884-730-375	Sequence 374, App
264	22	68.8	1237	7	US-11-052-554A-95	Sequence 95, Appl1	337	21	65.6	230	6	US-10-884-730-376	Sequence 375, App
265	22	68.8	1436	7	US-11-052-554A-140	Sequence 140, App	338	21	65.6	230	6	US-10-884-730-377	Sequence 376, App
266	22	68.8	2591	6	US-10-453-372-718	Sequence 718, App	339	21	65.6	231	6	US-10-467-657-1084	Sequence 1084, Ap
267	22	68.8	2602	6	US-10-453-372-716	Sequence 716, App	340	21	65.6	231	6	US-11-054-515-2010	Sequence 2010, Ap
268	22	68.8	2617	6	US-10-453-372-666	Sequence 666, App	341	21	65.6	237	7	US-11-054-515-2003	Sequence 2003, Ap
269	22	68.8	2617	6	US-10-453-372-732	Sequence 732, App	342	21	65.6	237	7	US-11-054-515-2005	Sequence 2005, Ap
270	22	68.8	2617	6	US-10-453-372-736	Sequence 736, App	343	21	65.6	237	7	US-11-054-515-2017	Sequence 2017, Ap
271	22	68.8	2617	6	US-10-453-372-738	Sequence 738, App	344	21	65.6	237	7	US-11-054-515-2019	Sequence 2019, Ap
272	22	68.8	2617	6	US-10-453-372-740	Sequence 740, App	345	21	65.6	237	7	US-11-054-515-2020	Sequence 2020, Ap
273	22	68.8	2617	6	US-10-453-372-742	Sequence 742, App	346	21	65.6	237	7	US-11-054-515-2027	Sequence 2027, Ap
274	22	68.8	2617	6	US-10-453-372-744	Sequence 744, App	347	21	65.6	237	7	US-11-054-515-2036	Sequence 2028, Ap
275	22	68.8	2617	6	US-10-453-372-746	Sequence 746, App	348	21	65.6	237	7	US-11-054-515-2043	Sequence 2036, Ap
276	22	68.8	2617	6	US-10-453-372-748	Sequence 748, App	349	21	65.6	237	7	US-11-054-515-2044	Sequence 2040, Ap
277	22	68.8	2617	6	US-10-453-372-750	Sequence 750, App	350	21	65.6	237	7	US-11-054-515-2045	Sequence 2046, Ap
278	22	68.8	2837	6	US-10-499-715-2	Sequence 2, Appl1	351	21	65.6	237	7	US-11-054-515-2043	Sequence 2043, Ap
279	22	68.8	3002	6	US-10-821-334-916	Sequence 916, App	352	21	65.6	237	7	US-11-054-515-2110	Sequence 2104, Ap
280	22	68.8	3716	7	US-11-052-554A-141	Sequence 141, App	353	21	65.6	237	7	US-11-054-515-2110	Sequence 2110, Ap
281	22	68.8	7968	7	US-11-186-731-5	Sequence 5, Appl1	354	21	65.6	237	7	US-11-054-515-2111	Sequence 2111, Ap
282	22	68.8	7	US-10-665-658-62	Sequence 62, Appl1	355	21	65.6	237	7	US-11-054-515-2112	Sequence 2112, Ap	
283	21	65.6	20	US-10-485-788A-623	Sequence 623, App	356	21	65.6	237	7	US-11-054-515-2115	Sequence 2115, Ap	
284	21	65.6	22	US-11-149-943-16	Sequence 16, Appl1	357	21	65.6	237	7	US-11-054-515-2118	Sequence 2118, Ap	
285	21	65.6	40	US-10-957-887B-239	Sequence 239, App	358	21	65.6	237	7	US-11-054-515-2118	Sequence 2118, Ap	
286	21	65.6	42	US-10-828-033-38	Sequence 38, Appl1	359	21	65.6	237	7	US-11-054-515-2034	Sequence 2034, Ap	
287	21	65.6	44	US-10-957-887B-240	Sequence 240, App	360	21	65.6	238	7	US-11-054-515-2034	Sequence 2034, Ap	
288	21	65.6	45	US-10-957-887B-158	Sequence 158, App	361	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
289	21	65.6	53	US-10-957-887B-191	Sequence 191, App	362	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
290	21	65.6	56	US-10-957-887B-26	Sequence 26, Appl1	363	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
291	21	65.6	62	US-10-467-657-336	Sequence 336, App	364	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
292	21	65.6	80	US-11-102-476-17	Sequence 17, Appl1	365	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
293	21	65.6	80	US-11-102-476-17	Sequence 17, Appl1	366	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
294	21	65.6	80	US-11-102-476-18	Sequence 18, Appl1	367	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
295	21	65.6	81	US-11-102-476-32	Sequence 32, Appl1	368	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
296	21	65.6	81	US-11-102-476-32	Sequence 32, Appl1	369	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
297	21	65.6	96	US-11-084-554-144	Sequence 144, App	370	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
298	21	65.6	96	US-11-084-554-147	Sequence 147, App	371	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
299	21	65.6	98	US-11-144-248-30	Sequence 30, Appl1	372	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
300	21	65.6	98	US-11-054-669-17	Sequence 17, Appl1	373	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
301	21	65.6	98	US-11-084-554-27	Sequence 27, Appl1	374	21	65.6	240	7	US-11-054-515-2036	Sequence 2036, Ap	
302	21	65.6	98	US-11-144-222-30	Sequence 30, Appl1	375	21	65.6	240	7	US-11-053-185-46	Sequence 46, Appl1	
303	21	65.6	103	7	US-11-007-282-12	Sequence 12, Appl1	376	21	65.6	245	6	US-10-467-657-7884	Sequence 7884, Ap
304	21	65.6	106	6	US-10-485-788A-644	Sequence 644, App	377	21	65.6	248	7	US-11-054-515-1965	Sequence 1965, Ap
305	21	65.6	106	6	US-11-053-076-12	Sequence 12, Appl1	378	21	65.6	248	7	US-11-054-515-1974	Sequence 1974, Ap
310	21	65.6	137	6	US-10-793-326-1980	Sequence 1980, App	384	21	65.6	250	7	US-11-054-515-1179	Sequence 1179, Ap
311	21	65.6	142	7	US-11-082-389-326	Sequence 99, Appl1	385	21	65.6	251	7	US-11-054-515-1343	Sequence 1343, Ap
312	21	65.6	142	7	US-10-925-366A-99	Sequence 99, Appl1	386	21	65.6	252	7	US-11-054-515-1431	Sequence 1431, Ap
313	21	65.6	153	6	US-10-821-334-1253	Sequence 1253, Ap	387	21	65.6	252	7	US-11-054-515-1431	Sequence 1431, Ap
314	21	65.6	167	7	US-11-052-554A-32	Sequence 32, Appl1	388	21	65.6	252	7	US-10-821-234-1582	Sequence 1582, Ap
315	21	65.6	167	7	US-11-052-554A-187	Sequence 187, App	389	21	65.6	253	6	US-10-878-556A-51	Sequence 51, Appl1
316	21	65.6	186	6	US-10-873-528-105	Sequence 105, App	390	21	65.6	253	6	US-10-878-556A-51	Sequence 51, Appl1
317	21	65.6	192	7	US-11-055-822-206	Sequence 206, App	390	21	65.6	253	6	US-10-878-556A-51	Sequence 51, Appl1

391	21	65.6	358	6	US-10-995-561-888	Sequence 888, App	464	21	65.6	816	7	US-11-057-058-10	Sequence 10, Appl
392	21	65.6	358	6	US-10-995-561-889	Sequence 889, App	465	21	65.6	817	6	US-10-954-468-41	Sequence 11, Appl
393	21	65.6	362	7	US-11-012-762-56	Sequence 89, Appl	466	21	65.6	915	6	US-10-821-234-1514	Sequence 1514, Ap
394	21	65.6	373	7	US-11-009-658-34	Sequence 34, Appl	467	21	65.6	916	6	US-10-995-561-1003	Sequence 1003, Ap
395	21	65.6	374	6	US-10-954-468-40	Sequence 40, Appl	468	21	65.6	917	6	US-10-995-561-1004	Sequence 1004, Ap
396	21	65.6	380	7	US-11-116-939-2	Sequence 2, Appl1	469	21	65.6	940	6	US-10-995-561-1004	Sequence 1004, Ap
397	21	65.6	381	6	US-10-821-234-1342	Sequence 1342, Ap	470	21	65.6	950	6	US-10-981-267-24	Sequence 24, Appl
398	21	65.6	388	6	US-10-995-561-887	Sequence 887, App	471	21	65.6	952	6	US-10-821-234-1557	Sequence 1557, Ap
399	21	65.6	396	7	US-11-120-308-172	Sequence 172, App	472	21	65.6	952	7	US-11-057-058-54	Sequence 54, Appl
400	21	65.6	401	6	US-10-467-657-5208	Sequence 5208, Ap	473	21	65.6	964	7	US-11-103-957-13	Sequence 13, Appl
401	21	65.6	410	6	US-10-821-234-912	Sequence 912, App	474	21	65.6	969	6	US-10-995-561-1001	Sequence 1001, Ap
402	21	65.6	410	6	US-10-858-730-233	Sequence 233, App	475	21	65.6	971	6	US-10-954-468-39	Sequence 39, Appl
403	21	65.6	421	6	US-10-067-974-2	Sequence 2, Appl1	476	21	65.6	985	6	US-10-995-561-997	Sequence 997, App
404	21	65.6	421	6	US-10-858-730-2	Sequence 16, Appl	477	21	65.6	994	6	US-10-995-561-997	Sequence 33, Appl
405	21	65.6	421	6	US-10-858-730-2	Sequence 202, Appl	478	21	65.6	997	7	US-11-057-058-33	Sequence 31, Appl
406	21	65.6	421	6	US-10-858-730-202	Sequence 202, App	479	21	65.6	1011	7	US-11-057-058-31	Sequence 1055, Ap
407	21	65.6	421	6	US-10-525-710-73	Sequence 73, Appl	480	21	65.6	1043	6	US-10-821-234-1055	Sequence 22, Appl
408	21	65.6	421	6	US-10-525-674-65	Sequence 65, Appl	481	21	65.6	1056	7	US-11-044-111-22	Sequence 41, Appl
409	21	65.6	421	7	US-11-055-822-26	Sequence 26, Appl	482	21	65.6	1107	7	US-11-057-058-41	Sequence 41, Appl
410	21	65.6	428	7	US-11-127-622-2	Sequence 2, Appl1	483	21	65.6	1294	7	US-11-052-554A-340	Sequence 340, App
411	21	65.6	428	7	US-11-127-877-73	Sequence 73, Appl	484	21	65.6	1343	7	US-11-052-554A-2	Sequence 2, Appl1
412	21	65.6	431	7	US-11-052-554A-210	Sequence 210, App	485	21	65.6	1571	7	US-10-052-554A-15	Sequence 145, App
413	21	65.6	433	6	US-10-641-678-34	Sequence 34, Appl	486	21	65.6	1613	6	US-10-055-877-145	Sequence 144, App
414	21	65.6	437	6	US-10-858-730-214	Sequence 214, App	487	21	65.6	1637	6	US-10-055-877-144	Sequence 21, Appl
415	21	65.6	437	6	US-10-858-730-283	Sequence 283, App	488	21	65.6	1770	7	US-11-103-957-21	Sequence 1004, Ap
416	21	65.6	437	6	US-10-858-730-288	Sequence 288, App	489	21	65.6	1902	6	US-10-453-372-1004	Sequence 1640, Ap
417	21	65.6	439	7	US-11-075-185-11	Sequence 11, Appl	490	21	65.6	2399	7	US-11-052-554A-92	Sequence 92, Appl
418	21	65.6	449	7	US-11-120-308-176	Sequence 176, App	491	21	65.6	2828	7	US-11-080-991-54	Sequence 54, Appl
419	21	65.6	455	6	US-10-467-657-5828	Sequence 5828, Ap	492	21	65.6	2828	7	US-11-186-284-49	Sequence 49, Appl
420	21	65.6	463	6	US-10-467-657-6352	Sequence 6352, Ap	493	21	65.6	3130	6	US-10-453-372-42	Sequence 42, Appl
421	21	65.6	463	6	US-10-467-657-7604	Sequence 7604, Ap	494	21	65.6	3483	6	US-10-453-372-40	Sequence 40, Appl
422	21	65.6	463	6	US-10-954-468-38	Sequence 38, Appl	495	21	65.6	3546	6	US-10-453-372-32	Sequence 32, Appl
423	21	65.6	464	6	US-10-763-712A-46	Sequence 46, Appl	496	21	65.6	4495	6	US-10-453-372-1002	Sequence 1002, Ap
424	21	65.6	468	7	US-10-763-712A-3	Sequence 237, App	497	21	65.6	4958	7	US-10-821-234-1538	Sequence 1538, Ap
425	21	65.6	468	7	US-11-000-463-237	Sequence 50, Appl	498	20.5	64.1	122	6	US-10-821-234-1538	Sequence 3015, Ap
426	21	65.6	473	7	US-11-144-224-50	Sequence 50, Appl	499	20	62.5	12	7	US-11-054-518-3015	Sequence 454, App
427	21	65.6	473	7	US-11-144-222-50	Sequence 232, App	500	20	62.5	15	7	US-10-929-988-404	Sequence 33, Appl
428	21	65.6	479	6	US-10-510-386-232	Sequence 298, App	501	20	62.5	17	7	US-11-006-031-33	Sequence 89, Appl
429	21	65.6	482	6	US-10-055-877-298	Sequence 28, Appl	502	20	62.5	20	6	US-10-889-197-30	Sequence 30, Appl
430	21	65.6	486	6	US-10-641-678-28	Sequence 1302, Ap	503	20	62.5	42	6	US-10-957-887B-99	Sequence 143, App
431	21	65.6	489	6	US-10-793-626-1302	Sequence 65, Appl	504	20	62.5	44	6	US-10-957-887B-143	Sequence 69, Appl
432	21	65.6	491	6	US-10-641-678-65	Sequence 2, Appl1	505	20	62.5	43	6	US-10-957-887B-59	Sequence 277, App
433	21	65.6	497	6	US-10-641-678-2	Sequence 6, Appl1	506	20	62.5	43	6	US-10-957-887B-303	Sequence 303, App
434	21	65.6	497	6	US-10-641-678-6	Sequence 8, Appl1	507	20	62.5	44	6	US-10-986-501-356	Sequence 356, App
435	21	65.6	497	6	US-10-641-678-8	Sequence 10, Appl	508	20	62.5	44	6	US-10-957-887B-173	Sequence 173, App
436	21	65.6	497	6	US-10-641-678-10	Sequence 12, Appl	509	20	62.5	44	6	US-10-957-887B-210	Sequence 210, App
437	21	65.6	497	6	US-10-641-678-12	Sequence 14, Appl	510	20	62.5	44	6	US-10-957-887B-252	Sequence 252, App
438	21	65.6	497	6	US-10-641-678-14	Sequence 16, Appl	511	20	62.5	45	6	US-10-957-887B-174	Sequence 174, App
439	21	65.6	497	6	US-10-641-678-16	Sequence 18, Appl	512	20	62.5	45	6	US-10-957-887B-178	Sequence 20, Appl
440	21	65.6	497	6	US-10-641-678-18	Sequence 22, Appl	513	20	62.5	45	6	US-10-523-038-20	Sequence 20, Appl
441	21	65.6	497	6	US-10-641-678-22	Sequence 24, Appl	514	20	62.5	46	6	US-10-523-038-20	Sequence 20, Appl
442	21	65.6	497	6	US-10-641-678-24	Sequence 26, Appl	515	20	62.5	46	6	US-10-957-887B-215	Sequence 275, App
443	21	65.6	497	6	US-10-641-678-26	Sequence 26, Appl	516	20	62.5	46	6	US-10-467-657-7896	Sequence 7896, App
444	21	65.6	497	6	US-10-641-678-30	Sequence 30, Appl	517	20	62.5	48	6	US-10-523-038-16	Sequence 16, Appl
445	21	65.6	497	7	US-11-212-443-189	Sequence 189, App	518	20	62.5	51	6	US-10-523-038-14	Sequence 14, Appl
446	21	65.6	499	6	US-10-793-626-1484	Sequence 189, App	519	20	62.5	51	6	US-10-523-038-18	Sequence 18, Appl
447	21	65.6	510	6	US-10-641-678-20	Sequence 20, Appl	520	20	62.5	51	6	US-10-467-657-1174	Sequence 1744, Ap
448	21	65.6	513	6	US-10-641-678-64	Sequence 34, App	521	20	62.5	65	6	US-10-467-657-8276	Sequence 8276, Ap
449	21	65.6	513	6	US-11-055-822-348	Sequence 348, App	522	20	62.5	65	6	US-10-925-366A-288	Sequence 288, App
450	21	65.6	515	6	US-10-467-657-1968	Sequence 1968, Ap	523	20	62.5	65	6	US-10-925-366A-12	Sequence 12, Appl
451	21	65.6	520	6	US-10-763-712A-54	Sequence 54, Appl	524	20	62.5	77	7	US-11-113-476-11	Sequence 11, Appl
452	21	65.6	520	6	US-11-052-554A-98	Sequence 98, Appl	525	20	62.5	77	7	US-11-102-476-61	Sequence 61, Appl
453	21	65.6	523	7	US-11-212-443-64	Sequence 64, Appl	526	20	62.5	90	7	US-10-678-790-61	Sequence 146, App
454	21	65.6	526	6	US-10-467-657-1772	Sequence 1772, Ap	527	20	62.5	107	6	US-10-925-366A-146	Sequence 288, App
455	21	65.6	528	6	US-10-821-234-921	Sequence 921, App	528	20	62.5	108	6	US-10-925-366A-288	Sequence 1175, Ap
456	21	65.6	529	6	US-10-467-962B-101	Sequence 101, App	529	20	62.5	109	6	US-10-821-234-1175	Sequence 12, Appl
457	21	65.6	530	6	US-10-954-468-35	Sequence 35, Appl	530	20	62.5	113	7	US-11-073-605-8	Sequence 8, Appl
458	21	65.6	531	6	US-11-052-554A-99	Sequence 99, Appl	531	20	62.5	114	6	US-10-925-366A-12	Sequence 3, Appl1
459	21	65.6	532	6	US-10-131-826A-406	Sequence 406, App	532	20	62.5	121	6	US-10-510-880-3	Sequence 60, Appl
460	21	65.6	533	6	US-10-821-234-888	Sequence 888, App	533	20	62.5	122	6	US-10-678-790-60	Sequence 5246, Ap
461	21	65.6	534	6	US-10-954-468-42	Sequence 42, Appl	534	20	62.5	127	6	US-10-467-657-5246	Sequence 8156, Ap
462	21	65.6	535	6	US-10-467-962B-57	Sequence 57, Appl	535	20	62.5	138	6	US-10-467-657-8156	Sequence 8156, Ap
463	21	65.6	810	6	US-10-954-468-37	Sequence 37, Appl	536	20	62.5	144	7	US-11-134-795-26	Sequence 26, Appl

683	20	62.5	146	6	US-10-835-615-404	Sequence 404, App	756	20	62.5	180	7	US-11-055-822-40	Sequence 40, Appl
684	20	62.5	146	6	US-10-835-615-405	Sequence 405, App	757	20	62.5	183	7	US-11-051-568-23	Sequence 23, Appl
685	20	62.5	146	6	US-10-835-615-406	Sequence 406, App	758	20	62.5	183	7	US-11-055-862-84	Sequence 84, Appl
686	20	62.5	146	6	US-10-835-615-407	Sequence 407, App	759	20	62.5	188	6	US-10-453-377-1052	Sequence 1052, Ap
687	20	62.5	146	6	US-10-835-615-408	Sequence 408, App	760	20	62.5	190	7	US-11-124-368A-224	Sequence 224, App
688	20	62.5	146	6	US-10-835-615-409	Sequence 409, App	761	20	62.5	190	7	US-11-124-368A-225	Sequence 225, App
689	20	62.5	146	6	US-10-835-615-410	Sequence 410, App	762	20	62.5	190	7	US-11-124-368A-227	Sequence 227, App
690	20	62.5	146	6	US-10-835-615-411	Sequence 411, App	763	20	62.5	191	6	US-10-995-561-824	Sequence 824, App
691	20	62.5	146	6	US-10-835-615-412	Sequence 412, App	764	20	62.5	195	7	US-11-055-822-782	Sequence 782, App
692	20	62.5	146	6	US-10-835-615-413	Sequence 413, App	765	20	62.5	197	7	US-11-055-822-908	Sequence 908, App
693	20	62.5	146	6	US-10-835-615-414	Sequence 414, App	766	20	62.5	198	6	US-10-821-628-1448	Sequence 1448, Ap
694	20	62.5	146	6	US-10-835-615-415	Sequence 415, App	767	20	62.5	204	6	US-10-793-628-2394	Sequence 2394, Ap
695	20	62.5	146	6	US-10-835-615-416	Sequence 416, App	768	20	62.5	217	7	US-11-205-109-22	Sequence 22, Appl
696	20	62.5	146	6	US-10-835-615-417	Sequence 417, App	769	20	62.5	220	7	US-11-174-150-32	Sequence 32, Appl
697	20	62.5	146	6	US-10-835-615-418	Sequence 418, App	770	20	62.5	221	7	US-11-102-978-11	Sequence 11, Appl
698	20	62.5	146	6	US-10-835-615-420	Sequence 420, App	771	20	62.5	229	6	US-10-131-826A-178	Sequence 178, App
699	20	62.5	146	6	US-10-835-615-421	Sequence 421, App	772	20	62.5	229	6	US-10-467-657-1754	Sequence 1754, Ap
700	20	62.5	146	6	US-10-835-615-422	Sequence 422, App	773	20	62.5	233	6	US-10-485-517-214	Sequence 214, App
701	20	62.5	146	6	US-10-835-615-423	Sequence 423, App	774	20	62.5	236	6	US-10-467-657-5280	Sequence 5280, Ap
702	20	62.5	146	6	US-10-835-615-424	Sequence 424, App	775	20	62.5	236	6	US-10-995-561-823	Sequence 823, App
703	20	62.5	146	6	US-10-835-615-425	Sequence 425, App	776	20	62.5	236	6	US-10-523-038-5	Sequence 5, Appl
704	20	62.5	146	6	US-10-835-615-426	Sequence 426, App	777	20	62.5	237	6	US-10-793-628-1744	Sequence 1744, Ap
705	20	62.5	146	6	US-10-835-615-427	Sequence 427, App	778	20	62.5	237	6	US-11-523-038-45	Sequence 45, Appl
706	20	62.5	146	6	US-10-835-615-428	Sequence 428, App	779	20	62.5	237	7	US-11-074-178-178	Sequence 178, App
707	20	62.5	146	6	US-10-835-615-429	Sequence 429, App	780	20	62.5	238	7	US-11-054-518-2053	Sequence 2053, Ap
708	20	62.5	146	6	US-10-835-615-430	Sequence 430, App	781	20	62.5	240	7	US-11-212-443-166	Sequence 166, App
709	20	62.5	146	6	US-10-835-615-431	Sequence 431, App	782	20	62.5	242	6	US-10-821-234-1073	Sequence 1073, Ap
710	20	62.5	146	6	US-10-835-615-432	Sequence 432, App	783	20	62.5	242	7	US-11-054-515-1830	Sequence 1830, Ap
711	20	62.5	146	6	US-10-835-615-433	Sequence 433, App	784	20	62.5	242	7	US-11-054-515-1844	Sequence 1844, Ap
712	20	62.5	146	6	US-10-835-615-434	Sequence 434, App	785	20	62.5	243	7	US-11-054-515-1515	Sequence 1515, Ap
713	20	62.5	146	6	US-10-835-615-435	Sequence 435, App	786	20	62.5	243	7	US-11-054-515-1533	Sequence 1533, Ap
714	20	62.5	146	6	US-10-835-615-436	Sequence 436, App	787	20	62.5	243	7	US-11-054-515-1633	Sequence 1633, Ap
715	20	62.5	146	6	US-10-835-615-437	Sequence 437, App	788	20	62.5	244	7	US-11-054-515-1124	Sequence 1124, Ap
716	20	62.5	146	6	US-10-835-615-438	Sequence 438, App	789	20	62.5	244	7	US-11-054-515-1491	Sequence 1491, Ap
717	20	62.5	146	6	US-10-835-615-439	Sequence 439, App	790	20	62.5	244	7	US-11-054-515-1498	Sequence 1498, Ap
718	20	62.5	146	6	US-10-835-615-444	Sequence 444, App	791	20	62.5	244	7	US-11-054-515-1524	Sequence 1524, Ap
719	20	62.5	146	6	US-10-835-615-450	Sequence 450, App	792	20	62.5	244	7	US-11-054-515-1568	Sequence 1568, Ap
720	20	62.5	146	6	US-10-835-615-451	Sequence 451, App	793	20	62.5	244	7	US-11-054-515-1569	Sequence 1569, Ap
721	20	62.5	146	6	US-10-835-615-453	Sequence 453, App	794	20	62.5	244	7	US-11-054-515-1582	Sequence 1582, Ap
722	20	62.5	146	6	US-10-835-615-459	Sequence 459, App	795	20	62.5	244	7	US-11-054-515-1606	Sequence 1606, Ap
723	20	62.5	146	6	US-10-835-615-463	Sequence 463, App	796	20	62.5	244	7	US-11-054-515-1845	Sequence 1845, Ap
724	20	62.5	146	6	US-10-835-615-469	Sequence 469, App	797	20	62.5	245	7	US-11-054-515-1516	Sequence 1516, Ap
725	20	62.5	146	6	US-10-835-615-471	Sequence 471, App	798	20	62.5	245	7	US-11-054-515-1521	Sequence 1521, Ap
726	20	62.5	146	6	US-10-835-615-475	Sequence 475, App	799	20	62.5	245	7	US-11-054-515-1523	Sequence 1523, Ap
727	20	62.5	146	6	US-10-835-615-477	Sequence 477, App	800	20	62.5	245	7	US-11-054-515-1528	Sequence 1528, Ap
728	20	62.5	146	6	US-10-835-615-478	Sequence 478, App	801	20	62.5	245	7	US-11-054-515-1532	Sequence 1532, Ap
729	20	62.5	146	6	US-10-835-615-479	Sequence 479, App	802	20	62.5	245	7	US-11-054-515-1547	Sequence 1547, Ap
730	20	62.5	146	6	US-10-835-615-480	Sequence 480, App	803	20	62.5	245	7	US-11-054-515-1550	Sequence 1550, Ap
731	20	62.5	146	6	US-10-835-615-481	Sequence 481, App	804	20	62.5	245	7	US-11-054-515-1714	Sequence 1714, Ap
732	20	62.5	146	6	US-10-835-615-482	Sequence 482, App	805	20	62.5	245	7	US-11-054-515-1743	Sequence 1743, Ap
733	20	62.5	146	6	US-10-835-615-483	Sequence 483, App	806	20	62.5	245	7	US-11-054-515-1839	Sequence 1839, Ap
734	20	62.5	146	6	US-10-835-615-484	Sequence 484, App	807	20	62.5	246	7	US-11-054-515-1860	Sequence 1860, Ap
735	20	62.5	146	6	US-10-835-615-502	Sequence 502, App	808	20	62.5	246	7	US-11-054-515-1589	Sequence 1589, Ap
736	20	62.5	146	6	US-10-835-615-508	Sequence 508, App	809	20	62.5	246	7	US-11-054-515-1834	Sequence 1834, Ap
737	20	62.5	146	6	US-10-835-615-509	Sequence 509, App	810	20	62.5	247	7	US-11-054-515-1492	Sequence 1492, Ap
738	20	62.5	146	6	US-10-835-615-510	Sequence 510, App	811	20	62.5	247	7	US-11-054-515-1687	Sequence 1687, Ap
739	20	62.5	146	6	US-10-835-615-511	Sequence 511, App	812	20	62.5	247	7	US-11-054-515-1711	Sequence 1711, Ap
740	20	62.5	146	6	US-10-835-615-512	Sequence 512, App	813	20	62.5	247	7	US-11-054-515-377	Sequence 377, App
741	20	62.5	146	6	US-10-835-615-513	Sequence 513, App	814	20	62.5	250	6	US-10-793-626-1124	Sequence 1124, Ap
742	20	62.5	146	6	US-10-835-615-514	Sequence 514, App	815	20	62.5	252	7	US-11-054-515-1144	Sequence 1144, Ap
743	20	62.5	146	6	US-10-835-615-568	Sequence 568, App	816	20	62.5	253	7	US-11-054-515-1353	Sequence 1353, Ap
744	20	62.5	146	6	US-10-835-615-618	Sequence 618, App	817	20	62.5	254	7	US-11-054-515-1301	Sequence 1301, Ap
745	20	62.5	146	6	US-10-835-615-667	Sequence 667, App	818	20	62.5	254	7	US-11-054-515-1334	Sequence 1334, Ap
746	20	62.5	146	6	US-10-835-615-669	Sequence 669, App	819	20	62.5	255	7	US-11-054-515-1463	Sequence 1463, Ap
747	20	62.5	146	6	US-10-835-615-695	Sequence 695, App	820	20	62.5	260	7	US-11-055-822-322	Sequence 322, App
748	20	62.5	146	6	US-10-835-615-695	Sequence 701, App	821	20	62.5	260	7	US-11-055-822-324	Sequence 324, App
749	20	62.5	146	6	US-10-835-615-703	Sequence 703, App	822	20	62.5	264	6	US-10-502-972-8	Sequence 12, Appl
750	20	62.5	146	6	US-10-835-615-705	Sequence 705, App	823	20	62.5	266	6	US-10-195-585-12	Sequence 8, Appl
751	20	62.5	146	6	US-10-835-615-815	Sequence 815, App	824	20	62.5	273	6	US-10-467-657-7792	Sequence 7792, Ap
752	20	62.5	146	6	US-10-835-615-825	Sequence 825, App	825	20	62.5	283	7	US-11-195-585-10	Sequence 10, Appl
753	20	62.5	146	6	US-11-044-285-1	Sequence 1, Appl1	826	20	62.5	288	7	US-11-135-855-30	Sequence 30, Appl
754	20	62.5	166	7	US-11-094-519A-47	Sequence 47, Appl	827	20	62.5	295	7	US-11-194-246-298	Sequence 298, App
755	20	62.5	180	7	US-11-055-822-30	Sequence 30, Appl	828	20	62.5	299	7	US-11-112-882-30	Sequence 30, Appl

829	20	62.5	300	6	US-10-467-657-4166	Sequence 4166, Ap	902	20	62.5	420	6	US-10-131-826A-260	Sequence 260, App
830	20	62.5	302	6	US-10-793-626-2170	Sequence 2170, Ap	903	20	62.5	420	7	US-11-183-914-4	Sequence 11, App1
831	20	62.5	303	7	US-11-135-855-31	Sequence 31, App1	904	20	62.5	423	7	US-11-047-383-11	Sequence 41, App1
832	20	62.5	306	7	US-11-017-550-35	Sequence 35, App1	905	20	62.5	424	6	US-10-485-517-264	Sequence 264, App
833	20	62.5	306	7	US-11-017-550-39	Sequence 39, App1	906	20	62.5	424	6	US-10-485-517-281	Sequence 281, App
834	20	62.5	306	7	US-11-017-550-42	Sequence 42, App1	907	20	62.5	429	6	US-10-967-457-74	Sequence 74, App1
835	20	62.5	306	7	US-11-017-550-47	Sequence 47, App1	908	20	62.5	429	7	US-11-000-463-302	Sequence 302, App
836	20	62.5	306	7	US-11-017-550-63	Sequence 63, App1	909	20	62.5	429	7	US-11-000-463-302	Sequence 302, App
837	20	62.5	314	7	US-11-018-018-4	Sequence 4, App1	910	20	62.5	441	6	US-10-821-234-1668	Sequence 1668, Ap
838	20	62.5	314	7	US-11-047-757-4	Sequence 4, App1	911	20	62.5	447	6	US-10-632-150-10	Sequence 10, App1
839	20	62.5	315	7	US-11-037-243-60	Sequence 60, App1	912	20	62.5	447	7	US-11-073-457-10	Sequence 10, App1
840	20	62.5	316	7	US-11-055-822-58	Sequence 58, App1	913	20	62.5	447	7	US-11-073-460-10	Sequence 10, App1
841	20	62.5	317	7	US-11-094-519A-38	Sequence 38, App1	914	20	62.5	448	6	US-10-873-528-56	Sequence 56, App1
842	20	62.5	322	7	US-11-067-121-15	Sequence 15, App1	915	20	62.5	448	7	US-11-119-569-4	Sequence 4, App11
843	20	62.5	324	6	US-10-995-561-765	Sequence 765, App	916	20	62.5	449	6	US-10-878-556A-57	Sequence 57, App1
844	20	62.5	325	7	US-11-143-980-45	Sequence 45, App1	917	20	62.5	451	6	US-10-995-561-886	Sequence 86, App1
845	20	62.5	325	7	US-11-052-554A-356	Sequence 356, App	918	20	62.5	451	6	US-10-451-378-6	Sequence 6, App1
846	20	62.5	325	7	US-11-055-822-980	Sequence 980, App	919	20	62.5	459	6	US-10-641-678-72	Sequence 72, App1
847	20	62.5	335	6	US-10-467-657-3818	Sequence 3818, Ap	920	20	62.5	462	6	US-10-828-203-24	Sequence 24, App1
848	20	62.5	335	6	US-10-517-939-232	Sequence 232, App	921	20	62.5	462	6	US-10-821-234-1548	Sequence 1548, Ap
849	20	62.5	338	6	US-11-152-892-12	Sequence 12, App1	922	20	62.5	465	6	US-10-821-234-1550	Sequence 28, App1
850	20	62.5	338	6	US-10-793-626-320	Sequence 320, App	923	20	62.5	468	6	US-10-957-569-28	Sequence 28, App1
851	20	62.5	339	6	US-10-517-939-154	Sequence 154, App	924	20	62.5	468	6	US-10-995-561-907	Sequence 907, App
852	20	62.5	340	6	US-10-055-877-69	Sequence 69, App1	925	20	62.5	470	6	US-11-076-187-2	Sequence 2, App11
853	20	62.5	340	6	US-10-453-372-1014	Sequence 1014, Ap	926	20	62.5	474	6	US-10-873-528-3	Sequence 3, App11
854	20	62.5	341	6	US-10-515-481-3	Sequence 3, App11	927	20	62.5	476	6	US-10-467-657-5978	Sequence 5978, Ap
855	20	62.5	341	6	US-10-515-481-6	Sequence 6, App11	928	20	62.5	476	6	US-10-467-657-7518	Sequence 7518, Ap
856	20	62.5	341	6	US-10-515-481-9	Sequence 9, App11	929	20	62.5	481	7	US-11-090-439-16	Sequence 16, App1
857	20	62.5	341	6	US-10-515-481-12	Sequence 12, App1	930	20	62.5	482	6	US-10-517-939-104	Sequence 104, App
858	20	62.5	345	6	US-10-512-109-17	Sequence 17, App1	931	20	62.5	485	6	US-10-467-657-2488	Sequence 2498, Ap
859	20	62.5	346	6	US-10-512-109-15	Sequence 15, App1	932	20	62.5	486	7	US-11-210-316-10	Sequence 10, App1
860	20	62.5	346	6	US-11-174-150-33	Sequence 33, App1	933	20	62.5	496	6	US-10-467-657-2096	Sequence 2096, Ap
861	20	62.5	348	7	US-11-067-121-5	Sequence 5, App1	934	20	62.5	515	6	US-10-055-877-60	Sequence 60, App1
862	20	62.5	349	7	US-11-067-121-14	Sequence 14, App1	935	20	62.5	516	6	US-10-641-678-39	Sequence 39, App1
863	20	62.5	351	6	US-10-821-234-969	Sequence 969, App	936	20	62.5	516	6	US-10-641-678-40	Sequence 40, App1
864	20	62.5	352	6	US-10-517-939-226	Sequence 226, App	937	20	62.5	516	6	US-10-641-678-41	Sequence 41, App1
865	20	62.5	354	6	US-10-995-561-717	Sequence 717, App	938	20	62.5	540	6	US-10-641-678-60	Sequence 60, App1
866	20	62.5	356	7	US-11-012-762-46	Sequence 46, App1	939	20	62.5	540	7	US-11-212-443-167	Sequence 167, App
867	20	62.5	356	7	US-11-012-762-46	Sequence 46, App1	940	20	62.5	542	6	US-10-517-939-262	Sequence 262, App
868	20	62.5	358	6	US-10-793-626-18	Sequence 18, App1	941	20	62.5	544	6	US-10-719-311-18	Sequence 18, App1
869	20	62.5	360	6	US-10-517-939-184	Sequence 184, App	942	20	62.5	546	6	US-11-143-980-38	Sequence 38, App1
870	20	62.5	361	6	US-10-517-939-212	Sequence 212, App	943	20	62.5	556	6	US-10-995-561-766	Sequence 766, App
871	20	62.5	361	6	US-11-012-762-42	Sequence 42, App1	944	20	62.5	556	6	US-10-995-561-767	Sequence 767, App
872	20	62.5	362	7	US-11-012-762-30	Sequence 30, App1	945	20	62.5	579	6	US-10-528-673-2	Sequence 2, App11
873	20	62.5	362	7	US-11-012-762-32	Sequence 32, App1	946	20	62.5	585	6	US-10-793-626-2124	Sequence 2124, Ap
874	20	62.5	363	6	US-10-995-561-541	Sequence 541, App1	947	20	62.5	590	7	US-11-131-212-73	Sequence 73, App1
875	20	62.5	363	6	US-10-454-437-94	Sequence 94, App1	948	20	62.5	595	7	US-11-102-476-33	Sequence 33, App1
876	20	62.5	369	6	US-10-763-712A-43	Sequence 43, App1	949	20	62.5	598	6	US-10-719-311-16	Sequence 16, App1
877	20	62.5	369	6	US-10-763-712A-45	Sequence 45, App1	950	20	62.5	604	6	US-10-517-939-34	Sequence 34, App1
878	20	62.5	369	6	US-10-763-712A-106	Sequence 106, App	951	20	62.5	606	6	US-10-055-877-58	Sequence 58, App1
879	20	62.5	370	7	US-11-121-731A-2	Sequence 2, App11	952	20	62.5	606	7	US-11-052-554A-163	Sequence 163, App
880	20	62.5	370	7	US-11-121-731A-2	Sequence 2, App11	953	20	62.5	607	6	US-11-080-991-88	Sequence 88, App1
881	20	62.5	372	6	US-10-793-626-2840	Sequence 2840, Ap	954	20	62.5	609	7	US-10-517-939-310	Sequence 310, App
882	20	62.5	376	6	US-10-995-561-540	Sequence 540, App	955	20	62.5	610	6	US-10-606-302-1	Sequence 1, App11
883	20	62.5	376	6	US-10-793-626-490	Sequence 490, App	956	20	62.5	612	6	US-10-467-657-764	Sequence 764, App
884	20	62.5	376	6	US-10-793-626-2260	Sequence 2260, Ap	957	20	62.5	633	7	US-11-119-683-3	Sequence 3, App11
885	20	62.5	377	7	US-11-121-731A-3	Sequence 3, App11	958	20	62.5	634	7	US-10-632-150-26	Sequence 26, App1
886	20	62.5	378	7	US-11-185	Sequence 12, App1	959	20	62.5	634	7	US-11-073-457-26	Sequence 26, App1
887	20	62.5	379	7	US-11-052-554A-193	Sequence 193, App	960	20	62.5	634	7	US-11-073-460-26	Sequence 26, App1
888	20	62.5	380	6	US-10-989-313-4	Sequence 4, App11	961	20	62.5	635	6	US-10-821-234-1673	Sequence 1673, Ap
889	20	62.5	380	7	US-11-185-230-2	Sequence 2, App11	962	20	62.5	655	6	US-10-055-877-40	Sequence 40, App1
890	20	62.5	381	6	US-10-517-939-326	Sequence 326, App	963	20	62.5	672	6	US-10-689-742-70	Sequence 70, App1
891	20	62.5	383	6	US-10-989-313-2	Sequence 2, App11	964	20	62.5	674	6	US-10-501-039-10	Sequence 10, App1
892	20	62.5	386	7	US-11-012-762-44	Sequence 44, App1	965	20	62.5	678	6	US-10-055-877-202	Sequence 102, App
893	20	62.5	387	7	US-11-074-176-232	Sequence 232, App	966	20	62.5	687	6	US-10-055-877-199	Sequence 199, App
894	20	62.5	395	6	US-10-467-657-2992	Sequence 2992, Ap	967	20	62.5	687	6	US-10-055-877-201	Sequence 201, App
895	20	62.5	397	6	US-10-821-234-1020	Sequence 1020, Ap	968	20	62.5	711	6	US-10-517-939-4	Sequence 4, App11
896	20	62.5	397	6	US-10-878-556A-165	Sequence 165, App	969	20	62.5	716	6	US-10-467-657-6200	Sequence 6200, Ap
897	20	62.5	398	6	US-10-828-033-23	Sequence 23, App1	970	20	62.5	718	6	US-10-878-556A-97	Sequence 97, App1
898	20	62.5	398	6	US-10-995-561-719	Sequence 719, App	971	20	62.5	728	6	US-10-467-657-8376	Sequence 8376, Ap
899	20	62.5	405	6	US-10-793-626-232	Sequence 232, App	972	20	62.5	730	7	US-11-082-389-358	Sequence 358, App
900	20	62.5	406	7	US-11-075-185-23	Sequence 23, App1	973	20	62.5	730	7	US-11-113-424-50	Sequence 50, App1
901	20	62.5	406	7	US-11-075-185-23	Sequence 23, App1	974	20	62.5	732	6	US-10-518-599-22	Sequence 22, App1

975 20 62.5 733 6 US-10-821-234-1147 Sequence 1147, Ap
976 20 62.5 734 6 US-10-719-311-4 Sequence 4, Appl
977 20 62.5 734 6 US-11-145-035-24 Sequence 24, Appl
978 20 62.5 744 6 US-10-467-657-1936 Sequence 1936, Ap
979 20 62.5 751 6 US-10-467-657-1418 Sequence 1418, Ap
980 20 62.5 751 6 US-11-114-906-8 Sequence 8, Appl
981 20 62.5 756 7 US-11-074-176-202 Sequence 202, App
982 20 62.5 761 7 US-11-212-443-22 Sequence 22, Appl
983 20 62.5 764 7 US-11-114-906-6 Sequence 6, Appl
984 20 62.5 769 6 US-10-485-517-401 Sequence 401, App
985 20 62.5 794 6 US-10-793-626-1050 Sequence 1050, Ap
986 20 62.5 825 6 US-11-074-176-20 Sequence 20, Appl
987 20 62.5 838 6 US-10-645-441-9 Sequence 9, Appl
988 20 62.5 838 7 US-11-114-906-40 Sequence 40, Appl
989 20 62.5 839 7 US-11-050-804-4 Sequence 4, Appl
990 20 62.5 844 6 US-10-763-712A-48 Sequence 48, Appl
991 20 62.5 851 7 US-11-114-906-38 Sequence 38, Appl
992 20 62.5 864 7 US-11-114-906-4 Sequence 4, Appl
993 20 62.5 865 6 US-10-467-9628-33 Sequence 33, Appl
994 20 62.5 869 6 US-10-453-372-50 Sequence 50, Appl
995 20 62.5 870 7 US-11-114-906-2 Sequence 2, Appl
996 20 62.5 872 7 US-11-077-550-145 Sequence 145, App
997 20 62.5 879 7 US-11-077-550-143 Sequence 143, App
998 20 62.5 887 7 US-11-077-550-147 Sequence 147, App
999 20 62.5 894 6 US-10-485-517-416 Sequence 416, App
1000 20 62.5 903 7 US-11-057-058-65 Sequence 65, Appl

ALIGNMENTS

RESULT 1
US-10-665-658-14
; Sequence 14, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-665-658-14

Query Match 100.0%; Score 32; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 1 SGGSTLOS 7

RESULT 2
US-10-665-658-61
; Sequence 61, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; TYPE: Amino Acid
; LENGTH: 7 amino acids
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-10-665-658-61

Query Match 100.0%; Score 32; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTLOS 7
Db 1 SGGSTLOS 7

RESULT 3
US-11-107-028-49
; Sequence 49, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 49
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-49

Query Match 100.0%; Score 32; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCSSTLOS 7
|||||
Db 50 SCSSTLOS 56

RESULT 4
US-11-107-028-51
; Sequence 51, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-107-028-51

Query Match 100.0%; Score 32; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCSSTLOS 7
|||||
Db 50 SCSSTLOS 56

RESULT 5
US-10-665-658-1
; Sequence 1, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-665-658-1
Query Match 100.0%; Score 32; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCSSTLOS 7
|||||
Db 50 SCSSTLOS 56

RESULT 6
US-10-665-658-2
; Sequence 2, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-665-658-2

Query Match 100.0%; Score 32; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.66; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 SGGSTLOS 7
Db 50 SGGSTLOS 56

RESULT 7
US-10-665-658-63
Sequence 63, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardiou, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-665-658-63

Query Match 90.6%; Score 29; DB 6; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.2e+04; 0; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

QY 1 SGGSTLOS 7
Db 1 AGSTLOS 7

RESULT 8
US-10-665-658-64
Sequence 64, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardiou, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-665-658-64

Query Match 90.6%; Score 29; DB 6; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.2e+04; 0; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

QY 1 SGGSTLOS 7
Db 1 AGSTLOS 7

Db 1 SGATLQS 7

RESULT 9

US-10-665-658-65
; Sequence 65, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: Amino Acid
; TOPOLOGY: <Unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-665-658-65

Query Match 84.4%; Score 27; DB 6; Length 7;
Best Local Similarity 85.7%; Pred. No. 5.2e+04;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLQS 7
Db 1 SGSALQS 7

RESULT 10

US-10-467-657-1544
; Sequence 1544, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1544
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1544

Query Match 84.4%; Score 27; DB 6; Length 275;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLQS 7
Db 238 SGSTLQA 244

RESULT 11

US-11-062-225-3
; Sequence 3, Application US/11062225
; Publication No. US20050272060A1
; GENERAL INFORMATION:
; APPLICANT: Tuli, Rakesh
; TITLE OF INVENTION: CHIMERIC & ENDOTOXIN PROTEIN WITH
; FILE REFERENCE: 07064-014001
; CURRENT APPLICATION NUMBER: US/11/062,225
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: US/10/107,581
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-062-225-3

Query Match 84.4%; Score 27; DB 7; Length 609;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLQS 7
Db 556 SGSNTLQS 562

RESULT 12

US-11-062-225-4
; Sequence 4, Application US/11062225
; Publication No. US20050272060A1
; GENERAL INFORMATION:
; APPLICANT: Tuli, Rakesh
; TITLE OF INVENTION: CHIMERIC & ENDOTOXIN PROTEIN WITH
; FILE REFERENCE: 07064-014001
; CURRENT APPLICATION NUMBER: US/11/062,225
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: US/10/107,581
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-062-225-4

Query Match 84.4%; Score 27; DB 7; Length 609;

Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 556 SGSNLOS 562

RESULT 13
US-11-062-225-5

; Sequence 5, Application US/11062225
; Publication No. US20050272060A1

; GENERAL INFORMATION:

; APPLICANT: Tull, Rakesh

; TITLE OF INVENTION: CHIMERIC & ENDOTOXIN PROTEIN WITH
EXTRAORDINARILY HIGH INSECTICIDAL ACTIVITY

; FILE REFERENCE: 07064-014001

; CURRENT APPLICATION NUMBER: US/11/062,225

; PRIOR FILING DATE: 2005-02-18

; PRIOR APPLICATION NUMBER: US/10/107,581

; PRIOR FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 609

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-11-062-225-5

Query Match 84.4%; Score 27; DB 7; Length 609;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 556 SGSNLOS 562

RESULT 14
US-11-062-225-6

; Sequence 6, Application US/11062225
; Publication No. US20050272060A1

; GENERAL INFORMATION:

; APPLICANT: Tull, Rakesh

; TITLE OF INVENTION: CHIMERIC & ENDOTOXIN PROTEIN WITH
EXTRAORDINARILY HIGH INSECTICIDAL ACTIVITY

; FILE REFERENCE: 07064-014001

; CURRENT APPLICATION NUMBER: US/11/062,225

; PRIOR FILING DATE: 2005-02-18

; PRIOR APPLICATION NUMBER: US/10/107,581

; PRIOR FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 609

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-11-062-225-6

Query Match 84.4%; Score 27; DB 7; Length 609;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 556 SGSNLOS 562

RESULT 15
US-11-062-225-7

; Sequence 7, Application US/11062225
; Publication No. US20050272060A1

; GENERAL INFORMATION:

; APPLICANT: Tull, Rakesh

; TITLE OF INVENTION: CHIMERIC & ENDOTOXIN PROTEIN WITH
EXTRAORDINARILY HIGH INSECTICIDAL ACTIVITY

; FILE REFERENCE: 07064-014001

; CURRENT APPLICATION NUMBER: US/11/062,225

; PRIOR FILING DATE: 2005-02-18

; PRIOR APPLICATION NUMBER: US/10/107,581

; PRIOR FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 609

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-11-062-225-7

Query Match 84.4%; Score 27; DB 7; Length 609;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 556 SGSNLOS 562

RESULT 16
US-11-062-225-8

; Sequence 8, Application US/11062225
; Publication No. US20050272060A1

; GENERAL INFORMATION:

; APPLICANT: Tull, Rakesh

; TITLE OF INVENTION: CHIMERIC & ENDOTOXIN PROTEIN WITH
EXTRAORDINARILY HIGH INSECTICIDAL ACTIVITY

; FILE REFERENCE: 07064-014001

; CURRENT APPLICATION NUMBER: US/11/062,225

; PRIOR FILING DATE: 2005-02-18

; PRIOR APPLICATION NUMBER: US/10/107,581

; PRIOR FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 609

; TYPE: PRT

; ORGANISM: Bacillus thuringiensis

US-11-062-225-8

Query Match 84.4%; Score 27; DB 7; Length 609;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
|||
Db 556 SGSNLOS 562

RESULT 17
US-11-219-995-9

; Sequence 9, Application US/11219995
; Publication No. US2006003379A1

; GENERAL INFORMATION:

; APPLICANT: Miyazono, Kohel

; TITLE OF INVENTION: SMAD6 AND USES THEREOF

; FILE REFERENCE: 10461-70148US01

; CURRENT APPLICATION NUMBER: US/11/219,995

; PRIOR FILING DATE: 2005-09-06

; PRIOR APPLICATION NUMBER: US 10/390,553

; PRIOR FILING DATE: 2003-03-17

; PRIOR APPLICATION NUMBER: US 09/923,922

; PRIOR FILING DATE: 2001-08-07

; PRIOR APPLICATION NUMBER: US 09/096,776

; PRIOR FILING DATE: 1998-06-12

; PRIOR APPLICATION NUMBER: US 60/049,990

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; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: US 60/053,040
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: US 60/066,173
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-219-995-9

Query Match
Best Local Similarity 81.2%; Score 26; DB 7; Length 552;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTLOS 7
DB 144 SGLTLOS 150

RESULT 18
US-10-467-657-102
; Sequence 102, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 102
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-102

Query Match
Best Local Similarity 78.1%; Score 25; DB 6; Length 154;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSTLOS 7
DB 108 GATLOS 113

RESULT 19
US-10-467-657-7744
; Sequence 7744, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
```

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; SEQ ID NO 7744
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-7744

Query Match
Best Local Similarity 78.1%; Score 25; DB 6; Length 154;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSTLOS 7
DB 108 GATLOS 113

RESULT 20
US-10-467-657-946
; Sequence 946, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 946
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-946

Query Match
Best Local Similarity 78.1%; Score 25; DB 6; Length 485;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTLO 6
DB 328 SGSTLE 333

RESULT 21
US-10-131-826A-210
; Sequence 210, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Ellen
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
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; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 210
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-210
```

```

Query Match          78.1%; Score 25; DB 6; Length 519;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SGSTLQ 6
       :|||||
Db      98 NGSSTLQ 103
```

```

RESULT 22
US-10-520-655-1
; Sequence 1, Application US/10520655
; Publication No. US2006000330A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
; APPLICANT: DIDBERG Otto
; APPLICANT: VERNET Thierly
; APPLICANT: MOUZ Nicolas
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PBP2X MINI-PROTEIN AND USES THEREOF.
; FILE REFERENCE: P263FR798
; CURRENT APPLICATION NUMBER: US/10/520,655
; CURRENT FILING DATE: 2005-01-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-520-655-1
```

```

Query Match          78.1%; Score 25; DB 6; Length 551;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SGSTLQ 6
       :|||||
Db      524 SGSTVQ 529
```

```

RESULT 23
US-10-623-155-169
; Sequence 169, Application US/10623155
```

```

; Publication No. US2005026116A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 169
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-169
```

```

Query Match          78.1%; Score 25; DB 6; Length 592;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 SGSTLQ 7
       :|||||
Db      436 SGSTHS 442
```

```

RESULT 24
US-10-467-657-5218
; Sequence 5218, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5218
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5218
```

```

Query Match          78.1%; Score 25; DB 6; Length 597;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SGSTLQ 6
       :|||||
Db      525 SGAHTLQ 530
```

```

RESULT 25
US-10-623-155-170
; Sequence 170, Application US/10623155
; Publication No. US2005026116A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
```

```
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-170
```

```
Query Match      78.1%; Score 25; DB 6; Length 791;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 SGGTLOS 7
        |||||:|
Db      436 SGGTTHS 442
```

```
RESULT 26
US-10-623-155-430
; Sequence 430, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 430
; LENGTH: 881
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-430
```

```
Query Match      78.1%; Score 25; DB 6; Length 881;
Best Local Similarity 71.4%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 SGGTLOS 7
        |||||:|
Db      413 SGGTTHS 419
```

```
RESULT 27
US-10-623-155-357
; Sequence 357, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-357
```

```
Query Match      78.1%; Score 25; DB 6; Length 920;
```

```
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 SGGTLOS 7
        |||||:|
Db      413 SGGTTHS 419
```

```
RESULT 28
US-10-623-155-161
; Sequence 161, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 943
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-161
```

```
Query Match      78.1%; Score 25; DB 6; Length 943;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 SGGTLOS 7
        |||||:|
Db      436 SGGTTHS 442
```

```
RESULT 29
US-11-057-058-67
; Sequence 67, Application US/11057058
; Publication No. US2005024400A1
; GENERAL INFORMATION:
; APPLICANT: Lebowitz, Jonathan
; APPLICANT: Maga, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SYM-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-057-058-67
```

```
Query Match      78.1%; Score 25; DB 7; Length 966;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 SGGTLOS 7
        |||||:|
Db      890 SGGTTHS 896
```

```
RESULT 30
US-11-067-811-4
; Sequence 4, Application US/11067811
; Publication No. US20050260688A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Morgan, Bruce A
; APPLICANT: Bishell-SciJffers, David
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HAIR GROWTH
; FILE REFERENCE: 10287-083001
; CURRENT APPLICATION NUMBER: US/11/067,811
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 60/548,272
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1113
; TYPE: PRT
; ORGANISM: Mus Musculus
; US-11-067-811-4

Query Match          78.1%; Score 25; DB 7; Length 1113;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGGSTLQ 6
Db      828 NGSSTLQ 833

RESULT 31
US-10-647-956A-2
; Sequence 2, Application US/10647956A
; Publication No. US20050251878A1
; GENERAL INFORMATION:
; APPLICANT: French-Constant, Richard
; APPLICANT: Bowen, David
; APPLICANT: Rochelleau, Thomas
; APPLICANT: Watefield, Nicholas
; TITLE OF INVENTION: DNA SEQUENCES FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: 61645
; CURRENT APPLICATION NUMBER: US/10/647,956A
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/817,514
; PRIOR FILING DATE: CURRENT FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/191806
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 2516
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
; US-10-647-956A-2

Query Match          78.1%; Score 25; DB 6; Length 2516;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GSTLQS 7
Db      2037 GSTLQ 2042

RESULT 32
US-10-925-366A-158
; Sequence 158, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Demildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Phillip
; APPLICANT: Bastran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
```

```

; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 158
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Antibody Domain
; US-10-925-366A-158

Query Match          75.0%; Score 24; DB 6; Length 108;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SGGSTLQS 7
Db      50 NGSSTLQS 56

RESULT 33
US-10-925-366A-160
; Sequence 160, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Demildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Phillip
; APPLICANT: Bastran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
```



```

; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 160
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Antibody Domain
US-10-925-366A-160

Query Match      75.0%; Score 24; DB 6; Length 108;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY      1 SGSTLOS 7
Db      50 NGSVALS 56

RESULT 34
US-10-925-366A-169
; Sequence 169, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Demildt, Rudolph M.T.
; APPLICANT: Benjamin, Moolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 169
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Antibody Domain
US-10-925-366A-169

Query Match      75.0%; Score 24; DB 6; Length 108;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;
```

```

QY      1 SGSTLOS 7
Db      50 NGSVALS 56

RESULT 35
US-10-689-742-2
; Sequence 2, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-2

Query Match      75.0%; Score 24; DB 6; Length 263;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      2 SGSTLOS 7
Db      44 CGTLOS 49

RESULT 36
US-10-793-626-588
; Sequence 588, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 588
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-588

Query Match      75.0%; Score 24; DB 6; Length 272;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 SGSTLOS 7
Db      51 TGSTLES 57
```

RESULT 37
US-10-858-730-122
; Sequence 122, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doren, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Thermobifida fusca
US-10-858-730-122

Query Match 75.0%; Score 24; DB 6; Length 312;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GSKTLOS 7
DB 95 TGHTLOS 101
RESULT 38
US-11-016-564-15
; Sequence 15, Application US/11016564
; Publication No. US20050287146A1
; GENERAL INFORMATION:
; APPLICANT: INHIBITEX, INC.
; TITLE OF INVENTION: METHOD OF INHIBITING CANDIDA-RELATED INFECTIONS
; FILE REFERENCE: P08140US03/BAS
; CURRENT APPLICATION NUMBER: US/11/016,564
; CURRENT FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: US 60/566,082
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: US 60/561,540
; PRIOR FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: US 60/530,654
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Candida albicans
US-11-016-564-15

Query Match 75.0%; Score 24; DB 7; Length 343;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GSKTLOS 7
DB 278 GSKLOS 283

RESULT 39
US-11-052-554A-194
; Sequence 194, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 194
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Shigella flexneri 2a str. 2457T
US-11-052-554A-194

Query Match 75.0%; Score 24; DB 7; Length 365;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSKTLOS 7
DB 315 GSKLOS 321

RESULT 40
US-11-052-554A-258
; Sequence 258, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 258
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes MGAS8232
US-11-052-554A-258

Query Match 75.0%; Score 24; DB 7; Length 495;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSKTLOS 7
DB 19 GSKLOS 24

RESULT 41
US-11-145-035-15
; Sequence 15, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS

```
FILE REFERENCE: 28335/41335
CURRENT APPLICATION NUMBER: US/11/145,035
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 10/038,972
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.3
SEQ ID NO 15
LENGTH: 533
TYPE: PRT
ORGANISM: adeno-associated virus 2
US-11-145-035-15

Query Match
Best Local Similarity 71.4%; Score 24; DB 7; Length 533;
Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 250 SGTLOS 256

RESULT 42
US-11-104-110-9
Sequence 9, Application US/11/104,110
Publication No. US2006002916A1
GENERAL INFORMATION:
APPLICANT: Ruglies, Sandra
APPLICANT: Nguyen, Jack
TITLE OF INVENTION: CLEAVAGE OF VEGF AND VEGF RECEPTOR BY WILDTYPE AND MUTANT MT-SPL
FILE REFERENCE: 25840-502
CURRENT APPLICATION NUMBER: US/11/104,110
CURRENT FILING DATE: 2005-04-12
PRIOR APPLICATION NUMBER: 60/561,720
PRIOR FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 10/677,977
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,388
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 592
TYPE: PRT
ORGANISM: Homo sapiens
US-11-104-110-9

Query Match
Best Local Similarity 71.4%; Score 24; DB 7; Length 592;
Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 583 SGTLOS 589

RESULT 43
US-11-145-035-14
Sequence 14, Application US/11/145,035
Publication No. US20050287122A1
GENERAL INFORMATION:
APPLICANT: Bartlett et al.
TITLE OF INVENTION: AAV VECTORS AND METHODS
FILE REFERENCE: 28335/41335
CURRENT APPLICATION NUMBER: US/11/145,035
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 10/038,972
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: US 60/260,124
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 45
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 14
LENGTH: 598
TYPE: PRT
ORGANISM: adeno-associated virus 2
US-11-145-035-14

Query Match
Best Local Similarity 71.4%; Score 24; DB 7; Length 598;
Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGTLOS 7
DB 315 SGTLOS 321

RESULT 44
US-10-131-826A-102
Sequence 102, Application US/10/131,826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 102
LENGTH: 607
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-102

Query Match
Best Local Similarity 83.3%; Score 24; DB 6; Length 607;
Pred. No. 2.9e+02;
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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGTLOS 7
|:|:|
Db 44 GGTLOS 49

RESULT 45
US-11-184-380-24

; Sequence 24, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chlorini, John
; APPLICANT: Kotlin, Robert M.
; TITLE OF INVENTION: AAVS NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT APPLICATION NUMBER: US/11/184,380
; PRIOR FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: synthetic construct
US-11-184-380-24

Query Match 75.0%; Score 24; DB 7; Length 735;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSGTLOS 7
|:|:|
Db 452 GGTLOS 458

RESULT 46
US-11-145-035-13
; Sequence 13, Application US/11145035
; Publication No. US20050287122A1
; GENERAL INFORMATION:
; APPLICANT: Bartlett et al.
; TITLE OF INVENTION: AAV VECTORS AND METHODS
; FILE REFERENCE: 28335/41335
; CURRENT APPLICATION NUMBER: US/11/145,035
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/038,972
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/260,124
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 735
; TYPE: PRT
; ORGANISM: adeno-associated virus 2
US-11-145-035-13

Query Match 75.0%; Score 24; DB 7; Length 735;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSGTLOS 7
|:|:|
Db 452 GGTLOS 458

RESULT 47
US-11-052-554A-341

; Sequence 341, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 341
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Shigella flexneri 2a str. 2457T
US-11-052-554A-341

Query Match 75.0%; Score 24; DB 7; Length 773;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSGTLOS 7
|:|:|
Db 214 GSGTLOS 220

RESULT 48
US-10-467-962B-4
; Sequence 4, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Bian, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 4
; LENGTH: 959
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-4

Query Match 75.0%; Score 24; DB 6; Length 959;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGTLOS 7
|:|:|
Db 216 GGTLOS 221

RESULT 49
US-10-995-561-905
; Sequence 905, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 905
; LENGTH: 1306
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-905
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Query Match          75.0%; Score 24; DB 6; Length 1306;
Best Local Similarity 71.4%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 SGGTLOS 7
        ||:||||
Db      1297 SGTTLSS 1303
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RESULT 50
US-10-995-561-904
; Sequence 904, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 904
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-904
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Query Match          75.0%; Score 24; DB 6; Length 1356;
Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      1 SGGTLOS 7
        ||:||||
Db      1347 SGTTLSS 1353
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Search completed: January 17, 2006, 12:13:35
Job time : 3.33333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:46:53 ; Search time 56.3182 Seconds
(without alignments)
70.215 Million cell updates/sec

Title: US-10-665-658-15

Perfect score: 52

Sequence: 1 OQHNEYPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database :

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	9	2 AAW62016	Aaw62016 Light cha
2	52	100.0	9	3 AAW82342	Aaw82342 Humanised
3	52	100.0	9	8 ADG39003	Adg39003 Humanised
4	52	100.0	9	8 ADRO3423	Adro3423 Humanised
5	52	100.0	107	9 AEA62455	Aea62455 Mouse 1B3
6	52	100.0	108	2 AAW62017	Aaw62017 Light cha
7	52	100.0	108	2 AAW63528	Aaw63528 Murine MH
8	52	100.0	108	2 AAW63529	Aaw63529 Humanised
9	52	100.0	108	3 AAY82344	Aay82344 Murine MH
10	52	100.0	108	3 AAY82343	Aay82343 Humanised
11	52	100.0	108	8 ADG38989	Adg38989 Mouse ant
12	52	100.0	108	8 ADG38990	Adg38990 Humanised
13	52	100.0	108	8 ADRO3365	Adro3365 Humanised
14	52	100.0	108	8 ADRO3364	Adro3364 Murine MH
15	52	100.0	108	8 ADM38457	Adm38457 CD11a 11g
16	52	100.0	108	8 ADM80645	Adm80645 Humanized
17	52	100.0	109	2 AAY29449	Aay29449 Human 11g
18	52	100.0	109	3 AAY77752	Aay77752 Human 11g
19	52	100.0	109	3 AAB30309	Aab30309 Human 11g
20	52	100.0	109	6 ABU13786	Abu13786 Human 11g
21	52	100.0	109	7 ABUS9499	Abus9499 Human 11g
22	52	100.0	109	7 AAB39082	Aab39082 Human 11g
23	52	100.0	214	8 ADF11659	Adf11659 anti-CD11
24	47	90.4	101	5 ABB07177	Abb07177 Mouse 09

25	47	90.4	101	8 ADI26670	Adi26670 Mouse ant
26	47	90.4	107	9 ADV66159	Adv66159 Human BPC
27	47	90.4	107	9 ADZ83517	Adz83517 AntiBpCam
28	47	90.4	108	8 ADI26700	Adi26700 Mouse ant
29	47	90.4	242	2 AAY17957	Aay17957 Mouse scF
30	47	90.4	242	2 AAY17961	Aay17961 Mouse scF
31	47	90.4	242	2 AAY17959	Aay17959 Mouse scF
32	47	90.4	491	9 ADZ83409	Adz83409 C-termina
33	47	90.4	494	9 ADV66089	Adv66089 Anti-CD3-
34	47	90.4	497	9 ADV66123	Adv66123 Anti-CD3-
35	47	90.4	497	9 ADV66125	Adv66125 Anti-CD3-
36	47	90.4	506	9 ADZ83427	Adz83427 Deimmuniz
37	47	90.4	515	9 ADV66113	Adv66113 Anti-CD3-
38	46	88.5	9	8 ADRO3427	Adro3427 Humanised
39	46	88.5	234	2 AAR64819	Aar64819 OMV10 SC
40	44	84.6	9	8 ADRO3426	Adro3426 Humanised
41	43	82.7	9	8 ADRO3428	Adro3428 Humanised
42	43	82.7	109	8 ADM38453	Adm38453 CD11a 11g
43	42	80.8	9	8 ADP47236	Adp47236 Human pho
44	42	80.8	9	8 ADRO3425	Adro3425 Humanised
45	42	80.8	9	9 ADX98316	Adx98316 Human ant
46	42	80.8	9	9 AEA45084	Aea45084 Apolipop
47	42	80.8	107	5 ABG77141	Abg77141 Anti-IGF-
48	42	80.8	107	7 ADC92785	Adc92785 Anti-huma
49	42	80.8	107	7 ADD05389	Add05389 Anti-MOCl
50	42	80.8	107	7 ADF09827	Adf09827 Human ant
51	42	80.8	107	7 ADK18843	Adk18843 Anti-huma
52	42	80.8	107	7 ADK18861	Adk18861 Anti-huma
53	42	80.8	107	7 ADK18590	Adk18590 Anti-huma
54	42	80.8	107	7 ADK18839	Adk18839 Anti-huma
55	42	80.8	107	7 ADK18594	Adk18594 Anti-huma
56	42	80.8	107	7 ADK18809	Adk18809 Anti-huma
57	42	80.8	107	7 ADK18805	Adk18805 Anti-huma
58	42	80.8	107	7 ADP03911	Adp03911 Murine-ex
59	42	80.8	107	7 ADP03917	Adp03917 Murine-ex
60	42	80.8	107	8 ADL25398	Adl25398 Human mbd
61	42	80.8	107	8 ADL25406	Adl25406 Human mbd
62	42	80.8	107	8 ADP22106	Adp22106 Human ant
63	42	80.8	107	8 ADP22134	Adp22134 Human ant
64	42	80.8	107	8 ADP22399	Adp22399 Human ant
65	42	80.8	107	8 ADP22138	Adp22138 Human ant
66	42	80.8	107	8 ADP22102	Adp22102 Human ant
67	42	80.8	107	8 ADP22270	Adp22270 Human ant
68	42	80.8	107	8 ADP22314	Adp22314 Human ant
69	42	80.8	107	8 ADP22367	Adp22367 Human ant
70	42	80.8	107	8 ADP22172	Adp22172 Human ant
71	42	80.8	107	8 ADP22302	Adp22302 Human ant
72	42	80.8	107	8 ADP22098	Adp22098 Human ant
73	42	80.8	107	8 ADP22122	Adp22122 Human ant
74	42	80.8	107	8 ADP22274	Adp22274 Human ant
75	42	80.8	107	8 ADP22350	Adp22350 Human ant
76	42	80.8	107	8 ADP22318	Adp22318 Human ant
77	42	80.8	107	8 ADP22346	Adp22346 Human ant
78	42	80.8	107	8 ADZ82848	Adz82848 Human ant
79	42	80.8	107	8 ADW96638	Adw96638 Human ger
80	42	80.8	107	9 ADW80210	Adw80210 Human ant
81	42	80.8	107	9 ADX98403	Adx98403 Human ant
82	42	80.8	108	7 ADK18849	Adk18849 Anti-huma
83	42	80.8	108	8 ADS16507	Ads16507 Human ant
84	42	80.8	108	8 ADS16565	Ads16565 Human ant
85	42	80.8	108	9 AEA45112	Aea45112 Apolipop
86	42	80.8	129	9 ADX98268	Adx98268 Human ant
87	42	80.8	168	8 ADS16614	Ads16614 Human ant
88	42	80.8	215	8 ADH10328	Adh10328 Anti-HIV-
89	42	80.8	236	3 AAY96297	Aay96297 Human IGF
90	42	80.8	3	3 AAB10863	Aab10863 S11-VBGP2
91	42	80.8	3	3 AAB10864	Aab10864 S11-scVGB
92	41	78.8	9	2 AAW93479	Aaw93479 max TTC8
93	41	78.8	9	3 AAB19759	Aab19759 Erythro
94	41	78.8	9	6 ABO10689	Abol0689 Murine E9
95	41	78.8	9	6 ABO10769	Abol0769 Murine E9
96	41	78.8	9	6 ABR44713	AbR44713 Murine E9
97	41	78.8	9	6 ABR44633	AbR44633 Murine J5

98	41	78.8	9	8	ADQ90855	Adg90855	Mouse com	171	41	78.8	492	8	ADQ91096	Adg91096	Antibody
99	41	78.8	9	8	ADQ90757	Adg90757	Mouse com	172	41	78.8	492	8	ADQ91098	Adg91098	Antibody
100	41	78.8	9	8	ADU67983	AdU67983	Mouse ant	173	41	78.8	492	8	ADQ91102	Adg91102	Antibody
101	41	78.8	9	8	ADU67885	AdU67885	Mouse ant	174	41	78.8	492	8	ADQ91078	Adg91078	Antibody
102	41	78.8	9	9	ADV50608	Adv50608	Murine/Ra	175	41	78.8	507	5	ABG71552	Abg71552	Murine sc
103	41	78.8	9	9	ADW04805	Adw04805	PAP-A im	176	40	76.9	109	8	ADG25815	Adg25815	Antic-CD30
104	41	78.8	9	9	ADZ45564	Adz45564	Murine fa	177	40	76.9	130	3	AAV56737	AAV56737	Antino aci
105	41	78.8	9	9	ADZ45508	Adz45508	Murine fa	178	40	76.9	268	8	ADR70385	Adr70385	Polioviru
106	41	78.8	9	9	AEA45083	Aea45083	Apolipop	179	40	76.9	268	8	ADR70386	Adr70386	Polioviru
107	41	78.8	9	9	AEA46155	Aea46155	Apolipop	180	39	75.0	9	3	ABR30600	AbR30600	Antic-IGE
108	41	78.8	102	3	AAV56683	AAV56683	Humanized	181	39	75.0	9	8	ADP47239	AdP47239	Human pho
109	41	78.8	107	2	AAW47087	AAW47087	Mouse J59	182	39	75.0	105	3	ABR30583	AbR30583	Antic-IGE
110	41	78.8	107	2	AAW90375	AAW90375	J591 mono	183	39	75.0	107	8	ADT88867	AdT88867	Human IGF
111	41	78.8	107	2	AAW36226	AAW36226	Monoclon	184	39	75.0	107	8	ADT88874	AdT88874	Human IGF
112	41	78.8	107	2	AAV56680	AAV56680	Anti-eyrt	185	39	75.0	127	6	AAE37204	Aae37204	Human AB-
113	41	78.8	107	6	ABO10753	AbO10753	Variable	186	39	75.0	127	6	AAE16223	Aae16223	Anti-huma
114	41	78.8	107	6	ABO10705	AbO10705	Variable	187	39	75.0	128	7	ABU64274	AbU64274	Human C40
115	41	78.8	107	6	ABO10703	AbO10703	Variable	188	39	75.0	168	7	ABR84721	AbR84721	Vector pG
116	41	78.8	107	6	ABR44614	AbR44614	Murine de	189	39	75.0	168	7	ABR84720	AbR84720	Vector pG
117	41	78.8	107	6	ABR44647	AbR44647	Murine J5	190	39	75.0	211	3	ABR30592	AbR30592	Variable
118	41	78.8	107	6	ABR44697	AbR44697	Murine E9	191	39	75.0	224	4	ABR75044	AbR75044	TRO005 Hu
119	41	78.8	107	6	ABR44649	AbR44649	Murine U5	192	39	75.0	674	4	ABR66321	AbR66321	Drosophil
120	41	78.8	107	6	ABR44616	AbR44616	Murine de	193	38	73.1	9	5	AAE19662	Aae19662	Human tum
121	41	78.8	107	6	ADQ91074	AdQ91074	Anti-EPCA	194	38	73.1	9	7	ABR82933	AbR82933	Antic-huma
122	41	78.8	107	8	ADQ90771	AdQ90771	Mouse J59	195	38	73.1	9	8	ADQ07651	AdQ07651	Lignt cha
123	41	78.8	107	8	ADQ90838	AdQ90838	Mouse E99	196	38	73.1	9	9	ADQ26406	AdQ26406	Antic-EGFR
124	41	78.8	107	8	ADU67966	AdU67966	Mouse ant	197	38	73.1	9	9	ADX26938	AdX26938	Murine mo
125	41	78.8	107	8	ADU67901	AdU67901	Mouse ant	198	38	73.1	9	9	ADY26701	AdY26701	Human ant
126	41	78.8	107	8	ADU67899	AdU67899	Mouse ant	199	38	73.1	9	9	ABR21693	AbR21693	Antic-Nogo
127	41	78.8	107	8	AEA62498	Aea62498	Anti-C35	200	38	73.1	9	9	ABR80872	AbR80872	Antibody
128	41	78.8	108	3	AAH19751	Aah19751	Erythro	201	38	73.1	10	9	AEA45471	Aea45471	Apolipop
129	41	78.8	108	3	AAH19752	Aah19752	Erythro	202	38	73.1	10	9	ABE00017	AbE00017	Novel den
130	41	78.8	108	3	AAH19749	Aah19749	Erythro	203	38	73.1	10	9	ABE00097	AbE00097	Lead bind
131	41	78.8	108	3	AAH19780	Aah19780	Erythro	204	38	73.1	107	2	AAW01591	Aaw01591	Human TNF
132	41	78.8	108	8	ADG25829	AdG25829	Antic-CD30	205	38	73.1	107	5	AAE19664	Aae19664	Human TNF
133	41	78.8	108	8	ADQ90773	AdQ90773	Deimmun	206	38	73.1	107	5	AAE19665	Aae19665	Human TNF
134	41	78.8	108	8	ADQ76072	AdQ76072	Heterorec	207	38	73.1	107	6	ABR54901	AbR54901	Lignt cha
135	41	78.8	108	9	ADW04801	AdW04801	PAP-A im	208	38	73.1	107	6	ABR82945	AbR82945	Antic-EGFR
136	41	78.8	108	9	ADZ45505	Adz45505	Murine fa	209	38	73.1	107	7	ADK18596	AdK18596	Antic-huma
137	41	78.8	108	9	ADZ51187	Adz51187	Amino aci	210	38	73.1	107	7	ADK18867	AdK18867	Antic-huma
138	41	78.8	108	9	ADZ42061	Adz42061	Human ant	211	38	73.1	107	7	ADK18804	AdK18804	Antic-huma
139	41	78.8	108	9	AEA45111	Aea45111	Apolipop	212	38	73.1	107	8	ADJ25410	AdJ25410	Human mab
140	41	78.8	110	4	AAH49747	Aah49747	Anti-IP4/	213	38	73.1	107	8	ADQ26400	AdQ26400	Antic-EGFR
141	41	78.8	112	3	AAH19746	Aah19746	Erythro	214	38	73.1	107	8	ADX27047	AdX27047	Human gro
142	41	78.8	126	6	ABO10707	AbO10707	Variable	215	38	73.1	107	9	ADY26948	AdY26948	Human gro
143	41	78.8	126	6	ABR44651	AbR44651	Murine J5	216	38	73.1	107	9	ADY26697	AdY26697	Antic-NGF-
144	41	78.8	126	6	ADQ90779	AdQ90779	Deimmun	217	38	73.1	107	9	ABE00091	AbE00091	Novel den
145	41	78.8	126	8	ADU67907	AdU67907	Mouse ant	218	38	73.1	107	9	ABE19277	AbE19277	IGG kappa
146	41	78.8	132	9	ADV50600	Adv50600	Murine/Ra	219	38	73.1	108	5	AAE19684	Aae19684	Mouse-hum
147	41	78.8	159	9	ADV50602	Adv50602	Murine/Ra	220	38	73.1	108	5	ABG92887	AbG92887	Human imm
148	41	78.8	223	4	AAH75041	Aah75041	TRO005 Hu	221	38	73.1	108	8	ADQ07679	AdQ07679	Amino aci
149	41	78.8	224	4	AAH75041	Aah75041	TRO005 Hu	222	38	73.1	109	5	ADU75738	AdU75738	Murine ht
150	41	78.8	233	8	ADU68009	Adv68009	Mouse ant	223	38	73.1	109	5	AAU75738	Aau75738	AAV293 an
151	41	78.8	240	9	ADV50624	Adv50624	Murine/Ra	224	38	73.1	112	9	ABE00011	AbE00011	Novel den
152	41	78.8	240	9	ADV50622	Adv50622	Murine/Ra	225	38	73.1	112	9	ABE21720	AbE21720	Antic-NOGO
153	41	78.8	240	9	ADV50631	Adv50631	Murine/Ra	226	38	73.1	112	9	ABE08754	AbE08754	Antic-NOGO
154	41	78.8	244	9	ADV50612	Adv50612	Murine/Ra	227	38	73.1	123	2	AAH86317	Aah86317	Antic-IL-8
155	41	78.8	268	8	ADR70319	Adr70319	Polioviru	228	38	73.1	123	2	AAH23784	Aah23784	Monoclon
156	41	78.8	450	3	AAV44991	AAV44991	W98CFV-1	229	38	73.1	123	2	AAW31574	Aaw31574	Antic IL-8
157	41	78.8	451	8	ADR43339	AdR43339	scFv anti	230	38	73.1	123	2	AAW42317	Aaw42317	Antic IL-8
158	41	78.8	456	3	AAV44992	AAV44992	W98CFV-1	231	38	73.1	123	2	AAW33739	Aaw33739	Antic IL-8
159	41	78.8	480	7	ADH26642	Adh26642	Granzyme	232	38	73.1	123	2	AAW69305	Aaw69305	Murine an
160	41	78.8	492	8	ADQ91080	AdQ91080	Antibody	233	38	73.1	123	2	AAW40120	Aaw40120	Murine mo
161	41	78.8	492	8	ADQ91090	AdQ91090	Antibody	234	38	73.1	123	2	AAV29437	Aav29437	Murine 5-
162	41	78.8	492	8	ADQ91082	AdQ91082	Antibody	235	38	73.1	123	3	AAV77742	Aav77742	Murine an
163	41	78.8	492	8	ADQ91084	AdQ91084	Antibody	236	38	73.1	123	3	AAH30299	Aah30299	Murine an
164	41	78.8	492	8	ADQ91104	AdQ91104	Antibody	237	38	73.1	123	6	ABU13776	AbU13776	Mouse ant
165	41	78.8	492	8	ADQ91106	AdQ91106	Antibody	238	38	73.1	123	6	ABU59489	AbU59489	Mouse ant
166	41	78.8	492	8	ADQ91088	AdQ91088	Antibody	239	38	73.1	126	7	AAE39072	Aae39072	Murine 5.
167	41	78.8	492	8	ADQ91086	AdQ91086	Antibody	240	38	73.1	127	2	AAV24100	Aav24100	p24 monoc
168	41	78.8	492	8	ADQ91092	AdQ91092	Antibody	241	38	73.1	127	2	AAH81313	Aah81313	Rat monoc
169	41	78.8	492	8	ADQ91094	AdQ91094	Antibody	242	38	73.1	142	7	ABR82929	AbR82929	Antic-huma
170	41	78.8	492	8	ADQ91100	Adq91100	Antibody	243	38	73.1	152	8	ADR52390	AdR52390	Human ant

244	38	73.1	208	8	ADK90585	Adk90585 Grafted 1	317	36	69.2	9	2	AAV06698	AAV06698 Ab2 varia
245	38	73.1	208	8	ADL13415	Adl13415 Mouse-der	318	36	69.2	9	2	AAV05033	AAV05033 Tumour an
246	38	73.1	214	5	AAE19696	Aae19696 Antibody	319	36	69.2	9	2	AAV05031	AAV05031 Tumour an
247	38	73.1	214	7	ADK01486	Adk01486 CDP870.1i	320	36	69.2	9	4	AAE62996	AAE62996 Complemen
248	38	73.1	214	8	ADK73140	Adk73140 Humanized	321	36	69.2	9	4	AAE62990	AAE62990 Complemen
249	38	73.1	214	8	ADH34232	Adh34232 Anti-huma	322	36	69.2	9	7	ADK82784	Adk82784 CDR regio
250	38	73.1	214	8	ADN98361	Adn98361 Human IgG	323	36	69.2	9	7	ADK82780	Adk82780 CDR regio
251	38	73.1	214	8	ADQ07672	Adq07672 Amino aci	324	36	69.2	9	7	ADK82780	Adk82780 CDR regio
252	38	73.1	214	8	ADU86568	Adu86568 Immunoglo	325	36	69.2	9	8	ADL27479	Adl27479 CDR from
253	38	73.1	214	8	ADU86567	Adu86567 Immunoglo	326	36	69.2	9	8	ADU39684	Adu39684 Human 5B5
254	38	73.1	214	9	ADK27044	Adk27044 Murine hT	327	36	69.2	9	8	ADU36528	Adu36528 Human ant
255	38	73.1	214	9	ADY26729	Ady26729 Anti-NGF-	328	36	69.2	9	8	ADU36540	Adu36540 Human ant
256	38	73.1	237	2	AAE86319	Aae86319 Anti-IL-8	329	36	69.2	9	8	ADU36522	Adu36522 Human ant
257	38	73.1	237	2	AAW33786	Aaw33786 Chimeric	330	36	69.2	9	8	ADU36516	Adu36516 Human ant
258	38	73.1	237	2	AAW31576	Aaw31576 Chimeric	331	36	69.2	9	8	ADU36534	Adu36534 Human ant
259	38	73.1	237	2	AAW42319	Aaw42319 Murine va	332	36	69.2	9	8	ADP22420	Adp22420 Human ger
260	38	73.1	237	2	AAW33741	Aaw33741 Chimeric	333	36	69.2	9	8	ADK82731	Adk82731 Mouse lig
261	38	73.1	237	2	AAW69307	Aaw69307 Anti-IL-8	334	36	69.2	9	8	ADT75013	Adt75013 Murine i
262	38	73.1	237	2	AAW40122	Aaw40122 Mab 5.12.	335	36	69.2	9	9	ADW77458	Adw77458 Human pla
263	38	73.1	237	2	AAW29446	Aaw29446 5.12.14 L	336	36	69.2	9	9	ADZ35823	Adz35823 Anti-glyc
264	38	73.1	237	3	AAW77744	Aaw77744 Chimeric	337	36	69.2	9	9	AEA38750	Aea38750 Human ger
265	38	73.1	237	3	AAW30301	Aaw30301 5-12-14 a	338	36	69.2	9	9	AEA45570	Aea45570 Apolipopo
266	38	73.1	237	6	ABU13778	Abu13778 Mouse ant	339	36	69.2	9	9	ABE20795	Abe20795 M-CSF spe
267	38	73.1	237	6	ABU59491	Abu59491 Mouse ant	340	36	69.2	9	9	ABE20795	Abe20795 M-CSF spe
268	38	73.1	237	6	AAE39074	Aae39074 Murine 5.	341	36	69.2	14	6	ABE5894	AbE5894 CDR3-junc
269	38	73.1	240	5	AAE36053	Aae36053 Human WIC	342	36	69.2	80	4	AAU32265	Aau32265 Novel hum
270	38	73.1	243	5	ABP46003	Abp46003 Human Bly	343	36	69.2	97	6	ABG77139	Abg77139 Human mab
271	38	73.1	243	5	ABP45932	Abp45932 Human Bly	344	36	69.2	100	8	ADR28544	Adr28544 Human ant
272	38	73.1	243	5	ADG96880	Adg96880 Single ch	345	36	69.2	100	8	ADK33828	Adk33828 Human ant
273	38	73.1	243	7	ADG96759	Adg96759 Single ch	346	36	69.2	104	7	ABO33828	AbO33828 Human ant
274	38	73.1	243	7	AAE82896	Aae82896 Anti-huma	347	36	69.2	104	7	AAW21938	Aaw21938 Anti-glyc
275	37	71.2	9	4	ADK98313	Adk98313 Human ant	348	36	69.2	107	2	AAW15939	Aaw15939 Variable
276	37	71.2	101	2	AAV34316	Aav34316 IgG anti-b	349	36	69.2	107	2	AAW59168	Aaw59168 Mouse pAF
277	37	71.2	102	2	ADY39435	Ady39435 Anti-Tie	350	36	69.2	107	2	AAW78434	Aaw78434 Antibody
278	37	71.2	102	2	AAW86138	Aaw86138 Protein s	351	36	69.2	107	2	AAW78434	Aaw78434 Antibody
279	37	71.2	107	2	AAW86137	Aaw86137 Murine 70	352	36	69.2	107	2	AAW05268	Aaw05268 Antibody
280	37	71.2	107	2	AAW86136	Aaw86136 Protein s	353	36	69.2	107	2	AAW05270	Aaw05270 Antibody
281	37	71.2	107	2	AAW86129	Aaw86129 Protein s	354	36	69.2	107	2	AAW05271	Aaw05271 Antibody
282	37	71.2	107	4	AAW82890	Aaw82890 Anti-huma	355	36	69.2	107	2	AAW05269	Aaw05269 Antibody
283	37	71.2	107	6	ABUS6813	Abus6813 Monkey Im	356	36	69.2	107	3	AAW96062	Aaw96062 Human ant
284	37	71.2	107	7	ADK61016	Adk61016 Human ant	357	36	69.2	107	4	AAW72882	Aaw72882 Human ant
285	37	71.2	107	7	AAO24242	Aao24242 708 anti-	358	36	69.2	107	4	AAW72880	Aaw72880 Human ant
286	37	71.2	107	7	ADOS1594	Ados1594 Human TAG	359	36	69.2	107	5	ABG98273	Abg98273 Murine an
287	37	71.2	107	7	ADG52884	Adg52884 Human ant	360	36	69.2	107	5	ABG98274	Abg98274 Murine an
288	37	71.2	107	8	ADP22118	Adp22118 Human ant	361	36	69.2	107	5	ABG98275	Abg98275 Murine an
289	37	71.2	107	8	ADW96639	Adw96639 Human ant	362	36	69.2	107	5	ABG98276	Abg98276 Murine an
290	37	71.2	107	9	ADW96640	Adw96640 Human ant	363	36	69.2	107	5	AAW47643	Aaw47643 Human G1C
291	37	71.2	107	9	ADW80211	Adw80211 Human ant	364	36	69.2	107	5	ABG97821	Abg97821 Human MFL
292	37	71.2	107	9	ADW80212	Adw80212 Human ant	365	36	69.2	107	5	ABG35324	Abg35324 Thrombopo
293	37	71.2	107	9	ADW80212	Adw80212 Human ant	366	36	69.2	107	5	ABG97977	Abg97977 Light cha
294	37	71.2	107	9	ADW98402	Adw98402 Human ant	367	36	69.2	107	5	ABP97651	Abp97651 Amino aci
295	37	71.2	107	9	ABE19281	Abe19281 IgG kappa	368	36	69.2	107	6	ABR54891	AbR54891 Light cha
296	37	71.2	108	2	AAW54012	Aaw54012 Anti-CD4	369	36	69.2	107	6	ABR54891	AbR54891 Light cha
297	37	71.2	108	2	AAW48864	Aaw48864 Chimeric	370	36	69.2	107	6	ABR63606	AbR63606 Human gly
298	37	71.2	108	8	ADR87272	Adr87272 Anti-LIV-	371	36	69.2	107	6	ADK61017	Adk61017 Human ant
299	37	71.2	125	9	ADZ70612	Adz70612 Human pro	372	36	69.2	107	7	ADK61015	Adk61015 Human ant
300	37	71.2	127	6	AAE37206	Aae37206 Human AB-	373	36	69.2	107	7	ADC97978	Adc97978 Anti-huma
301	37	71.2	127	9	AAE16227	Aae16227 Anti-huma	374	36	69.2	107	7	ADD05393	AdD05393 Anti-MUC1
302	37	71.2	129	3	AAV56722	Aav56722 Amino aci	375	36	69.2	107	7	ADP09931	AdP09931 Human ant
303	37	71.2	129	3	ADW98262	Adw98262 Human ant	376	36	69.2	107	7	ADG88415	Adg88415 VL chain
304	37	71.2	134	9	ADK61106	Adk61106 Human ant	377	36	69.2	107	7	ADK18841	Adk18841 Anti-huma
305	37	71.2	152	8	ADK52354	Adk52354 Human ant	378	36	69.2	107	7	ADK18816	Adk18816 Anti-huma
306	37	71.2	164	2	AAW34317	Aaw34317 IgG anti-b	379	36	69.2	107	7	ADK18885	Adk18885 Anti-huma
307	37	71.2	224	2	AAW75040	Aaw75040 TRO005 Hu	380	36	69.2	107	7	ADK18840	Adk18840 Anti-huma
308	37	71.2	236	5	ABG77160	Abg77160 Germline	381	36	69.2	107	7	ADK18892	Adk18892 Anti-huma
309	37	71.2	236	8	ADK28582	Adk28582 Human ant	382	36	69.2	107	7	ADK18841	Adk18841 Anti-huma
310	37	71.2	242	3	AAW58236	Aaw58236 Internai	383	36	69.2	107	7	ADK18879	Adk18879 Anti-huma
311	37	71.2	264	2	AAW73049	Aaw73049 Humanized	384	36	69.2	107	7	ADK18612	Adk18612 Anti-huma
312	37	71.2	450	8	ADN20942	Adn20942 Bacterial	385	36	69.2	107	7	ADK18602	Adk18602 Anti-huma
313	37	71.2	532	2	AAW73051	Aaw73051 Z3dCh2.2	386	36	69.2	107	7	ADK18810	Adk18810 Anti-huma
314	37	71.2	643	2	AAW73050	Aaw73050 Z3gZ623.7	387	36	69.2	107	7	ADK18844	Adk18844 Anti-huma
315	37	71.2	1094	8	ADK52927	Adk52927 Bacterial	388	36	69.2	107	7	ADK18806	Adk18806 Anti-huma
316	36	69.2	9	2	AAW59175	Aaw59175 Mouse pAF	389	36	69.2	107	7	ADK18808	Adk18808 Anti-huma

390	36	69.2	107	7	ADK18807	Adk18807	Anti-huma	463	36	69.2	129	2	AAR27054	Aar27054	Anti-CEA
391	36	69.2	107	7	ADK18604	Adk18604	Anti-huma	464	36	69.2	129	2	AAR30481	Aar30481	hCEA spec
392	36	69.2	107	7	ADK18600	Adk18600	Anti-huma	465	36	69.2	129	5	ABG97823	Abg97823	Human HEF
393	36	69.2	107	7	ADP03912	Adp03912	Murine-ex	466	36	69.2	129	5	ABG35326	Abg35326	Thrombopo
394	36	69.2	107	7	ADP03908	Adp03908	Murine-ex	467	36	69.2	133	2	AAW21936	Aaw21936	Variable
395	36	69.2	107	7	ADP03996	Adp03996	Murine-ex	468	36	69.2	133	2	AAW21934	Aaw21934	Variable
396	36	69.2	107	8	ADL26704	Adl26704	Moube ant	469	36	69.2	133	2	AAW21933	Aaw21933	Variable
397	36	69.2	107	8	ADL25422	Adl25422	Human mAb	470	36	69.2	133	2	AAV05266	Aav05266	Antibody
398	36	69.2	107	8	ADL25418	Adl25418	Human mAb	471	36	69.2	133	2	AAV05264	Aav05264	Antibody
399	36	69.2	107	8	ADL25426	Adl25426	Human mAb	472	36	69.2	133	2	AAV05263	Aav05263	Antibody
400	36	69.2	107	8	ADL25442	Adl25442	Human mAb	473	36	69.2	133	5	ABG98315	Abg98315	Murine hu
401	36	69.2	107	8	ADO07289	Ado07289	Human pro	474	36	69.2	133	5	ABG98314	Abg98314	Murine hu
402	36	69.2	107	8	ADO07291	Ado07291	Human pro	475	36	69.2	133	5	ABG98317	Abg98317	Murine wi
403	36	69.2	107	8	ADO36490	Ado36490	Human ant	476	36	69.2	134	5	AAW47645	Aaw47645	Human pro
404	36	69.2	107	8	ADO36506	Ado36506	Human ant	477	36	69.2	136	5	ABG77135	Abg77135	Abci-IGF-
405	36	69.2	107	8	ADO36498	Ado36498	Human ant	478	36	69.2	136	8	ADR28536	Adr28536	Human ant
406	36	69.2	107	8	ADO36502	Ado36502	Human ant	479	36	69.2	145	8	ADL27476	Adl27476	Human mAb
407	36	69.2	107	8	ADO36494	Ado36494	Human ant	480	36	69.2	154	8	ADL25472	Adl25472	Human mAb
408	36	69.2	107	8	ADP22368	Adp22368	Human ant	481	36	69.2	164	7	ADD28242	Add28242	Human het
409	36	69.2	107	8	ADP22166	Adp22166	Human ant	482	36	69.2	164	9	ADV86829	Adv86829	Bacillus
410	36	69.2	107	8	ADP22240	Adp22240	Human ant	483	36	69.2	177	4	ABG01825	Abg01825	Novel hum
411	36	69.2	107	8	ADP22401	Adp22401	Human ant	484	36	69.2	213	6	ABM67103	Abm67103	Photorhab
412	36	69.2	107	8	ADP22310	Adp22310	Human ant	485	36	69.2	214	9	AEC20772	Aec20772	M-CSF spe
413	36	69.2	107	8	ADP22154	Adp22154	Human ant	486	36	69.2	232	7	ADF72730	Adf72730	Divalent
414	36	69.2	107	8	ADP22126	Adp22126	Human ant	487	36	69.2	234	4	AAB90612	Aab90612	Human sec
415	36	69.2	107	8	ADP22328	Adp22328	Human ant	488	36	69.2	234	5	ABG65461	Abg65461	Human alb
416	36	69.2	107	8	ADP22407	Adp22407	Human ant	489	36	69.2	234	8	ADL78728	Adl78728	Albumin f
417	36	69.2	107	8	ADP22158	Adp22158	Human ant	490	36	69.2	236	5	ABG77163	Abg77163	Germine
418	36	69.2	107	8	ADP22354	Adp22354	Human ant	491	36	69.2	236	5	ABG77164	Abg77164	Germine
419	36	69.2	107	8	ADR43402	Adr43402	Human ant	492	36	69.2	236	8	ADR28586	Adr28586	Human ant
420	36	69.2	107	8	ADR31547	Adr31547	Human ant	493	36	69.2	236	8	ADR28585	Adr28585	Human ant
421	36	69.2	107	9	ADV21397	Adv21397	Human ant	494	36	69.2	236	9	ADX57905	Adx57905	Human 2-1
422	36	69.2	107	9	AEB19267	Aeb19267	IgG kappa	495	36	69.2	236	2	ADX57906	Adx57906	Human ger
423	36	69.2	107	9	AEC08123	Aec08123	Human ant	496	36	69.2	238	2	AAW14936	Aaw14936	2A2 Human
424	36	69.2	108	2	AAR21294	Aar21294	Murine VL	497	36	69.2	238	2	AAW14931	Aaw14931	Murine an
425	36	69.2	108	2	AAW19885	Aaw19885	CEA-speci	498	36	69.2	239	5	ABP45911	Abp45911	Human Bly
426	36	69.2	108	2	AAW19895	Aaw19895	CEA-speci	499	36	69.2	239	5	ABP45871	Abp45871	Human Bly
427	36	69.2	108	2	AAW59169	Aaw59169	Mouse PAF	500	36	69.2	239	6	ABP60529	Abp60529	APRIL bin
428	36	69.2	108	2	AAW21817	Aaw21817	Mouse PAF	501	36	69.2	239	7	ADG30415	Adg30415	Human GMB
429	36	69.2	108	4	AAW62953	Aaw62953	Amino aci	502	36	69.2	239	7	ADG30447	Adg30447	Human GMB
430	36	69.2	108	4	AAW62959	Aaw62959	Amino aci	503	36	69.2	239	7	ADG96698	Adg96698	Single ch
431	36	69.2	108	8	ADO36412	Ado36412	Intracell	504	36	69.2	239	7	ADG96738	Adg96738	Single ch
432	36	69.2	108	8	ADT75006	Adt75006	Light cha	505	36	69.2	240	6	ABP60528	Abp60528	APRIL bin
433	36	69.2	108	8	ADT75000	Adt75000	Light cha	506	36	69.2	240	7	ADG30465	Adg30465	Human GMB
434	36	69.2	108	8	ADT75004	Adt75004	Light cha	507	36	69.2	241	5	ABP45937	Abp45937	Human Bly
435	36	69.2	108	8	ADT75005	Adt75005	Light cha	508	36	69.2	241	5	ABP45878	Abp45878	Human Bly
436	36	69.2	108	8	ADT74999	Adt74999	Light cha	509	36	69.2	241	5	ABP45890	Abp45890	Human Bly
437	36	69.2	108	9	AEB11691	Aeb11691	Anti-Pseu	510	36	69.2	241	6	ABP60527	Abp60527	APRIL bin
438	36	69.2	109	8	ADT75002	Adt75002	Light cha	511	36	69.2	241	7	ADF72729	Adf72729	Monovalen
439	36	69.2	109	8	ADT74991	Adt74991	Consensu	512	36	69.2	241	7	ADG96705	Adg96705	Single ch
440	36	69.2	109	8	ADT75008	Adt75008	Light cha	513	36	69.2	241	7	ADG96764	Adg96764	Single ch
441	36	69.2	109	8	ADT74996	Adt74996	Light cha	514	36	69.2	241	7	ABP45924	Abp45924	Single ch
442	36	69.2	109	8	ADT74997	Adt74997	Light cha	515	36	69.2	243	5	ABP45872	Abp45872	Human Bly
443	36	69.2	110	2	AAW93001	Aaw93001	Humani sed	516	36	69.2	243	5	ABP45934	Abp45934	Human Bly
444	36	69.2	110	2	AAW93005	Aaw93005	Monoclon	517	36	69.2	243	5	ABP46052	Abp46052	Human Bly
445	36	69.2	110	2	AAW92999	Aaw92999	Monoclon	518	36	69.2	243	5	ABP45879	Abp45879	Single ch
446	36	69.2	110	2	AAW93007	Aaw93007	Humani sed	519	36	69.2	243	7	ADG96699	Adg96699	Single ch
447	36	69.2	112	4	AAW84286	Aaw84286	Amino aci	520	36	69.2	243	7	ADG96879	Adg96879	Single ch
448	36	69.2	113	7	ADD28269	Add28269	Human het	521	36	69.2	243	7	ADG96761	Adg96761	Single ch
449	36	69.2	115	5	ABB07359	Abb07359	22A5 IGM	522	36	69.2	243	9	ADV21484	Adv21484	Mature fo
450	36	69.2	115	5	ADT74992	Adt74992	Light cha	523	36	69.2	244	2	AAW06715	Aaw06715	Antibody
451	36	69.2	116	5	ABB07179	Abb07179	AKuR4 kAp	524	36	69.2	244	8	ADR28085	Adr28085	Antibody
452	36	69.2	116	8	ADJ26674	Adj26674	Human ant	525	36	69.2	244	8	ADL28085	Adl28085	Antibody
453	36	69.2	116	8	ADJ26674	Adj26674	Human ant	526	36	69.2	244	8	ADL28085	Adl28085	Antibody
454	36	69.2	119	8	ADL25468	Adl25468	Human mAb	527	36	69.2	245	2	AAW06714	Aaw06714	Antibody
455	36	69.2	126	2	AAW43691	Aaw43691	PBI.3/Hum	528	36	69.2	245	2	AAW06717	Aaw06717	Antibody
456	36	69.2	126	2	AAW43692	Aaw43692	PBI.3/Hum	529	36	69.2	245	5	ABP45891	Abp45891	Human Bly
457	36	69.2	126	2	AAW62675	Aaw62675	CY1748RLB	530	36	69.2	245	5	ABP45889	Abp45889	Human Bly
458	36	69.2	126	2	AAW62676	Aaw62676	CY1748RLC	531	36	69.2	245	5	ABP45889	Abp45889	Human Bly
459	36	69.2	126	2	AAW62677	Aaw62677	CY1748RLD	532	36	69.2	245	7	ADG96718	Adg96718	Single ch
460	36	69.2	127	7	ADC61102	Adc61102	Human ant	533	36	69.2	245	8	ADG96718	Adg96718	Single ch
461	36	69.2	127	7	ADC61102	Adc61102	Human ant	534	36	69.2	245	8	ADG96718	Adg96718	Single ch
462	36	69.2	127	7	ADC61110	Adc61110	Human ant	535	36	69.2	245	8	ADG96718	Adg96718	Single ch

536	36	69.2	245	8	AD039733	Human c-m	609	35	67.3	9	8	ADR46835	Adt46835	Human ant
537	36	69.2	246	5	ABP45909	Human Bly	610	35	67.3	9	8	ADU07245	Adt07245	Human 7P3
538	36	69.2	246	5	ABP46051	Abp46051	611	35	67.3	9	8	ADT88312	Adt88312	Human IL-
539	36	69.2	246	7	ADG96878	Adg96878	612	35	67.3	9	8	ADU15326	Adt15326	Clostridi
540	36	69.2	246	7	ADG96736	Adg96736	613	35	67.3	9	8	ADY26806	Ady26806	Human ant
541	36	69.2	247	5	ABP45912	Abp45912	614	35	67.3	9	9	ADY26812	Ady26812	Human ant
542	36	69.2	247	5	ABP44958	Abp44958	615	35	67.3	9	9	ADY70264	Ady70264	Human Mab
543	36	69.2	247	5	ABP45166	Abp45166	616	35	67.3	9	9	AEA45642	Adt45642	Novel den
544	36	69.2	247	5	ADG30471	Adg30471	617	35	67.3	10	9	AEBO0081	Adt0081	Novel den
545	36	69.2	247	7	ADG95785	Adg95785	618	35	67.3	105	8	ADU07255	Adt07255	Human 7P3
546	36	69.2	247	7	ADG96739	Adg96739	619	35	67.3	105	8	ADT88322	Adt88322	Human IL-
547	36	69.2	247	7	ADG95993	Adg95993	620	35	67.3	107	2	AAW86131	Adt86131	Protein s
548	36	69.2	247	7	ADG98058	Adg98058	621	35	67.3	107	2	AAW48004	Adt48004	Human mon
549	36	69.2	247	8	ADN99189	Adn99189	622	35	67.3	107	6	ABR54892	Adt54892	Light cha
550	36	69.2	247	8	ADN99189	Adn99189	623	35	67.3	107	6	ADP03990	Adp03990	Murine-ex
551	36	69.2	248	5	ABP44997	Abp44997	624	35	67.3	107	7	ADP03910	Adp03910	Murine-ex
552	36	69.2	248	5	ABP45410	Abp45410	625	35	67.3	107	7	ADP03915	Adp03915	Murine-ex
553	36	69.2	248	5	ABP45689	Abp45689	626	35	67.3	107	8	ADP46825	Adt46825	Human ant
554	36	69.2	248	5	ABP45760	Abp45760	627	35	67.3	107	8	ADP46825	Adt46825	Human ant
555	36	69.2	248	5	ABP45767	Abp45767	628	35	67.3	107	8	ADP46825	Adt46825	Human ant
556	36	69.2	248	7	ADG96516	Adg96516	629	35	67.3	107	8	ADP46825	Adt46825	Human ant
557	36	69.2	248	7	ADG96587	Adg96587	630	35	67.3	107	8	ADP46825	Adt46825	Human ant
558	36	69.2	248	7	ADG96594	Adg96594	631	35	67.3	107	8	ADP46825	Adt46825	Human ant
559	36	69.2	248	7	ADG95824	Adg95824	632	35	67.3	107	8	ADP46825	Adt46825	Human ant
560	36	69.2	248	7	ADG96237	Adg96237	633	35	67.3	107	8	ADP46825	Adt46825	Human ant
561	36	69.2	249	5	ABP44915	Abp44915	634	35	67.3	107	8	ADP46825	Adt46825	Human ant
562	36	69.2	249	5	ABP44907	Abp44907	635	35	67.3	107	8	ADP46825	Adt46825	Human ant
563	36	69.2	249	5	ABP44908	Abp44908	636	35	67.3	107	8	ADP46825	Adt46825	Human ant
564	36	69.2	249	5	ABP45177	Abp45177	637	35	67.3	107	8	ADP46825	Adt46825	Human ant
565	36	69.2	249	7	ADG95742	Adg95742	638	35	67.3	107	8	ADP46825	Adt46825	Human ant
566	36	69.2	249	7	ADG95735	Adg95735	639	35	67.3	107	8	ADP46825	Adt46825	Human ant
567	36	69.2	249	7	ADG96004	Adg96004	640	35	67.3	107	8	ADP46825	Adt46825	Human ant
568	36	69.2	249	7	ADG95734	Adg95734	641	35	67.3	107	8	ADP46825	Adt46825	Human ant
569	36	69.2	250	5	ABP44921	Abp44921	642	35	67.3	107	8	ADP46825	Adt46825	Human ant
570	36	69.2	250	7	ADG95748	Adg95748	643	35	67.3	107	8	ADP46825	Adt46825	Human ant
571	36	69.2	251	5	ABP44911	Abp44911	644	35	67.3	107	8	ADP46825	Adt46825	Human ant
572	36	69.2	251	5	ABP45309	Abp45309	645	35	67.3	107	8	ADP46825	Adt46825	Human ant
573	36	69.2	251	7	ADG96136	Adg96136	646	35	67.3	107	8	ADP46825	Adt46825	Human ant
574	36	69.2	251	7	ADG95738	Adg95738	647	35	67.3	107	8	ADP46825	Adt46825	Human ant
575	36	69.2	254	9	ADX01984	Adx01984	648	35	67.3	107	8	ADP46825	Adt46825	Human ant
576	36	69.2	255	5	ABP45592	Abp45592	649	35	67.3	107	8	ADP46825	Adt46825	Human ant
577	36	69.2	255	5	ADP45734	Adp45734	650	35	67.3	107	8	ADP46825	Adt46825	Human ant
578	36	69.2	255	7	ADG96419	Adg96419	651	35	67.3	107	8	ADP46825	Adt46825	Human ant
579	36	69.2	256	5	ABG97826	Abg97826	652	35	67.3	107	8	ADP46825	Adt46825	Human ant
580	36	69.2	256	5	ABG35329	Abg35329	653	35	67.3	107	8	ADP46825	Adt46825	Human ant
581	36	69.2	257	8	ADR70320	Adr70320	654	35	67.3	107	8	ADP46825	Adt46825	Human ant
582	36	69.2	259	8	ADR28054	Adr28054	655	35	67.3	107	8	ADP46825	Adt46825	Human ant
583	36	69.2	277	9	ABE34727	Abt34727	656	35	67.3	107	8	ADP46825	Adt46825	Human ant
584	36	69.2	295	4	ABE34033	Abt34033	657	35	67.3	107	8	ADP46825	Adt46825	Human ant
585	36	69.2	330	2	AAW94267	Aw94267	658	35	67.3	107	8	ADP46825	Adt46825	Human ant
586	36	69.2	331	2	AAW94268	Aw94268	659	35	67.3	107	8	ADP46825	Adt46825	Human ant
587	36	69.2	333	3	AAW70111	Aw70111	660	35	67.3	107	8	ADP46825	Adt46825	Human ant
588	36	69.2	337	6	ABU52328	Abu52328	661	35	67.3	107	8	ADP46825	Adt46825	Human ant
589	36	69.2	337	6	ADL23991	Adl23991	662	35	67.3	107	8	ADP46825	Adt46825	Human ant
590	36	69.2	356	4	ABG17996	Abg17996	663	35	67.3	107	8	ADP46825	Adt46825	Human ant
591	36	69.2	496	9	ADV21523	Adv21523	664	35	67.3	107	8	ADP46825	Adt46825	Human ant
592	36	69.2	496	9	ADV21533	Adv21533	665	35	67.3	107	8	ADP46825	Adt46825	Human ant
593	36	69.2	498	9	ADV21503	Adv21503	666	35	67.3	107	8	ADP46825	Adt46825	Human ant
594	36	69.2	498	9	ADV21513	Adv21513	667	35	67.3	107	8	ADP46825	Adt46825	Human ant
595	36	69.2	592	2	AAW94269	Aw94269	668	35	67.3	107	8	ADP46825	Adt46825	Human ant
596	36	69.2	809	5	ABU03210	Abu03210	669	35	67.3	107	8	ADP46825	Adt46825	Human ant
597	36	69.2	809	8	ADJ15651	Adj15651	670	35	67.3	107	8	ADP46825	Adt46825	Human ant
598	36	69.2	809	8	ADJ15986	Adj15986	671	35	67.3	107	8	ADP46825	Adt46825	Human ant
599	36	69.2	809	8	ADN97887	Adn97887	672	35	67.3	107	8	ADP46825	Adt46825	Human ant
600	36	69.2	809	8	ADN97887	Adn97887	673	35	67.3	107	8	ADP46825	Adt46825	Human ant
601	36	69.2	809	8	ADN97887	Adn97887	674	35	67.3	107	8	ADP46825	Adt46825	Human ant
602	36	69.2	809	8	ADN97887	Adn97887	675	35	67.3	107	8	ADP46825	Adt46825	Human ant
603	36	69.2	809	8	ADN97887	Adn97887	676	35	67.3	107	8	ADP46825	Adt46825	Human ant
604	36	69.2	809	8	ADN97887	Adn97887	677	35	67.3	107	8	ADP46825	Adt46825	Human ant
605	36	69.2	809	8	ADN97887	Adn97887	678	35	67.3	107	8	ADP46825	Adt46825	Human ant
606	36	69.2	809	8	ADN97887	Adn97887	679	35	67.3	107	8	ADP46825	Adt46825	Human ant
607	36	69.2	809	8	ADN97887	Adn97887	680	35	67.3	107	8	ADP46825	Adt46825	Human ant
608	36	69.2	809	8	ADN97887	Adn97887	681	35	67.3	107	8	ADP46825	Adt46825	Human ant

682	35	67.3	291	8	ADN06993	Adn06993 Human ERG	755	34	65.4	110	2	AAR21307	Aar21307 Murine VL
683	35	67.3	543	8	ADR46829	Adr46829 Human pbl	756	34	65.4	110	2	AAR21306	Aar21306 Murine VL
684	35	67.3	411	7	ADD12876	Add12876 CD28/meia	757	34	65.4	110	2	AAR21287	Aar21287 Murine VL
685	35	67.3	681	7	ABO76994	Ab076994 Pseudomon	758	34	65.4	110	2	AAR21305	Aar21305 Murine VL
686	35	67.3	692	6	ABU03568	Abu03568 Angiotensin	759	34	65.4	110	2	AAR21304	Aar21304 Murine VL
687	35	67.3	1092	6	ADN20021	Adn20021 Bacteriophage	760	34	65.4	110	5	AAU81280	Aau81280 Human trk
688	35	67.3	1094	7	ADC31585	Adc31585 Human nov	761	34	65.4	110	8	ADJ54097	Adj54097 CAB-1 lig
689	34	65.4	9	2	AAR30450	Aar30450 C242:11 M	762	34	65.4	110	8	ADT75125	Adt75125 Light cha
690	34	65.4	9	4	AAE7506	Aae7506 Human lig	763	34	65.4	110	8	ADT75128	Adt75128 Light cha
691	34	65.4	9	5	AAU81252	Aau81252 Human trk	764	34	65.4	110	8	ADT75054	Adt75054 Light cha
692	34	65.4	9	5	AAU81260	Aau81260 Murine tr	765	34	65.4	110	8	ADT75053	Adt75053 Light cha
693	34	65.4	9	6	AAE38081	Aae38081 Human sfl	766	34	65.4	110	8	ADT59992	Adt59992 CAB1 lig
694	34	65.4	9	8	ADO43568	Ado43568 Complement	767	34	65.4	110	9	AEA99644	Aea99644 Human CAB
695	34	65.4	9	8	ADO43562	Ado43562 Complement	768	34	65.4	111	8	ADT75134	Adt75134 Light cha
696	34	65.4	9	8	AD519321	Ad519321 Light cha	769	34	65.4	111	8	ADT75132	Adt75132 Light cha
697	34	65.4	9	8	ADT75072	Adt75072 Murine li	770	34	65.4	111	8	ADT75132	Adt75132 Light cha
698	34	65.4	9	8	ADW07057	Adw07057 Anti-Psaa	771	34	65.4	112	2	AAR14392	Aar14392 L3 region
699	34	65.4	9	9	ADY70252	Ady70252 Human Mab	772	34	65.4	112	8	ADR36880	Adr36880 Mouse lig
700	34	65.4	9	9	AEA44030	Aea44030 Anti-TPO	773	34	65.4	112	9	AEA89803	Aea89803 Antibody
701	34	65.4	9	9	AEA44039	Aea44039 Anti-TPO	774	34	65.4	112	9	AEA44055	Aea44055 Anti-TPO
702	34	65.4	9	9	AEA44212	Aea44212 Anti-TPO	775	34	65.4	112	9	AEA44086	Aea44086 Anti-TPO
703	34	65.4	9	9	AEA43997	Aea43997 Anti-TPO	776	34	65.4	112	9	AEA44232	Aea44232 Anti-TPO
704	34	65.4	9	9	AEA43997	Aea43997 Anti-TPO	777	34	65.4	112	9	AEA44060	Aea44060 Anti-TPO
705	34	65.4	9	9	AEA44179	Aea44179 Anti-TPO	778	34	65.4	112	9	AEA44226	Aea44226 Anti-TPO
706	34	65.4	9	9	AEA9634	Aea9634 Human IP1	779	34	65.4	112	9	AEA44173	Aea44173 Anti-TPO
707	34	65.4	9	9	AEA96640	Aea96640 Human CAB	780	34	65.4	112	2	AAW48757	Aaw48757 TAI antib
708	34	65.4	9	9	AEA9662	Aea9662 Human SW1	781	34	65.4	114	2	AAW48757	Aaw48757 TAI antib
709	34	65.4	9	9	AEA96628	Aea96628 Human CAB	782	34	65.4	116	7	ADJ688500	Adj688500 Human hea
710	34	65.4	9	9	AEA96655	Aea96655 Human CAB	783	34	65.4	125	3	AAO282964	Aao282964 Human sec
711	34	65.4	27	8	AD884423	Ad884423 Human ant	784	34	65.4	125	7	ADB08431	Adb08431 Novel pro
712	34	65.4	27	8	AD868565	Ad868565 Human EPO	785	34	65.4	130	3	AAV56733	Aav56733 Amino aci
713	34	65.4	52	6	ABU56905	Abu56905 BONT/A Hc	786	34	65.4	132	6	ADA43065	Ada43065 Human ant
714	34	65.4	84	9	ADZ59997	Adz59997 CAB1 cons	787	34	65.4	132	9	AEA89785	Aea89785 Antibody
715	34	65.4	99	8	ADJ27402	Adj27402 Amino aci	788	34	65.4	133	2	AAR33951	Aar33951 CTMO1 VL
716	34	65.4	107	4	AAE67511	Aae67511 Light cha	789	34	65.4	133	2	AAR33954	Aar33954 GL1 varia
717	34	65.4	107	5	ABG32512	Abg32512 Human VK	790	34	65.4	133	2	AAW29754	Aaw29754 CDR-graft
718	34	65.4	107	6	ABR54895	AbR54895 Light cha	791	34	65.4	133	2	AAV56878	Aav56878 GL2 varia
719	34	65.4	107	6	ABR54902	AbR54902 Light cha	792	34	65.4	133	3	AAV56874	Aav56874 MAb CT-M
720	34	65.4	107	6	ABR54886	AbR54886 Light cha	793	34	65.4	133	8	ADO43553	Ado43553 Amino aci
721	34	65.4	107	6	ABR54899	AbR54899 Light cha	794	34	65.4	133	8	ADO43549	Ado43549 Amino aci
722	34	65.4	107	6	ABR54882	AbR54882 Light cha	795	34	65.4	141	2	AAW30454	Aaw30454 C242:11 M
723	34	65.4	107	6	ABR54883	AbR54883 Light cha	796	34	65.4	141	2	AAW32541	Aaw32541 C242 kapp
724	34	65.4	107	6	ABR54893	AbR54893 Light cha	797	34	65.4	145	5	ABP10448	Abp10448 Human ORF
725	34	65.4	107	6	AAE38063	Aae38063 Human SFL	798	34	65.4	145	5	ABP63932	Abp63932 Human ORF
726	34	65.4	107	7	AAO24247	Aao24247 708 anti-I	799	34	65.4	147	2	AAV34310	Aav34310 IGM antib
727	34	65.4	107	7	ADO51597	Ado51597 Human TAG	800	34	65.4	147	2	ADZ88798	Adz88798 Breast sp
728	34	65.4	107	7	ADP03918	Adp03918 Murine-ex	801	34	65.4	158	2	AAV34965	Aav34965 Chlamydia
729	34	65.4	107	8	ADP22220	Adp22220 Human ant	802	34	65.4	158	2	ADZ88800	Adz88800 Breast sp
730	34	65.4	107	8	ADP22404	Adp22404 Human ant	803	34	65.4	158	9	ADZ88799	Adz88799 Breast sp
731	34	65.4	107	8	ADS84366	Ads84366 Human ant	804	34	65.4	182	9	ADY64610	Ady64610 S. manson
732	34	65.4	107	8	ADS19318	Ads19318 Light cha	805	34	65.4	184	8	AD884439	Ad884439 Human ant
733	34	65.4	107	8	ADR68508	Adr68508 Anti-EPO-	806	34	65.4	184	8	ADR68581	Adr68581 Human ant
734	34	65.4	107	8	ADR38671	Adr38671 Mouse lig	807	34	65.4	214	7	ADP11431	Adp11431 18B2 anti
735	34	65.4	107	8	ADR88865	Adt88865 Human IGF	808	34	65.4	214	7	ADP11423	Adp11423 2B11 anti
736	34	65.4	107	8	ADT88863	Adt88863 Human IGF	809	34	65.4	215	2	AAW43674	Aaw43674 Mouse ant
737	34	65.4	107	9	ADW07059	Adw07059 Anti-Psaa	810	34	65.4	215	2	AAW99644	Aaw99644 Anti-bGH
738	34	65.4	107	9	ADY70210	Ady70210 Human mon	811	34	65.4	215	2	AAW97377	Aaw97377 Murine an
739	34	65.4	107	9	AEI19269	Aei19269 IGG kappa	812	34	65.4	219	8	ADJ35160	Adj35160 Humanised
740	34	65.4	107	9	AEI19271	Aei19271 IGG kappa	813	34	65.4	223	1	AAW40031	Aaw40031 Kappa ant
741	34	65.4	107	9	AEI19258	Aei19258 IGG kappa	814	34	65.4	223	7	ADC00122	Adc00122 Enterohae
742	34	65.4	107	9	AEI19275	Aei19275 IGG kappa	815	34	65.4	224	4	AAW99396	Aaw99396 Human int
743	34	65.4	107	9	AEI19278	Aei19278 IGG kappa	816	34	65.4	224	4	AAW57029	Aaw57029 Anti-IL8
744	34	65.4	107	9	AEI19259	Aei19259 IGG kappa	817	34	65.4	225	2	AAW05710	Aaw05710 TRY4.0. 9/
745	34	65.4	107	9	AEI19262	Aei19262 IGG kappa	818	34	65.4	225	2	AAW06478	Aaw06478 TRY4.0. 3/
746	34	65.4	107	9	AEI19262	Aei19262 IGG kappa	819	34	65.4	225	2	AAW43675	Aaw43675 Single ch
747	34	65.4	108	2	AAW34019	Aaw34019 BW 835 VK	820	34	65.4	225	2	AAW99645	Aaw99645 Single ch
748	34	65.4	108	7	AAW62757	Aaw62757 Human HIV	821	34	65.4	234	2	AAW48576	Aaw48576 Human kcp
749	34	65.4	108	7	ADP11399	Adp11399 2B11 anti	822	34	65.4	236	2	AAW48576	Aaw48576 Single ch
750	34	65.4	108	7	ADP11407	Adp11407 18B2 anti	823	34	65.4	236	2	AAW48576	Aaw48576 Single ch
751	34	65.4	109	2	AAW59986	Aaw59986 UT.6 lig	824	34	65.4	239	2	AAW43679	Aaw43679 Single ch
752	34	65.4	109	2	AAW88753	Aaw88753 secp UT.6	825	34	65.4	239	2	AAW66757	Aaw66757 Anti-toba
753	34	65.4	109	5	AAU81278	Aau81278 Murine tr	826	34	65.4	239	2	AAW99649	Aaw99649 Single ch
754	34	65.4	109	9	ADW86131	Adw86131 Novel cyt	827	34	65.4	239	2	AAW02191	Aaw02191 18-2-3/TR

828	34	65.4	239	9	AEB48570	Aeb48570	Human	Kap	901	34	65.4	605	9	AEA99649	Aea99649	Human	CAB
829	34	65.4	241	2	AAR06482	Aar06482	18-2-3-/T		902	34	65.4	605	9	AEA99622	Aea99622	Human	CAB
830	34	65.4	242	2	AAR06483	Aar06483	18-2-3-/T		903	34	65.4	605	9	AEA99663	Aea99663	Human	CAB
831	34	65.4	242	2	AAR43680	Aar43680	Single ch		904	34	65.4	605	9	AEA99621	Aea99621	Human	CAB
832	34	65.4	242	2	AAR99650	Aar99650	Single ch		905	34	65.4	651	2	AAR06460	Aar06460	Bt	PGS1208
833	34	65.4	242	2	AAW02192	AAw02192	18-2-3/TR		906	34	65.4	651	2	AAR33769	Aar33769	Bt	Isolat
834	34	65.4	244	8	ADK18141	Adk18141	CAB1-scfv		907	34	65.4	651	2	AAW06419	Aaw06419	Chimeric	
835	34	65.4	244	8	ADJ54093	Adj54093	CAB-1 scf		908	34	65.4	651	2	AAW26649	Aaw26649	Chimeric	
836	34	65.4	244	9	AEB17982	Aeb17982	Mouse scf		909	34	65.4	651	2	AAW23197	Aaw23197	Amino aci	
837	34	65.4	246	2	AAR43677	Aar43677	Single ch		910	34	65.4	651	2	AAW23200	Aaw23200	Amino aci	
838	34	65.4	246	2	AAR99647	Aar99647	Single ch		911	34	65.4	651	2	AAW23199	Aaw23199	Amino aci	
839	34	65.4	247	1	AAP80155	Aap80155	Frs and C		912	34	65.4	652	2	AAW14047	Aaw14047	B. thuring	
840	34	65.4	247	1	AAP80156	Aap80156	Bioeynte		913	34	65.4	652	2	AAW23174	Aaw23174	Amino aci	
841	34	65.4	250	2	AAR06481	Aar06481	TRY104b.		914	34	65.4	652	2	AAW23178	Aaw23178	Amino aci	
842	34	65.4	250	2	AAR43678	Aar43678	Single ch		915	34	65.4	652	2	AAW23203	Aaw23203	Amino aci	
843	34	65.4	250	2	AAR99648	Aar99648	Single ch		916	34	65.4	652	2	AAW23175	Aaw23175	Amino aci	
844	34	65.4	250	2	AAW02190	AAw02190	TRY104b		917	34	65.4	652	2	AAW23209	Aaw23209	Amino aci	
845	34	65.4	254	9	AEA44057	Aea44057	Anti-TPO		918	34	65.4	652	2	AAW23172	Aaw23172	Amino aci	
846	34	65.4	255	9	ADY66108	Ady66108	S. manson		919	34	65.4	652	2	AAW23184	Aaw23184	Amino aci	
847	34	65.4	256	9	ADY52918	Ady52918	Gloebact		920	34	65.4	652	2	AAW23190	Aaw23190	Amino aci	
848	34	65.4	256	9	ADY52980	Ady52980	Gloebact		921	34	65.4	652	2	AAW23183	Aaw23183	Amino aci	
849	34	65.4	257	5	AU87032	Aau87032	Adenoviru		922	34	65.4	652	2	AAW23193	Aaw23193	Amino aci	
850	34	65.4	266	8	ADH77307	Adh77307	Yeast K11		923	34	65.4	652	2	AAW23195	Aaw23195	Amino aci	
851	34	65.4	270	2	AAR75719	Aar75719	MFE-23 an		924	34	65.4	652	2	AAW23179	Aaw23179	Amino aci	
852	34	65.4	270	4	AAU58204	Aau58204	Propionib		925	34	65.4	652	2	AAW23211	Aaw23211	Amino aci	
853	34	65.4	270	6	ABM54723	Abm54723	Propionib		926	34	65.4	652	2	AAW23189	Aaw23189	Amino aci	
854	34	65.4	271	5	AAO19417	Aao19417	Human mol		927	34	65.4	652	2	AAW23207	Aaw23207	Amino aci	
855	34	65.4	275	7	ABO80481	Ab080481	Pseudomon		928	34	65.4	652	2	AAW23173	Aaw23173	Amino aci	
856	34	65.4	275	8	ADL0618	Adl0618	M. catatr		929	34	65.4	652	2	AAW23191	Aaw23191	Amino aci	
857	34	65.4	284	6	ADA14411	Ada14411	Mouse spe		930	34	65.4	652	2	AAW23196	Aaw23196	Amino aci	
858	34	65.4	284	6	ADA14413	Ada14413	Mouse spe		931	34	65.4	652	2	AAW23198	Aaw23198	Amino aci	
859	34	65.4	285	9	AEB17984	Aeb17984	Humanized		932	34	65.4	652	2	AAW23201	Aaw23201	Amino aci	
860	34	65.4	285	9	AEB17986	Aeb17986	Humanized		933	34	65.4	652	2	AAW23182	Aaw23182	Amino aci	
861	34	65.4	285	9	AEB18012	Aeb18012	Humanized		934	34	65.4	652	2	AAW23185	Aaw23185	Amino aci	
862	34	65.4	287	9	AEB18011	Aeb18011	Humanized		935	34	65.4	652	2	AAW23187	Aaw23187	Amino aci	
863	34	65.4	287	9	AEB48564	Aeb48564	Human Kap		936	34	65.4	652	2	AAW23212	Aaw23212	Amino aci	
864	34	65.4	290	9	AEB48564	Aeb48564	Human Kap		937	34	65.4	652	2	AAW23177	Aaw23177	Amino aci	
865	34	65.4	301	8	ADS30011	Ads30011	Bacterial		938	34	65.4	652	2	AAW23181	Aaw23181	Amino aci	
866	34	65.4	309	5	AAO19411	Aao19411	Human mol		939	34	65.4	652	2	AAW23186	Aaw23186	Amino aci	
867	34	65.4	309	9	AEA19985	Aea19985	Novel hum		940	34	65.4	652	2	AAW23176	Aaw23176	Amino aci	
868	34	65.4	330	9	ABB90710	Abb90710	Chlamydia		941	34	65.4	652	2	AAW23204	Aaw23204	Amino aci	
869	34	65.4	340	6	ABM65653	Abm65653	Propionib		942	34	65.4	652	2	AAW23192	Aaw23192	Amino aci	
870	34	65.4	343	9	AEA19986	Aea19986	Novel hum		943	34	65.4	652	2	AAW23188	Aaw23188	Amino aci	
871	34	65.4	362	2	AAV35611	AAv35611	Chlamydia		944	34	65.4	652	2	AAW23194	Aaw23194	Amino aci	
872	34	65.4	362	5	AU87035	Aau87035	Adenoviru		945	34	65.4	652	2	AAW23202	Aaw23202	Amino aci	
873	34	65.4	382	2	AAW26651	Aaw26651	Chimeric		946	34	65.4	652	2	AAW23205	Aaw23205	Amino aci	
874	34	65.4	403	2	AAW26648	Aaw26648	Chimeric		947	34	65.4	652	2	AAW23180	Aaw23180	Amino aci	
875	34	65.4	444	9	AEB27176	Aeb27176	Pinus rad		948	34	65.4	652	3	AAW70441	Aaw70441	Bacillus	
876	34	65.4	465	5	AU87036	Aau87036	Adenoviru		949	34	65.4	652	3	AAW70442	Aaw70442	Bacillus	
877	34	65.4	472	5	AAE23629	Aae23629	Lactobaci		950	34	65.4	652	3	AAW70443	Aaw70443	Synthetic	
878	34	65.4	473	2	AAW26646	Aaw26646	Chimeric		951	34	65.4	652	6	ABU09192	Abu09192	Bacillus	
879	34	65.4	511	4	ABE64793	Abb64793	Drosophila		952	34	65.4	652	6	ABU09193	Abu09193	Bacillus	
880	34	65.4	514	2	AAW26647	Aaw26647	Chimeric		953	34	65.4	652	6	ABU09194	Abu09194	Bacillus	
881	34	65.4	524	9	AEA44228	Aea44228	Anti-TPO		954	34	65.4	652	7	ABW01051	Abw01051	Bacillus	
882	34	65.4	524	9	AEA44189	Aea44189	Anti-TPO		955	34	65.4	652	7	ABW01052	Abw01052	Bacillus	
883	34	65.4	524	9	AEA44199	Aea44199	Anti-TPO		956	34	65.4	652	7	ABW01050	Abw01050	Bacillus	
884	34	65.4	524	9	AEA44232	Aea44232	Anti-TPO		957	34	65.4	652	8	ADR89425	Adr89425	cry3Bb. 1	
885	34	65.4	524	9	AEA43937	Aea43937	Anti-TPO		958	34	65.4	653	2	AAW23208	Aaw23208	Amino aci	
886	34	65.4	524	9	AEA44195	Aea44195	Anti-TPO		959	34	65.4	653	3	AAW70444	Aaw70444	Bacillus	
887	34	65.4	553	2	AAW11508	AAw11508	Single ch		960	34	65.4	653	3	AAW70446	Aaw70446	Bacillus	
888	34	65.4	553	2	AAW73223	AAw73223	H22-anti-		961	34	65.4	653	3	AAW70445	Aaw70445	Bacillus	
889	34	65.4	553	4	AAAB1960	Aab1960	Bispecific		962	34	65.4	653	6	ABU09200	Abu09200	Bacillus	
890	34	65.4	553	4	AAAB5455	Aab55455	Bispecific		963	34	65.4	653	6	ABU09195	Abu09195	Bacillus	
891	34	65.4	556	4	AAU80040	Aau80040	ScFv-rear		964	34	65.4	653	6	ABU09197	Abu09197	Bacillus	
892	34	65.4	556	4	AAU97935	Aau97935	ScFv-rear		965	34	65.4	653	6	ABU09197	Abu09197	Bacillus	
893	34	65.4	572	2	AAAR26574	Aaar26574	Sequence		966	34	65.4	653	6	ABU09198	Abu09198	Bacillus	
894	34	65.4	605	9	AEA99619	Aea99619	Human CAB		967	34	65.4	653	7	ABW09202	Abw09202	Bacillus	
895	34	65.4	605	9	AEA99702	Aea99702	Human CAB		968	34	65.4	653	7	ABW01054	Abw01054	Bacillus	
896	34	65.4	605	9	AEA99646	Aea99646	Human SW1		969	34	65.4	653	7	ABW01055	Abw01055	Bacillus	
897	34	65.4	605	9	AEA99704	Aea99704	Human CAB		970	34	65.4	653	7	ABW01053	Abw01053	Bacillus	
898	34	65.4	605	9	AEA99620	Aea99620	Human CAB		971	34	65.4	659	1	AAW92106	Aaw92106	Bacillus	
899	34	65.4	605	9	AEA99647	Aea99647	Human CAB		972	34	65.4	659	1	AAW23213	Aaw23213	Amino aci	
900	34	65.4	605	9	AEA99617	Aea99617	Human CAB		973	34	65.4	659	8	ADR89424	Adr89424	cry3Ba. 1	

974	34	65.4	692	2	AAW26650	AAW26650 Chimeric
975	34	65.4	842	2	ADN15287	ADN15287 Bacterial
976	34	65.4	942	6	ABU27012	ABU27012 Protein e
977	34	65.4	998	4	ABB61387	ABB61387 Drosophi1
978	34	65.4	998	4	ABB61350	ABB61350 Drosophi1
979	34	65.4	2285	4	ABB63057	ABB63057 Drosophi1
980	34	65.4	10421	6	ABU33707	ABU33707 Protein e
981	33	63.5	9	2	AAW41384	AAW41384 CDR3 of 1
982	33	63.5	9	3	AAV95235	AAV95235 Humanised
983	33	63.5	9	3	AAV79431	AAV79431 Tie2 rece
984	33	63.5	9	5	AAU76520	AAU76520 Anti-Inte
985	33	63.5	9	5	AAE15818	AAE15818 Human mab
986	33	63.5	9	7	ADP44928	ADP44928 Anti-CCR5
987	33	63.5	9	7	ADK17402	ADK17402 Anti-huma
988	33	63.5	9	8	ADE85716	ADE85716 Human Eph
989	33	63.5	9	8	ADG42824	ADG42824 scFv 1.9h
990	33	63.5	9	8	ADT75080	ADT75080 Murine 1h
991	33	63.5	9	8	ADJ38423	ADJ38423 Mouse anti
992	33	63.5	9	8	ADU15288	ADU15288 Clostridi
993	33	63.5	9	9	ADW04813	ADW04813 PAP-A im
994	33	63.5	9	9	ADY32293	ADY32293 Human Eph
995	33	63.5	9	9	ADY59153	ADY59153 Anti-Tag-
996	33	63.5	9	9	ADZ48269	ADZ48269 Pharmaceu
997	33	63.5	9	9	AEAS3563	AEAS3563 Novel hum
998	33	63.5	9	9	AEK44930	AEK44930 Apolipoep
999	33	63.5	9	9	AEA45477	AEA45477 Apolipoep
1000	33	63.5	9	9	AEA45562	AEA45562 Apolipoep

ALIGNMENTS

CC	AAW62016	standard; peptide; 9 AA.
XX	AAW62016;	
XX	01-OCT-1998	(first entry)
XX	Light chain variable region	complementarity determining region 3.
DE	Complementarity determining region; light chain variable region;	
KW	humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;	
KW	human CD11a I domain; MHM24 epitope; alpha subunit;	
KW	lymphocyte function-associated antigen 1; LFA-1; immunoassay;	
KW	in vivo imaging; diagnosis; CD11a-associated disease.	
XX	Mus sp.	
OS	Homo sapiens.	
XX	WO9823761-A1.	
PN	04-JUN-1998.	
PD	20-OCT-1997;	97WO-US019041.
XX	27-NOV-1996;	96US-00757205.
PR	(GETH) GENENTECH INC.	
XX	Jardieu PM, Presta LG;	
PA	WPI; 1998-322737/28.	
XX	New humanised anti-CD11a antibody - used in immunoassays for CD11a, and	
DR	also to treat conditions such as immunological or inflammatory disease.	
XX	Claim 8; Page 2; 66pp; English.	
XX	AAW62014-16 represent complementarity determining regions of the light	
CC	chain variable region of humanised antibody MHM24F(ab)-8. The fragments	
CC	make a humanised anti-CD11a antibody that binds specifically	

CC to the human CD14 I domain (M6M2 epitope). CD14 refers to the alpha
CC subunit of lymphocyte function-associated antigen 1 (LFA-1) from any
CC mammal. The humanised anti-CD14 antibodies are used to determine
CC presence of CD14 in usual immunoassays or by *in vivo* imaging.
CC particularly for diagnosis of CD14-associated diseases (typically immune
CC responses and inflammation such as psoriasis, Crohn's disease, rheumatoid
CC arthritis, transplant rejection, leukaemia, etc
XX
SQ Sequence 9 AA;

Query Match	100.0%	Score 52	DB 2	Length 9
Best Local Similarity	100.0%	Pred. No.	2e+06	
Matches 9; Conservative	0	Mismatches	0	Indels 0; Gaps 0

QY	1	QQHNEYPLT	9
Db	1	QQHNEYPLT	9

RESULT 2
AAV82342
ID AAV82342 standard; peptide; 9 AA.

22-JUN-2000 (first entry)

KM Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant
 KM antitumour; antiviral; inflammation; immunological response; LFA-1;
 KM lymphocyte function-associated antigen-1; psoriasis; rthritis; eczema
 KM inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
 KM viral infection; transplant rejection; graft rejection.

OS	Homo sapiens.
OS	Mus sp.

PN US6037454-A.

14-MAR-2000

20-NOV-1997: 97US-00974899.

AA 27-NOV-1996; 96US-0031971P.
PR

AA
PA (GETH) GENENTECH INC.

PI Jardieu PM, Presta LG,

WPI; 2000-282241/24.

PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.

PT region complementarity determining regions.

PS Claim 4; COL 57-58; 38pp; English.

The present invention describes a humanised anti-CD11a antibody (Ab) that binds specifically to the human CD11a I-domain. The Ab has anti-inflammatory, immunosuppressant, antitumour and antiviral activities. The Ab blocks lymphocyte function-associated antigen (LFA-1) which is involved in leucocyte adhesion associated with inflammatory and immunological responses. The Ab are used: (i) optionally when coupled to a cytotoxin, to treat or prevent disorders mediated by lymphocyte function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis, inflammatory bowel disease, eczema, systemic lupus erythematosus, rheitis, leukaemia, viral infections and many others, also for inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for tumour pre-treatment; (iv) for delivery of enzymes that convert prodrugs to active anticancer agent; and (v) for affinity chromatography. The Ab retain about the same activity in adhesion and mixed lymphocyte response assays as the murine antibodies from which they are derived. The murine

CC anti-CD11a antibody MEM24 has IC50 0.09 nM for preventing adhesion
CC between Jurkat cells (expressing LFA-1) and normal epidermal
CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
CC The fully humanized version of MEM24 had IC50 0.13 nM. The present
CC sequence represents the light chain variable region CDR3 of the humanised
CC anti-CD11a Ab
CC
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
QY 1 QOHNEXPLT 9
Db 1 QOHNEXPLT 9
RESULT 3
ADG39003
ID ADG39003 standard; peptide; 9 AA.
AC ADG39003;
DT 26-FEB-2004 (first entry)
DE Humanised Mouse anti-CD11a antibody light chain variable region CDR3.
XX
XX Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
XX VL; cluster of differentiation 11a; mixed lymphocyte response assay;
XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; prodrug activating enzyme; humanised;
XX complementarity determining region; CDR.
XX
XX Synthetic.
XX Mus sp.
XX US2003207336-A1.
XX
XX 06-NOV-2003.
XX
XX 28-FEB-2001; 2001US-00795798.
XX
XX 27-NOV-1996; 96US-0031971P.
XX 20-NOV-1997; 97US-00974899.
XX 20-OCT-1999; 99US-00420745.
XX
XX (GETH) GENENTECH INC.
XX
XX Jardieu PM, Presta LG;
XX
XX WPI; 2004-051511/05.
XX
XX Humanized anti-CD11a antibody useful for treating lymphocyte function-
XX associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
XX ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
XX
XX Claim 8; SEQ ID NO 15; 43pp; English.
XX
XX The invention relates to a Humanised anti-cluster of differentiation
XX (CD11a) antibody having specificity to human CD11a I-domain or CD11a with
XX a kd value of not more than 1x10⁻⁸ M, or concentration for 50 %
XX inhibition (IC50) (nm) value of not more than 1 nM in mixed lymphocyte
XX response assay or for preventing adhesion of Jurkat cells to normal human
XX epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
XX -1. Also included are a kit comprising the antibody and instructions for
XX use to detect the CD11a protein, an isolated nucleic acid encoding the
XX antibody, a vector comprising the nucleic acid, a host cell comprising
XX the vector and producing the antibody by culturing the cell so that the
XX antibody is expressed. The antibody binds to epitope MEM24 on CD11a. The

CC antibody is useful for determining the presence of CD11a protein and for
CC treating lymphocyte function-associated antigen I mediated disorder such
CC as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
CC rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
CC and diabetes mellitus. The antibody is useful when conjugated to a
CC prodrug activating enzyme, or as an affinity purification agent. The
CC present sequence is a CDR (complementarity determining region) of the
CC light chain variable region (VL) of the humanised mouse anti-CD11a I
CC domain monoclonal antibody MEM24.
CC
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 52; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
QY 1 QOHNEXPLT 9
Db 1 QOHNEXPLT 9
RESULT 4
ADR03423
ID ADR03423 standard; peptide; 9 AA.
AC ADR03423;
DT 21-OCT-2004 (first entry)
DE Humanised MEM24 CDR-L3 peptide.
XX
XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
XX rhinovirus infection; inflammatory skin disease; psoriasis;
XX inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX adult respiratory distress syndrome; allergic disease; eczema; asthma;
XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
XX SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
XX tuberculosis; sarcoidosis; polyomyelitis;
XX chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
XX skin hypersensitivity disorder; poison ivy; poison oak;
XX B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
XX graft versus host disease; cancer; gene therapy;
XX murine anti-human CD11a monoclonal antibody; MEM24; variable light chain;
XX VL; murine; human; fusion protein; complementarity determining region;
XX CDR.
XX
XX Mus sp.
XX Homo sapiens.
XX Chimeric.
XX US2004146507-A1.
XX
XX 29-JUL-2004.
XX
XX 03-DEC-2003; 2003US-00727737.
XX
XX 27-NOV-1996; 96US-0031945P.
XX 20-NOV-1997; 97US-00975329.
XX
XX (GETH) GENENTECH INC.
XX
XX Jardieu PM, Presta LG;
XX
XX WPI; 2004-552640/53.
XX
XX New antibody mutant of a species-dependent antibody, useful for treating
XX PT and preventing infectious diseases, psoriasis, inflammatory bowel
XX PT disease, allergic conditions, autoimmune diseases, or cancer.
XX
XX Example; SEQ ID NO 60; 54pp; English.
XX
XX The present invention relates to an antibody mutant of a species-
XX dependent antibody with beneficial properties. The invention is useful

for treating and preventing infectious diseases such as human immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin disease such as psoriasis, inflammatory bowel diseases such as Crohn's disease and ulcerative colitis, adult respiratory distress syndrome, allergic diseases such as eczema and asthma, autoimmune diseases such as rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes mellitus, Reynaud's syndrome, immunological diseases such as tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary disease (COPD), CNS inflammatory disorder, skin hypersensitivity disorders such as poison ivy and poison oak, B-cell malignancies such as chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host disease and cancer. The invention is also useful in gene therapy. The present sequence is humanised murine anti-human CD11a monoclonal antibody (MHM24) CDR-1/3 peptide. This sequence is used in the exemplification of the invention.

Sequence 9 AA:

Query Match 100.0%; Score 52; DB 8; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOHNEYPIT 9
| | | | |
Db 1 QOHNEYPIT 9

RESULT 5
AEA62455
ID AEA62455 standard; protein; 107 AA.

AEA62455;

25-AUG-2005 (first entry)

Mouse 1B3 anti-C35 antibody kappa chain variable region.

C35 antigen; cell growth; cancer; cytostatic; apoptosis; immunotherapy; hyperproliferation; antibody; light chain variable region.

Mus sp.

WO2005055936-A2.

23-JUN-2005.

06-DEC-2004; 2004WO-US040573.

04-DEC-2003; 2003US-0526572P.

23-DEC-2003; 2003US-0531688P.

(VACC-) VACCINEX INC.

Evans BE, Paris MJ, Sahaarabudhe DM, Smith ES, Zauderer M;

WPI: 2005-458501/46.

N-PsDB; AEA62454.

Killing cancer cells, by administering apoptosis-inducing therapy and administering antibody specific for intracellular, cancer-associated protein other than C35, or antibody specific for C35.

Disclosure, SEQ ID NO 10, 255bp; English.

The invention relates to killing (M1) cancer cells, comprising administering an apoptosis-inducing therapy to cancer cells, and administering to the cells an antibody specific for an intracellular, cancer-associated protein, provided that the protein is not C35 antigen, where protein becomes exposed on the cell surface in cells undergoing apoptosis, where the antibody is conjugated to or complexed with a toxin. The non-C35 antigen protein is a prenylated protein. Also included are an isolated antibody (I) specific for C35 (chosen from an antibody comprising the VH region encoded by clone 1B3G, the VL region encoded by

clone 1B3K, the VH region encoded by clone 1F2G, the VL region encoded by clone 1F2K, the VH region encoded by clone H0609, the VL region encoded by clone L0010, an antibody comprising at least one of CDR1 or CDR2 of the VH region encoded by AEA62495, an antibody comprising at least one of CDR1 or CDR2 of the VH region encoded by AEA62499, an antibody comprising at least one of CDR1, CDR2, or CDR3 of the VL region encoded by AEA62497, a chimeric antibody, or a humanized antibody, a polynucleotide encoding the antibody, a vector comprising the polynucleotide, a host cell comprising the vector and a composition comprising the antibody and a carrier. The method is useful for killing cancer cells in a mammal preferably human in need of eradication of smaller tumors and/or micrometastases, or in need of cancer treatment for C35-associated cancer chosen from breast cancer, ovarian cancer, bladder cancer, lung cancer, prostate cancer, pancreatic cancer, colon cancer, melanoma and other hyperproliferative disorders. The antibody is useful for detecting, diagnosing or monitoring C35-associated cancers. The antibody comprises a chimeric antibody comprising human immunoglobulin constant regions fused to the variable regions of mouse anti-35 antibodies (named 1F2, 1B3, MAb 165 and MAb 171). The present sequence represents a kappa chain variable region of a mouse anti-C35 antibody.

Sequence 107 AA:

Query Match 100.0%; Score 52; DB 9; Length 107;

Best Local Similarity 100.0%; Pred. No. 0.053; Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOHNEYPIT 9
| | | | |
Db 89 QOHNEYPIT 97

RESULT 6
AAM62017
ID AAM62017 standard; peptide; 108 AA.

AAM62017;

01-OCT-1998 (first entry)

Light chain variable region of humanised anti-CD11a antibody.

Complementarily determining region; light chain variable region; humanised antibody; MHM24F(ab)-8; anti-CD11a antibody;

human CD11a I domain; MHM24 epitope; alpha subunit;

lymphocyte function-associated antigen 1; LFA-1; immunoassay; in vivo imaging; diagnosis; CD11a-associated disease.

Mus sp.

Homo sapiens.

WO9823761-A1.

04-JUN-1998.

20-OCT-1997; 97WO-US019041.

27-NOV-1996; 96US-00757205.

(GETH) GENENTECH INC.

Jardieu PM, Presta IG;

WPI: 1998-322737/28.

New humanised anti-CD11a antibody - used in immunoassays for CD11a, and also to treat conditions such as immunological or inflammatory disease.

Claim 9; Page 48; 66pp; English.

The present sequence represents the light chain variable region of a humanised anti-CD11a antibody that binds specifically to the human CD11a I domain (MHM24 epitope). CD11a refers to the alpha subunit of lymphocyte

CC function-associated antigen 1 (LFA-1) from any mammal. The humanised anti-
 CC CD11a antibodies are used to determine presence of CD11a in usual
 CC immunosays or by in vivo imaging, particularly for diagnosis of CD11a-
 CC associated diseases (typically immune responses and inflammation such as
 CC psoriasis, Crohn's disease, rheumatoid arthritis, transplant rejection,
 CC leukaemia, etc

XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 52; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEYPPLT 9
 |||||
 DB 89 OOHNEYPPLT 97

RESULT 7

AAW63528
 ID AAW63528 standard; protein; 108 AA.

XX
 AC AAW63528;

XX
 DT 06-OCT-1998 (first entry)

XX
 DE Murine MEM24 light chain.

XX Antibody mutant production; species-dependent antibody; malignancy;
 KW infection; haematopoesis; lymphocyte function-associated antigen-1;
 KW intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 KW autoimmune disease; transplant rejection; tumour cell invasion;
 KW human immune deficiency virus infection; light chain.

XX
 OS Mus sp.

XX
 PN WO9823746-A1.

XX
 PD 04-JUN-1998.

XX
 PF 29-OCT-1997; 97WO-US020169.

XX
 PR 27-NOV-1996; 96US-00756150.

XX
 PA (GETH) GENENTECH INC.

XX
 PI Jardieu PM, Presta LG;

XX
 DR WPI; 1998-322726/28.

XX
 PT Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD11a.

XX
 PS Disclosure; Page 52-53; 71pp; English.

XX This sequence represents the light chain of the murine antibody MEM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use

XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 52; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEYPPLT 9
 |||||
 DB 89 OOHNEYPPLT 97

RESULT 8

AAW63529
 ID AAW63529 standard; protein; 108 AA.

XX
 AC AAW63529;

XX
 DT 06-OCT-1998 (first entry)

XX
 DE Humanised MEM24 light chain.

XX Antibody mutant production; species-dependent antibody; malignancy;
 KW infection; haematopoesis; lymphocyte function-associated antigen-1;
 KW intercellular adhesion molecule-1; inflammatory disease; CD11a; therapy;
 KW autoimmune disease; transplant rejection; tumour cell invasion;
 KW human immune deficiency virus infection; light chain.

XX
 OS Synthetic.

XX
 PN WO9823746-A1.

XX
 PD 04-JUN-1998.

XX
 PF 29-OCT-1997; 97WO-US020169.

XX
 PR 27-NOV-1996; 96US-00756150.

XX
 PA (GETH) GENENTECH INC.

XX
 PI Jardieu PM, Presta LG;

XX
 DR WPI; 1998-322726/28.

XX
 PT Mutants of species-dependent antibodies with affinity for non-human
 PT mammalian antigen - greater than for parent antibody, particularly used
 PT for pre-clinical trial(s) in rhesus monkey(s) of therapeutic antibodies
 PT directed against CD11a.

XX
 PS Disclosure; Page 53; 71pp; English.

XX This sequence represents the light chain of the humanised antibody MEM24,
 CC and was used to produce a mutant of the invention. The mutants are of a
 CC species-dependent antibody (Ab), and have an amino acid substitution in a
 CC variable region of the Ab, and binding affinity for an antigen (Ag) from
 CC a non-human mammal at least 10 times stronger than for the wild type Ab
 CC against the Ag. The mutant antibodies are particularly intended for
 CC administration to a non-human mammal in preclinical studies (e.g. of
 CC infection, immunity, haematopoesis or transplantation). They can also be
 CC used diagnostically (to identify specific proteins) or therapeutically,
 CC e.g. where directed against CD11a (lymphocyte function-associated antigen
 CC -1) or intercellular adhesion molecule-1 against a wide variety of
 CC inflammatory or autoimmune diseases, malignancies, transplant rejection,
 CC human immune deficiency virus infection and tumour cell invasion.
 CC Conversion to the mutant form allows useful antibodies to be produced
 CC from antibodies which normally have affinity for non-human analogues of
 CC the Ag too low to be of any use

XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 52; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEYP.LT 9
Db 89 OOHNEYP.LT 97

RESULT 9
AAV82344
ID AAV82344 standard; protein; 108 AA.

AC AAV82344;
DT 22-JUN-2000 (first entry)

DE Murine MHM24 light chain amino acid sequence SEQ ID NO:1.

XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
KW antitumour; antiviral; inflammation; immunological response; LFA-1;
KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
KW viral infection; transplant rejection; graft rejection.

OS Mus sp.

PN US6037454-A.

PD 14-MAR-2000.

PF 20-NOV-1997; 97US-00974899.

PR 27-NOV-1996; 96US-0031971P.

PA (GETH) GENENTECH INC.

PI Jardieu PM, Presta LG;

DR WPI; 2000-282241/24.

PT New humanised anti-CD11a antibody, useful for treating or preventing e.g.
PT inflammation and transplant rejection, contains human heavy variable
PT region complementarily determining regions.

PS Example; Fig 1; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that
CC binds specifically to the human CD11a I-domain. The Ab has anti-
CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
CC involved in leucocyte adhesion associated with inflammatory and
CC immunological responses. The Ab are used: (i) optionally when coupled to
CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
CC rhinitis, leukaemia, viral infections and many others, also for
CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
CC to active anticancer agent; and (v) for affinity chromatography. The Ab
CC retain about the same activity in adhesion and mixed lymphocyte response
CC assays as the murine antibodies from which they are derived. The murine
CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
CC between Jurkat cells (expressing LFA-1) and normal epidermal
CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
CC sequence represents the amino acid sequence of murine MHM24 light chain,
CC which is used in the exemplification of the present invention

XX Sequence 108 AA;

Query Match 100.0%; Score 52; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEYP.LT 9

Db 89 OOHNEYP.LT 97

RESULT 10
AAV82343
ID AAV82343 standard; protein; 108 AA.

AC AAV82343;
DT 22-JUN-2000 (first entry)

DE Humanised anti-CD11a antibody light chain variable region SEQ ID NO:2.

XX Humanised; anti-CD11a; antibody; anti-inflammatory; immunosuppressant;
KW antitumour; antiviral; inflammation; immunological response; LFA-1;
KW lymphocyte function-associated antigen-1; psoriasis; rhinitis; eczema;
KW inflammatory bowel disease; systemic lupus erythematosus; leukaemia;
KW viral infection; transplant rejection; graft rejection.

OS Homo sapiens.

PN US6037454-A.

PD 14-MAR-2000.

PF 20-NOV-1997; 97US-00974899.

PR 27-NOV-1996; 96US-0031971P.

PA (GETH) GENENTECH INC.

PI Jardieu PM, Presta LG;

DR WPI; 2000-282241/24.

PT New humanized anti-CD11a antibody, useful for treating or preventing e.g.
PT inflammation and transplant rejection, contains human heavy variable
PT region complementarily determining regions.

PS Claim 5; Fig 1; 38pp; English.

XX The present invention describes a humanised anti-CD11a antibody (Ab) that
CC binds specifically to the human CD11a I-domain. The Ab has anti-
CC inflammatory, immunosuppressant, antitumour and antiviral activities. The
CC Ab blocks lymphocyte function-associated antigen (LFA-1) which is
CC involved in leucocyte adhesion associated with inflammatory and
CC immunological responses. The Ab are used: (i) optionally when coupled to
CC a cytotoxin, to treat or prevent disorders mediated by lymphocyte
CC function-associated antigen-1 (LFA-1; CD11a/CD18), e.g. psoriasis,
CC inflammatory bowel disease, eczema, systemic lupus erythematosus,
CC rhinitis, leukaemia, viral infections and many others, also for
CC inhibiting graft rejection; (ii) when labeled, to detect CD11a; (iii) for
CC tumour pretreatment; (iv) for delivery of enzymes that convert prodrugs
CC to active anticancer agent; and (v) for affinity chromatography. The Ab
CC retain about the same activity in adhesion and mixed lymphocyte response
CC assays as the murine antibodies from which they are derived. The murine
CC anti-CD11a antibody MHM24 has IC50 0.09 nM for preventing adhesion
CC between Jurkat cells (expressing LFA-1) and normal epidermal
CC keratinocytes that express ICAM-1 (intracellular adhesion molecule-1).
CC The fully humanized version of MHM24 had IC50 0.13 nM. The present
CC sequence represents the light chain variable region of the humanised anti-
CC -CD11a Ab

XX Sequence 108 AA;

Query Match 100.0%; Score 52; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEYP.LT 9

Db 89 QQHNEYPLT 97

RESULT 11
ADG38989
ID ADG38989 standard; protein; 108 AA.
AC ADG38989;
DT 26-FEB-2004 (first entry)
XX Mouse anti-CD11a antibody light chain variable region.
XX
XX Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
XX VL; cluster of differentiation 11a; mixed lymphocyte response assay;
XX Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
XX ICAM-1; lymphocyte function-associated antigen 1 mediated disorder;
XX psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
XX rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; prodrug activating enzyme.
XX Mus sp.
XX OS
XX US2003207336-A1.
XX
XX 06-NOV-2003.
XX
XX 28-FEB-2001; 2001US-00795798.
XX PF
XX 27-NOV-1996; 96US-0031971P.
XX PR 20-NOV-1997; 97US-00974899.
XX PR 20-OCT-1999; 99US-00420745.
XX PA
XX (GETH) GENENTECH INC.
XX
XX Jardiou PM, Presta LG;
XX WPI; 2004-051511/05.
XX
XX Humanized anti-CD11a antibody useful for treating lymphocyte function-
XX associated antigen mediated disorder e.g. psoriasis, Crohn's disease,
XX ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.
XX
XX Example; SEQ ID NO 1; 43pp; English.
XX
XX The invention relates to a Humanised anti-cluster of differentiation
XX (CD)11a antibody having specificity to human CD11a I-domain or CD11a with
XX a kd value of not more than 1x10-8 M, or concentration for 50 %
XX inhibition (IC50) (mM) value of not more than 1 nM in mixed lymphocyte
XX response assay or for preventing adhesion of Jurkat cells to normal human
XX epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)
XX -1. Also included are a kit comprising the antibody and instructions for
XX use to detect the CD11a protein, an isolated nucleic acid encoding the
XX antibody, a vector comprising the nucleic acid, a host cell comprising
XX the vector and producing the antibody by culturing the cell so that the
XX antibody is expressed. The antibody binds to epitope MWM24 on CD11a. The
XX antibody is useful for determining the presence of CD11a protein and for
XX treating lymphocyte function-associated antigen 1 mediated disorder such
XX as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma,
XX rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis
XX and diabetes mellitus. The antibody is useful when conjugated to a
XX prodrug activating enzyme, or as an affinity purification agent. The
XX present sequence is the light chain variable region (VL) of the wild-type
XX mouse anti-CD11a I domain monoclonal antibody MWM24.
XX
XX Sequence 108 AA;
XX
XX Query Match 100.0%; Score 52; DB 8; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 89 QQHNEYPLT 97

RESULT 12

ID ADG38990
ADG38990 standard; protein, 108 AA.

XX DT 26-FEB-2004 (first entry)

XX Humanised Mouse anti-CD11a antibody light chain variable region.

XX MM Mouse; CD11a; I-domain; monoclonal antibody; light chain variable region;
KM VL; cluster of differentiation 11a; mixed lymphocyte response assay;
KM Jurkat cell; epidermal keratinocyte; intercellular adhesion molecule;
KM ICMV; lymphocyte function-associated antigen 1 mediated disorder;
KM psoriasis; Crohn's disease; ulcerative colitis; dermatitis; asthma;
KM rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KM diabetes mellitus; prodrug activating enzyme; humanised.

XX OS Synthetic.
OS Mus sp.

PV US2003207336-A1.

PM 06-NOV-2003.

PF 28-FEB-2001; 2001US-00795798.

PR 27-NOV-1996; 96US-0031971P.
PR 20-NOV-1997; 97US-00974899.
PR 20-OCT-1999; 99US-00420745.

PA (GETH) GENENTECH INC.

PI Jardieu PM, Presta LG;

DR WPI; 2004-051511/05.

XX Humanized anti-CD11a antibody useful for treating lymphocyte function-associated antigen mediated disorder e.g. psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis.

XX Claim 9; SEQ ID NO 2; 43pp; English.

PS The invention relates to a Humanised anti-cluster of differentiation (CD11a) antibody having specificity to human CD11a I-domain or CD11a with a kd value of not more than 1x10⁻⁸ M, or concentration for 50 % inhibition (IC50) (nM) value of not more than 1 nM in mixed lymphocyte response assay or for preventing adhesion of Jurkat cells to normal human epidermal keratinocytes expressing intercellular adhesion molecule (ICAM)-1. Also included are a kit comprising the antibody and instructions for use to detect the CD11a protein, an isolated nucleic acid encoding the antibody, a vector comprising the nucleic acid, a host cell comprising the vector and producing the antibody by culturing the cell so that the antibody is expressed. The antibody binds to epitope MEM24 on CD11a. The antibody is useful for determining the presence of CD11a protein and for treating lymphocyte function-associated antigen 1 mediated disorder such as psoriasis, Crohn's disease, ulcerative colitis, dermatitis, asthma, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis and diabetes mellitus. The antibody is useful when conjugated to a prodrug activating enzyme, or as an affinity purification agent. The present sequence is the light chain variable region (VL) of the humanised mouse anti-CD11a I domain monoclonal antibody MEM24.

SQ Sequence 108 AA;

Query Match 100.0%; Score 52; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

1 QQHNEYPLT 9

Db 89 QOHNEXPLT 97

RESULT 13
ADRO3365

ID ADRO3365 standard; protein; 108 AA.

AC ADRO3365;

DT 21-OCT-2004 (first entry)

DE Humanised MEM24 F(ab)-8 antibody variable light chain protein.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
XX rhinovirus infection; inflammatory skin disease; psoriasis;
XX inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX adult respiratory distress syndrome; allergic disease; eczema; asthma;
XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
XX SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
XX tuberculosis; sarcoidosis; polymyositis;
XX chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
XX skin hypersensitivity disorder; poison ivy; poison oak;
XX B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
XX graft versus host disease; cancer; gene therapy;
XX murine anti-human CD11a monoclonal antibody; MEM24; variable light chain;
XX VL; murine; human; fusion protein.

OS Mus sp.
OS Homo sapiens.
OS Chimeric.

XX US2004146507-A1.

XX 29-JUL-2004.

XX 03-DEC-2003; 2003US-00727737.

XX 27-NOV-1996; 96US-0031945P.

XX 20-NOV-1997; 97US-00975329.

XX (GETH) GENENTECH INC.

XX Jardiou PM, Presta LG;

XX WPI; 2004-552640/53.

XX New antibody mutant of a species-dependent antibody, useful for treating
XX PT and preventing infectious diseases, psoriasis, inflammatory bowel
XX PT disease, allergic conditions, autoimmune diseases, or cancer.

XX Example; SEQ ID NO 2; 54pp; English.

XX The present invention relates to an antibody mutant of a species-
XX CC dependent antibody with beneficial properties. The invention is useful
XX CC for treating and preventing infectious diseases such as human
XX CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
XX CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
XX CC disease and ulcerative colitis, adult respiratory distress syndrome,
XX CC allergic diseases such as eczema and asthma, autoimmune diseases such as
XX CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
XX CC mellitus, Reynaud's syndrome, immunological diseases such as
XX CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
XX CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
XX CC disorders such as poison ivy and poison oak, B-cell malignancies such as
XX CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
XX CC disease and cancer. The invention is also useful in gene therapy. The
XX CC present sequence is humanised murine anti-human CD11a monoclonal antibody
XX CC (MEM24) F(ab)-8 variable light chain protein. This sequence is used in
XX CC the exemplification of the invention.

XX Sequence 108 AA;

Query Match 100.0%; Score 52; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOHNEXPLT 9

Db 89 QOHNEXPLT 97

RESULT 14
ADRO3364

ID ADRO3364 standard; protein; 108 AA.

AC ADRO3364;

DT 21-OCT-2004 (first entry)

DE Murine MEM24 antibody variable light chain protein.

XX CD11a antibody; human immunodeficiency virus infection; HIV infection;
XX rhinovirus infection; inflammatory skin disease; psoriasis;
XX inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX adult respiratory distress syndrome; allergic disease; eczema; asthma;
XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
XX SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
XX tuberculosis; sarcoidosis; polymyositis;
XX chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
XX skin hypersensitivity disorder; poison ivy; poison oak;
XX B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
XX graft versus host disease; cancer; gene therapy;
XX murine anti-human CD11a monoclonal antibody; MEM24; variable light chain;
XX VL; murine.

OS Mus sp.

XX US2004146507-A1.

XX 29-JUL-2004.

XX 03-DEC-2003; 2003US-00727737.

XX 27-NOV-1996; 96US-0031945P.

XX 20-NOV-1997; 97US-00975329.

XX (GETH) GENENTECH INC.

XX Jardiou PM, Presta LG;

XX WPI; 2004-552640/53.

XX New antibody mutant of a species-dependent antibody, useful for treating
XX PT and preventing infectious diseases, psoriasis, inflammatory bowel
XX PT disease, allergic conditions, autoimmune diseases, or cancer.

XX Example; SEQ ID NO 1; 54pp; English.

XX The present invention relates to an antibody mutant of a species-
XX CC dependent antibody with beneficial properties. The invention is useful
XX CC for treating and preventing infectious diseases such as human
XX CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
XX CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
XX CC disease and ulcerative colitis, adult respiratory distress syndrome,
XX CC allergic diseases such as eczema and asthma, autoimmune diseases such as
XX CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
XX CC mellitus, Reynaud's syndrome, immunological diseases such as
XX CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
XX CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
XX CC disorders such as poison ivy and poison oak, B-cell malignancies such as
XX CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
XX CC disease and cancer. The invention is also useful in gene therapy. The
XX CC present sequence is murine anti-human CD11a monoclonal antibody (MEM24)
XX CC variable light chain protein. This sequence is used in the
XX CC exemplification of the invention.

XX SQ Sequence 108 AA;
Query Match 100.0%; Score 52; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 OOHNEYPPLT 9
|||
DB 89 OOHNEYPPLT 97
RESULT 15
ADM38457
ID ADM38457 standard; protein; 108 AA.
XX AC ADM38457;
XX DT 24-MAR-2005 (first entry)
XX DE CD1a light chain variable region #2.
XX KW monoclonal antibody; CD1a; light-chain variable region;
XX KM heavy-chain variable region.
XX OS Homo sapiens.
XX PN CN1439651-A.
XX PD 03-SEP-2003.
XX PF 20-FEB-2002; 2002CN-00110866.
XX PR 20-FEB-2002; 2002CN-00110866.
XX (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
XX PI Wang H, Wang J;
XX DR WPI; 2004-169719/17.
XX PT Recombinant human CD1a monoclonal antibody and its preparation and
XX medicinal composition.
XX PS Claim 1; Page 14; 16pp; Chinese.
XX CC The present invention relates to a recombinant monoclonal antibody for
XX human CD1a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
XX No.5 in light-chain variable region and the amino acid sequence shown by
XX SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
XX bioactivity and the expression in host cell are greatly increased. The
XX DNA molecule for coding the antibody, its preparation process and the
XX medicinal composition containing it are also disclosed. The present
XX sequence represents a light chain variable region of human CD1a.
XX SQ Sequence 108 AA;
Query Match 100.0%; Score 52; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 OOHNEYPPLT 9
|||
DB 89 OOHNEYPPLT 97
RESULT 16
ADX80645
ID ADX80645 standard; protein; 108 AA.
XX AC ADX80645;
XX DT 05-MAY-2005 (first entry)

XX DE Humanized CD1a variable light chain amino acid sequence, seq id 5.
XX KW Protein purification; leaching; protein A affinity chromatography; CD1a;
XX KM antibody.
XX OS Synthetic.
XX PN US2005038231-A1.
XX PD 17-FEB-2005.
XX PF 24-JUN-2004; 2004US-00877532.
XX PR 28-JUL-2003; 2003US-0490500P.
XX (GETH) GENENTECH INC.
XX PA Fahrner RL, Laverdiere A, McDonald PJ, O'leary RM;
XX PI WPI; 2005-172327/18.
XX DR
XX PT Purifying a protein, e.g. antibody or immunoadhesin, comprises reducing
XX the temperature of a composition subjected to protein A affinity
XX chromatography to 3-20 degrees C, where protein A leaching is reduced.
XX PS Disclosure; SEQ ID NO 5; 27pp; English.
XX CC The invention relates to a method of purifying a protein which comprises
XX a CH2/CH3 region by protein A affinity chromatography. The method
XX involves reducing the temperature of a composition comprising the protein
XX and one or more impurities subjected to protein A affinity chromatography
XX to 3-20 degrees Celsius, where protein A leaching is reduced. Preferably
XX the protein is antibody. The antibody is selected from Trastuzumab,
XX humanized 2C4, humanized CD1a antibody, and humanized VEGF antibody.
XX Preferably, the antibody binds HER2 antigen, where the antibody is
XX Trastuzumab or humanized 2C4. The protein is an immunoadhesin,
XX specifically a TNF receptor immunoadhesin. The methods are useful for
XX purifying a protein, which comprises a CH2/CH3 region by protein A
XX affinity chromatography and for reducing leaching of protein A during
XX protein A affinity chromatography. The current sequence represents the
XX variable light chain amino acid sequence of CD1a.
XX SQ Sequence 108 AA;
Query Match 100.0%; Score 52; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 OOHNEYPPLT 9
|||
DB 89 OOHNEYPPLT 97
RESULT 17
AAV29449
ID AAV29449 standard; protein; 109 AA.
XX AC AAV29449;
XX DT 05-OCT-1999 (first entry)
XX DE Human light chain kappa-I consensus framework.
XX KW Antibody; humanized; anti-IL-8 monoclonal antibody; interleukin 8;
XX diagnosis; inflammatory disorder; conjugate; immunoglobulin;
XX fusion protein.
XX OS Homo sapiens.
XX PN WO9937779-A1.
XX PD 29-JUL-1999.

XX 19-JAN-1999; 99WO-US001081.
PR 22-JAN-1998; 98US-00012116.
PR 20-FEB-1998; 98WO-US003337.
PR 24-JUL-1998; 98US-00121952.
PR 24-JUL-1998; 98US-00122513.
XX (GETH) GENENTECH INC.
XX Hseel V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z, Zapata GA;
XX WPI, 1999-469134/39.
XX WPI, 1999-469134/39.
XX New conjugates of nonproteinaceous polymers with antibody fragments, used
PT for treating inflammatory disorders.
XX Disclosure; Fig 29; 360pp; English.
XX The present invention describes a novel conjugate having one or more
CC antibody fragments covalently attached to one or more nonproteinaceous
CC polymer molecules, where the apparent size of the conjugate is at least
CC about 500 kDa. Conjugates of antibody fragments which bind the human
CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for
CC treating inflammatory disorders e.g. acute lung injury, ischemic
CC reperfusion disorder, and autoimmune diseases. They can also be used for
CC treating e.g. inflammatory skin diseases including psoriasis and atopic
CC dermatitis, systemic sclerosis and sclerodermis, and asthmatic diseases.
CC The conjugates can also be used as reagents in an animal model system for
CC in vivo study of the biological functions of the antigen recognised by
CC the conjugate. The present sequence represents the human light chain
CC kappa-I consensus framework from the present invention
XX SQ Sequence 109 AA;

Query Match 100.0%; Score 52; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. NO. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OQHNEYPIT 9
DB 90 OQHNEYPIT 98

RESULT 18

AA77752
ID AA77752 standard; protein; 109 AA.

AC AA77752;

DT 06-JUN-2000 (first entry)

XX Human light chain k1 consensus framework.

XX Interleukin-8; IL-8; monoclonal antibody; Mab; anti-IL-8; 6G4.2.5V1IN35A;
KW inflammatory disorder; adult respiratory distress syndrome; chimeric;
KW affinity purification; 6G4.2.5.

XX Homo sapiens.

XX US6025158-A.

XX 15-FEB-2000.

XX 20-FEB-1998; 98US-00027449.

XX 21-FEB-1997; 97US-0038664P.
PR 22-JAN-1998; 98US-0074330P.

XX (GETH) GENENTECH INC.

XX Presta LG, Leong SR, Gonzalez TN;
XX

DR WPI; 2000-181809/16.
XX New nucleic acid molecule encodes a polypeptide which is an anti-
PT interleukin-8 monoclonal antibody or antibody fragment useful for the
PT production of anti-interleukin-8 monoclonal antibodies or fragments.
XX Example; Fig 29; 188pp; English.

XX The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
CC (Mab). The anti-IL-8 Mab comprises a sequence containing the CDRs
CC (complementarity determining regions) of the humanized anti-IL-8
CC 6G4.2.5V1IN35A light chain; and amino acids 24-253 of the humanized anti-
CC IL-8 6G4.2.5V1IN35A heavy chain. The anti-IL-8 Mabs and fragments can be
CC used in diagnosis, for affinity purification of IL-8 from recombinant
CC cell culture or natural sources and for the treatment of inflammatory
CC disorders e.g. adult respiratory distress syndrome. Nucleic acids
CC encoding the anti-IL-8 Mab can be associated in a vector with another
CC gene encoding another protein or protein fragment to produce a fusion
CC protein which can make isolation and/or purification of the protein an
CC easier process
XX SQ Sequence 109 AA;

Query Match 100.0%; Score 52; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. NO. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OQHNEYPIT 9
DB 90 OQHNEYPIT 98

RESULT 19

AAB30309
ID AAB30309 standard; protein; 109 AA.

AC AAB30309;

DT 12-FEB-2001 (first entry)

XX Human light chain kappa consensus framework SEQ ID NO: 47.

XX Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;
KW adult respiratory distress syndrome; multiple organ failure;
KW bacterial pneumonia; inflammatory bowel disease.

XX Homo sapiens.

XX US6133426-A.

XX 17-OCT-2000.

XX 20-FEB-1998; 98US-00026985.

XX 21-FEB-1997; 97US-0038664P.
PR 22-JAN-1998; 98US-0074330P.

XX (GETH) GENENTECH INC.

XX Presta LG, Leong SR, Gonzalez TN;
XX

XX WPI; 2000-686027/67.

XX Humanized anti-interleukin 8 monoclonal antibody variant useful for
PT treating inflammatory disorders, such as adult respiratory distress
PT syndrome, hypovolemic shock and ulcerative colitis.
XX

XX Disclosure; Col 161-162; 240pp; English.

XX The present invention provides a number of humanised monoclonal anti-IL-8
CC antibodies which can be used in the diagnosis and treatment of
CC inflammatory disorders, including adult respiratory distress syndrome,
CC septic shock, multiple organ failure, bacterial pneumonia and

CC inflammatory bowel disease. The present sequence comprises one of the
 CC antibodies of the invention
 XX

SO Sequence 109 AA;

Query Match 100.0%; Score 52; DB 3; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQHNEYPLT 9
 |||||
 DB 90 QQHNEYPLT 98

RESULT 20

ABU13786
 ID ABU13786 standard; protein; 109 AA.

XX ABU13786;

DT 25-FEB-2003 (first entry)

DE Human light chain kappa consensus framework sequence.

XX Antibody; monoclonal antibody; 5.12.14; 6G4.2.5; interleukin-8; mAb;
 KW antiinflammatory; respiratory; acute lung injury; polyethylene glycol;
 KW PEG; lung injury; adult respiratory distress syndrome; ARDS; asthma;
 KW inflammatory disease; inflammatory bowel disease; psoriasis; sclerosis;
 KW ischaemic reperfusion disorder; stroke; multiple sclerosis; meningitis;
 KW osteoarthritis; septic shock; autoimmune disease; rheumatoid arthritis;
 KW alcoholic hepatitis; cystic fibrosis; human.

OS Homo sapiens.

PN US6468532-B1.

PD 22-OCT-2002.

PF 20-JAN-1999; 98US-00234340.

XX 22-JAN-1998; 98US-0074330P.

PR 20-FEB-1998; 98US-0075467P.

PR 24-JUL-1998; 98US-0094003P.

PR 24-JUL-1998; 98US-0094013P.

XX (GETH) GENENTECH INC.

PI Hsai V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;

XX WPI; 2003-138230/13.

PT Treating acute lung injury in mammal by administering to mammal a 500 kD

XX conjugate comprising F(ab')₂ antibody fragment that binds to human

XX interleukin-8, covalently attached to one or two polyethylene glycol

XX molecules.

PS Example G; Fig 29; 259pp; English.

XX The invention relates to treating acute lung injury in a mammal,
 CC comprising administering to the mammal an effective amount of a conjugate
 CC of a single antibody fragment covalently attached to 1 or 2 polyethylene
 CC glycol (PEG) molecules, where the antibody fragment is a F(ab')₂
 CC comprising: (a) first chain that is either a light chain or a heavy chain
 CC ; (b) a first opposite chain that is either a heavy chain opposite the
 CC first light chain or a light chain opposite the first heavy chain; (c) a
 CC second chain that is either a light chain or a heavy chain; and (d) a
 CC second opposite chain that is either a heavy chain opposite the second
 CC light chain or a light chain opposite the second heavy chain; where every
 CC PEG molecule is covalently attached to a first cysteine residue in the
 CC first or second chain that would ordinarily form a disulphide bridge with
 CC a second cysteine residue in the first or second opposite chain, where
 CC the disulphide bridge is avoided by substitution of another amino acid
 CC residue for the second cysteine residue in the first or second opposite

CC chain, where the F(ab')₂ comprises an antigen binding site that binds to
 CC human interleukin-8 (IL-8), and where the apparent size of the conjugate
 CC is at least about 500 kD. The antigen binding sites may be derived from
 CC murine monoclonal antibodies 5.12.14 or 6G4.2.5. The method is useful for
 CC treating lung injury, including adult respiratory distress syndrome
 CC (ARDS) in a mammal and inflammatory diseases (such as asthma,
 CC inflammatory bowel disease, psoriasis and sclerosis), ischaemic
 CC reperfusion disorder, stroke, multiple sclerosis, meningitis,
 CC osteoarthritis, septic shock, autoimmune disease (e.g. rheumatoid
 CC arthritis), alcoholic hepatitis, cystic fibrosis and many other diseases
 CC and disorders listed in the specification. The present sequence
 CC represents a human antibody sequence included for comparison with the
 CC mouse humanised monoclonal antibody sequences

SO Sequence 109 AA;

Query Match 100.0%; Score 52; DB 6; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQHNEYPLT 9
 |||||
 DB 90 QQHNEYPLT 98

RESULT 21

ABUS9499
 ID ABUS9499 standard; protein; 109 AA.

XX ABUS9499;

DT 22-APR-2003 (first entry)

DE Human light chain kappa consensus framework.

XX Interleukin-8; IL-8; humanised antibody; antibody; 5.12.14; 6G4.2.5;
 KW inflammatory disorder; psoriasis; atopic dermatitis; sclerosis;
 KW systemic scleroderma; inflammatory bowel disease; Crohn's disease;
 KW ulcerative colitis; ischaemia; reperfusion; myocardial infarction;
 KW stroke; adult respiratory distress syndrome; rheumatoid arthritis;
 KW alcoholic hepatitis; acute lung injury; asthma; cerebral oedema;
 KW myocardial ischaemia; cranial trauma; asphyxia; Behcet's disease;
 KW dermatomyositis; polymyositis; multiple sclerosis; meningitis;
 KW encephalitis; uveitis; osteoarthritis; lupus nephritis; trauma;
 KW autoimmune disease; Sjogren's syndrome; vasculitis; septicemia;
 KW central nervous system inflammatory disorder; sepsis; sarcoidosis;
 KW multiple organ injury syndrome; bacterial pneumonia; glomerulonephritis;
 KW inflammation of the lung; human.

OS Homo sapiens.

PN US6458355-B1.

PD 01-OCT-2002.

PF 24-JUL-1998; 98US-00121952.

XX 22-JAN-1998; 98US-0074330P.

PR 20-FEB-1998; 98US-0075467P.

XX (GETH) GENENTECH INC.

PI Hsai V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;

XX WPI; 2003-208759/20.

PT Treating inflammatory disorder in a mammal, involves administering a

XX conjugate of polyethylene glycol and a single antibody fragment

XX comprising antigen binding site that binds to human interleukin-8, to

XX mammal.

PS Example 3G; Fig 29; 259pp; English.

CC The invention relates to treating an inflammatory disorder in a mammal,
CC comprising administering to the mammal, an effective amount of a
CC conjugate of a single antibody fragment (e.g. the heavy or light chains
CC of the humanised mouse monoclonal antibodies 5.112.14 and 664.2.5, which
CC also have their intramolecular disulphide bridges ablated by substitution
CC mutations) covalently attached to one or two polyethylene glycol (PEG)
CC molecules. The antibodies comprise an antigen binding site that binds to
CC human interleukin-8 (IL-8), and the apparent size of the conjugate is at
CC least 500 kDa. The method is useful for treating an inflammatory disorder
CC e.g. ischaemic reperfusion disorder such as surgical tissue reperfusion
CC injury, myocardial ischaemia or myocardial infarction, or hypovolemic
CC shock, in a mammal e.g. human. The method is useful for treating
CC inflammatory disorders including psoriasis, atopic dermatitis, systemic
CC scleroderma and sclerosis, responses associated with inflammatory bowel
CC disease, ischaemic reperfusion disorders, myocardial ischaemic
CC conditions, cerebral oedema secondary to stroke, cranial trauma,
CC asphyxia, adult respiratory distress syndrome, acute lung injury,
CC Behcet's disease, dermatomyositis, polymyositis, multiple sclerosis,
CC dermatitis, meningitis, encephalitis, uveitis, osteoarthritis, lupus
CC nephritis, autoimmune diseases such as rheumatoid arthritis, Sjogren's
CC syndrome, vasculitis, central nervous system inflammatory disorder,
CC multiple organ injury syndrome secondary to septicemia or trauma,
CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex
CC mediated diseases including glomerulonephritis, sepsis, sarcoidosis,
CC immunopathologic responses to tissue/organ transplantation, inflammations
CC of the lung, inflammatory bowel disease such as ulcerative colitis and
CC asthma. The present sequence represents the light or heavy chain of human
CC IgG, used to design the humanising mutations in the two mouse antibodies
CC
SQ Sequence 109 AA;

Query Match 100.0%; Score 52; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OQHNEYPLT 9
| | | | | | | | | |
DB 90 OQHNEYPLT 98

RESULT 22

AAE39082
ID AAE39082 standard; protein; 109 AA.

AC AAE39082;

DT 18-DEC-2003 (first entry)

DE Human light chain kappa consensus framework protein.

XX Interleukin-8 mediated disease; adult respiratory distress syndrome; IL;
XX bacterial pneumonia; inflammatory bowel disease; hypovolemic shock; ARDS;
XX ulcerative colitis; ischaemic reperfusion injury; myocardial infarction;
XX acute lung injury; inflammatory disease; asthma; antibody; human.

OS Homo sapiens.

XX US2003021790-A1.

XX 30-JAN-2003.

PF 29-NOV-2000; 2000US-00726258.

XX 22-JAN-1998; 98US-0074330P.

PR 20-FEB-1998; 98US-0075467P.

PR 24-JUL-1998; 98US-0094003P.

PR 24-JUL-1998; 98US-0094013P.

PR 20-JAN-1999; 99US-00234182.

XX (GETH) GENENTECH INC.
XX Hseil V, Koumenis I, Leong S, Presta L, Shahrokh Z, Zapata G;
PI
XX

DR WPI; 2003-605694/57.

XX Novel conjugates comprising antibody fragments covalently attached to
PT nonproteaceous polymer molecules, useful for treating inflammatory
PT diseases, acute lung injury, ischemic reperfusion injury, pneumonia and
PT asthma.

XX Example; Fig 29; 266pp; English.

XX The invention relates to novel conjugates comprising antibody fragments
CC covalently attached to nonproteaceous polymer molecules. The invention
CC is useful for treating interleukin (IL)-8 mediated diseases or disorders
CC such as inflammatory diseases, acute lung injury e.g. adult respiratory
CC distress syndrome (ARDS), ischaemic reperfusion injury e.g. myocardial
CC infarction, hypovolemic shock, inflammatory bowel disease e.g. ulcerative
CC colitis, bacterial pneumonia and asthma. The invention is also useful as
CC a reagent in an animal model system for in vivo study of the biological
CC functions of the antigen recognised by the conjugate. The present
CC sequence is human light chain kappa consensus framework protein. This
CC sequence is used in the exemplification of the invention

SQ Sequence 109 AA;

Query Match 100.0%; Score 52; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OQHNEYPLT 9
| | | | | | | | | |
DB 90 OQHNEYPLT 98

RESULT 23

ADP11669
ID ADP11669 standard; protein; 214 AA.

AC ADP11669;

DT 26-FEB-2004 (first entry)

DE anti-CD11a rhumAb light chain amino acid sequence #SEQ ID 3.

XX Purifying; target protein; non-affinity purification;
XX high-performance tangential flow filtration; HPTFF; pharmaceutical;
XX diagnostic; therapeutic; antibody.

OS Synthetic.

XX WO2003102132-A2.

XX 11-DEC-2003.

PF 25-APR-2003; 2003WO-US013054.

PR 26-APR-2002; 2002US-0375953P.

XX (GETH) GENENTECH INC.

XX Fahner RL, Folman D, Lebretton B, Van Reis R;

XX WPI; 2004-043096/04.

XX Purifying target protein from mixture containing host cell protein
PT involves subjecting mixture to non-affinity purification, high-
PT performance tangential flow filtration and isolating purified protein.

XX Disclosure; SEQ ID NO 3; 77pp; English.

XX The invention relates to a method for purifying a target protein from a
CC mixture containing a host cell protein. This method comprises subjecting
CC the mixture to a non-affinity purification followed by high-performance
CC tangential flow filtration (HPTFF) and isolating the protein in a purity
CC containing less than 100 parts/million (ppm) of the host cell protein,

XX The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease, or
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of an anti-EpCam single chain antibody.

XX Sequence 107 AA;

Query Match 90.4%; Score 47; DB 9; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.48; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 1;

OY 1 QOHNEYPYT 9
 |||||
 DB 89 QOHNEYPYT 97

RESULT 28
 ADI26700
 ID ADI26700 standard; protein; 108 AA.

AC ADI26700;

DT 15-APR-2004 (first entry)

DE Mouse anti Igm antibody O1 Kappa light chain protein.

KW Mouse; antibody; Igm; remyelination; neuronal growth; autoantibody;
 KW demyelination disease; multiple sclerosis; central nervous system; CNS;

KW axon; glial cell proliferation;
 KW Theiler's murine encephalomyelitis virus infection; CNS injury;

KW spinal cord injury.

XX Mus sp.

OS US2003185827-A1.

PN 02-OCT-2003.

PF 13-NOV-2001; 2001US-00010729.

PR 29-APR-1994; 94US-00236520.

PR 08-JAN-1996; 96US-00692084.

PR 07-JUN-1997; 97US-00779784.

PR 28-MAY-1999; 99US-00322862.

PR 30-MAY-2000; 2000US-00580787.

PR 05-DEC-2000; 2000US-00730473.

XX (MAYO-) MAYO FOUND.

XX Rodriguez M, Miller DJ, Pease LR;

XX WPI; 2004-119219/12.

XX N-PSDB; ADI26701.

XX New human immunoglobulin M antibody for treating or preventing a
 PT demyelinating disease of the central nervous system in a human or
 PT domestic animal, such as multiple sclerosis.
 XX Example 19; Fig 68; 159pp; English.
 XX

CC The invention relates to an antibody (I) produced by injecting an
 CC immunocompetent host with an antibody peptide, and harvesting the
 CC antibody, where the peptide comprises a human anti-IgM antibody fragment
 CC given in the specification, or active fragments. Also included are
 CC stimulating remyelination of central nervous system (CNS) axons in a
 CC mammal (comprising administering a monoclonal antibody, or mixtures,
 CC monomers, active fragments, or recombinant antibodies derived from it,
 CC characterised by their ability to bind structures and cells within the
 CC CNS, including oligodendrocytes), stimulating the proliferation of glial
 CC cells in CNS axons in a mammal (comprising administering a monoclonal
 CC antibody, or mixtures, monomers, active fragments, or recombinant
 CC antibodies derived from it, characterised by their ability to bind
 CC structures and cells within the CNS), treating or preventing a
 CC demyelinating disease of the CNS in a mammal (comprising administering a
 CC monoclonal antibody, or mixtures, monomers, active fragments, or
 CC recombinant antibodies derived from it, characterised by their ability to
 CC bind structures and cells within the CNS, and to stimulate remyelination
 CC of axons of the CNS), stimulating, in vitro, the proliferation of glial
 CC cells from mixed cell culture, stimulating remyelination of CNS axons in
 CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 CC antibody/or a peptide analogue, hapten, or active fragment of it, where
 CC the DNA sequence consists of a sequence encoding an anti Igm antibody), a
 CC probe capable of screening for the antibody, an assay for screening drugs
 CC and other agents for the ability to modulate the production or mimic the
 CC activities of mAb SH1G22, SH1G46, or combinations of them, a
 CC recombinant virus transformed with recombinant antibody nucleic acids or
 CC vector, imaging a portion of the CNS using the antibody and diagnosing or
 CC monitoring demyelination and/or remyelination of the CNS comprising using
 CC CNS image. The antibody is used to stimulate remyelination of CNS axons,
 CC and to stimulate the proliferation of glial cells in CNS axons,
 CC optionally in vitro. The antibody is used to treat or prevent a
 CC demyelinating disease of the CNS in a human or domestic animal, such as
 CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 CC preferably the mammal is a mouse infected with Strain DA of Theiler's
 CC murine encephalomyelitis virus. The antibody is used to treat a spinal
 CC cord injury and used to screen drugs and other agents for the ability to
 CC modulate the production or mimic the activities of the antibody. The
 CC antibody can be used to image a portion of the CNS which can be used to
 CC diagnose or monitor demyelination and/or remyelination of the CNS. The
 CC present sequence is a variable region of a mouse anti-IgM antibody (or
 CC fragment).

XX Sequence 108 AA;

Query Match 90.4%; Score 47; DB 8; Length 108;
 Best Local Similarity 88.9%; Pred. No. 0.49; Mismatches 0; Gaps 0;
 Matches 8; Conservative 0; Indels 1;

OY 1 QOHNEYPYT 9
 |||||
 DB 89 QOHNEYPYT 97

RESULT 29
 AA117957
 ID AA117957 standard; protein; 242 AA.

AC AA117957;

DT 04-AUG-1999 (first entry)

DE Mouse scFv fragment 3-1.

KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;

KW autoimmune disease; scFv-antibody; single-chain Fv, mouse.

XX Mus sp.

XX WO9925818-A1.

XX 27-MAY-1999.

XX 16-NOV-1998; 98WO-EP007313.

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XX 17-NOV-1997; 97EP-00120096.
XX (KUFE/) KUFER P.
XX Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX WPI; 1999-338004/28.
XX N-PSDB; AAX77240.
XX Phage display system for identification of binding site domains retaining
XX capacity to bind an epitope.
XX Claim 27; Fig 6.3; 152pp; English.
XX The invention relates to a method of identifying binding site domains
XX (BSD) that retain the capacity of binding to a predetermined epitope when
XX positioned C-terminal of at least one further domain in a recombinant bi-
XX or multivalent polypeptide. The method comprises (a) testing a panel of
XX BSD displayed on the surface of a biological display system as part of a
XX fusion protein for binding to a predetermined epitope, where the fusion
XX protein comprises an additional domain positioned N-terminal of the BSD
XX and an amino acid sequence that mediates anchoring of the fusion protein
XX to the surface of the display system; and (b) identifying a BSD that
XX binds to the predetermined epitope. The method is useful to identify bi-
XX or multivalent polypeptides that comprise antibody binding sites capable
XX of efficiently binding to the corresponding antigen. The polypeptides or
XX antibodies identified by the method are useful therapeutically and
XX diagnostically, for e.g. cancer and autoimmune diseases. scFv-antibody
XX fragments that bind independently of their position within bifunctional
XX single-chain fusion proteins can be isolated from combinatorial antibody
XX libraries using the new in vitro method. Sequences AAY17957-965 represent
XX mouse scFv fragments
XX
SQ Sequence 242 AA;
Query Match 90.4%; Score 47; DB 2; Length 242;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QOHNREYPLT 9
DB 224 QOHNREYPT 232
RESULT 30
AAY17961
ID AAY17961 standard; protein; 242 AA.
XX
AC AAY17961;
XX
DT 04-AUG-1999 (first entry)
XX
DE Mouse scFv fragment 4-4.
XX
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
XX autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
OS Mus sp.
XX
PN WO9925818-A1.
XX
PD 27-MAY-1999.
XX
PF 16-NOV-1998; 98WO-EP007313.
XX
PR 17-NOV-1997; 97EP-00120096.
XX
PA (KUFE/) KUFER P.
XX
PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
DR WPI; 1999-338004/28.

```

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DR N-PSDB; AAX77244.
XX
XX Phage display system for identification of binding site domains retaining
XX capacity to bind an epitope.
XX Claim 27; Fig 6.7; 152pp; English.
XX The invention relates to a method of identifying binding site domains
XX (BSD) that retain the capacity of binding to a predetermined epitope when
XX positioned C-terminal of at least one further domain in a recombinant bi-
XX or multivalent polypeptide. The method comprises (a) testing a panel of
XX BSD displayed on the surface of a biological display system as part of a
XX fusion protein for binding to a predetermined epitope, where the fusion
XX protein comprises an additional domain positioned N-terminal of the BSD
XX and an amino acid sequence that mediates anchoring of the fusion protein
XX to the surface of the display system; and (b) identifying a BSD that
XX binds to the predetermined epitope. The method is useful to identify bi-
XX or multivalent polypeptides that comprise antibody binding sites capable
XX of efficiently binding to the corresponding antigen. The polypeptides or
XX antibodies identified by the method are useful therapeutically and
XX diagnostically, for e.g. cancer and autoimmune diseases. scFv-antibody
XX fragments that bind independently of their position within bifunctional
XX single-chain fusion proteins can be isolated from combinatorial antibody
XX libraries using the new in vitro method. Sequences AAY17957-965 represent
XX mouse scFv fragments
XX
SQ Sequence 242 AA;
Query Match 90.4%; Score 47; DB 2; Length 242;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QOHNREYPLT 9
DB 224 QOHNREYPT 232
RESULT 31
AAY17959
ID AAY17959 standard; protein; 242 AA.
XX
AC AAY17959;
XX
DT 04-AUG-1999 (first entry)
XX
DE Mouse scFv fragment 3-8.
XX
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
XX autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
OS Mus sp.
XX
PN WO9925818-A1.
XX
PD 27-MAY-1999.
XX
PF 16-NOV-1998; 98WO-EP007313.
XX
PR 17-NOV-1997; 97EP-00120096.
XX
PA (KUFE/) KUFER P.
XX
PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
DR WPI; 1999-338004/28.
XX
DR N-PSDB; AAX77242.
XX
XX Phage display system for identification of binding site domains retaining
XX capacity to bind an epitope.
XX Claim 27; Fig 6.5; 152pp; English.
XX The invention relates to a method of identifying binding site domains
XX

```

CC (BSD) that retain the capacity of binding to a predetermined epitope when
CC positioned C-terminal of at least one further domain in a recombinant bi-
CC or multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that
CC binds to the predetermined epitope. The method is useful to identify bi-
CC or multivalent polypeptides that comprise antibody binding sites capable
CC of efficiently binding to the corresponding antigen. The polypeptides or
CC antibodies identified by the method are useful therapeutically and
CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC fragments that bind independently of their position within bifunctional
CC single-chain fusion proteins can be isolated from combinatorial antibody
CC libraries using the new in vitro method. Sequences AAY17957-965 represent
CC mouse scFv fragments
XX

SQ Sequence 242 AA;

Query Match 90.4%; Score 47; DB 2; Length 242;
Best Local Similarity 88.9%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQHNEYPLT 9
| | | | |
Db 224 QQHNEYPYT 232

RESULT 32
AD283409
ID AD283409 standard; protein; 491 AA.
XX

AC AD283409;

DT 14-JUL-2005 (first entry)

DE C-terminal Epcam binder SEQ ID NO 31.

XX neoplasia; inflammation; immune disorder; infection; allergy;

KW graft versus host disease; Cytostatic; Antiinflammatory;
KM Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
Epcam.

OS Synthetic.

PN WO2005040220-A1.

PD 06-MAY-2005.

PF 15-OCT-2004; 2004WO-BP011646.

PR 16-OCT-2003; 2003BP-00023581.

PA (MICR-) MICROMET AG.

PI Hofmeister R, Kohleisen B, Lenkeri-Schuetz U, Itin C, Baeuerle P;
PI Carr FJ, Hamilton AA, Williams S;

XX WPI; 2005-333494/34.

DR N-PSDB; AD283408.

XX New cytotoxicity active CD3 specific binding construct comprises a first
PT domain specifically binding to human CD3 and an Ig-derived second binding
PT domain, useful for treating, preventing, or ameliorating, e.g.
PT proliferative disease.

XX Claim 20; SEQ ID NO 31; 639pp; English.

PS The invention relates to a cytotoxicity active CD3 specific binding
CC construct comprising a first domain specifically binding to human CD3 and
CC an Ig-derived second binding domain. The CD3 specific binding construct
CC above or the construct produced by the process, nucleic acid molecule,

CC vector, or host is useful for the preparation of a pharmaceutical
CC composition for the prevention, treatment, or amelioration of a
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host disease, or
CC host-versus-graft diseases. The cytotoxicity active CD3 specific binding
CC construct is useful for treating, preventing, or ameliorating
CC proliferative disease, a tumor, an inflammatory disease, an immunological
CC disorder, an autoimmune disease, an infectious disease, viral disease,
CC allergic reactions, parasitic reactions, graft-versus-host disease, or
CC host-versus-graft diseases. The present sequence represents the amino
CC acid sequence of an anti-Epcam binder.
XX

SQ Sequence 491 AA;

Query Match 90.4%; Score 47; DB 9; Length 491;
Best Local Similarity 88.9%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQHNEYPLT 9
| | | | |
Db 473 QQHNEYPYT 481

RESULT 33
ADV66089
ID ADV66089 standard; protein; 494 AA.
XX

AC ADV66089;

DT 24-FEB-2005 (first entry)

DE Anti-CD3-anti-Epcam bispecific single chain antibody - SEQ ID 12.

XX bispecific single chain antibody; epithelial cell adhesion molecule;
KW Epcam; CD3; tumor; cancer; cytostatic.

XX Unidentified.

PN WO2004106383-A1.

PD 09-DEC-2004.

PF 26-MAY-2004; 2004WO-BP005687.

PR 31-MAY-2003; 2003BP-00012133.

PR 31-MAY-2003; 2003BP-00012134.

PA (MICR-) MICROMET AG.

PI Kufer P, Berry M, Offner S, Brieschwein K, Wolf A, Raum T;
PI Kohleisen B, Lenkeri-Schuetz U, Baeuerle P;

XX WPI; 2005-021271/02.

DR N-PSDB; ADV66088.

XX New pharmaceutical composition having a bispecific single chain antibody
PT construct, useful for preventing, treating or ameliorating a tumorous
PT disease, such as an epithelial or minimal residual cancer.

XX Claim 12; SEQ ID NO 12; 227pp; English.

XX The invention comprises a composition that contains a bispecific single
CC chain antibody consisting of at least two domains, where one of domains
CC binds to human epithelial cell adhesion molecule (Epcam) antigen, and the
CC second domain binds to human CD3 antigen. The bispecific antibody
CC construct of the invention is useful for the prevention, treatment or
CC amelioration of a tumorous disease, such as an epithelial or minimal
CC residual cancer. The present amino acid sequence represents a bispecific
CC single chain antibody of the invention.

XX Sequence 494 AA;

Query Match 90.4%; Score 47; DB 9; Length 494;
 Best Local Similarity 88.9%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOHNEYPYT 9
 |||||
 DB 470 QOHNEYPYT 478

RESULT 34

ADV66123
 ID ADV66123 standard; protein; 497 AA.

XX
 AC ADV66123;

XX
 DT 24-FEB-2005 (first entry)

XX
 DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 46.

XX
 KW bispecific single chain antibody; epithelial cell adhesion molecule;
 EPCAM; CD3; tumor; cancer; cytostatic.

XX
 OS Unidentified.

XX
 PN WO2004106383-A1.

XX
 PD 09-DEC-2004.

XX
 PF 26-MAY-2004; 2004WO-EP005687.

XX
 PR 31-MAY-2003; 2003EP-00012133.

XX
 PR 31-MAY-2003; 2003EP-00012134.

XX
 PA (MIGR-) MICROMET AG.

XX
 PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkeri-Schuetz U, Baeuerle P;

XX
 DR WPI: 2005-021271/02.

XX
 DR N-PSDB; ADV66122.

XX
 PT New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.

XX
 PS Claim 12; SEQ ID NO 46; 227pp; English.

XX
 CC The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.

XX
 SQ Sequence 497 AA;

Query Match 90.4%; Score 47; DB 9; Length 497;
 Best Local Similarity 88.9%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOHNEYPYT 9
 |||||
 DB 473 QOHNEYPYT 481

RESULT 35

ADV66125
 ID ADV66125 standard; protein; 497 AA.

XX
 AC ADV66125;

XX

DT 24-FEB-2005 (first entry)

XX
 DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 48.

XX
 KW bispecific single chain antibody; epithelial cell adhesion molecule;
 EPCAM; CD3; tumor; cancer; cytostatic.

XX
 OS Unidentified.

XX
 PN WO2004106383-A1.

XX
 PD 09-DEC-2004.

XX
 PF 26-MAY-2004; 2004WO-EP005687.

XX
 PR 31-MAY-2003; 2003EP-00012133.

XX
 PR 31-MAY-2003; 2003EP-00012134.

XX
 PA (MIGR-) MICROMET AG.

XX
 PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkeri-Schuetz U, Baeuerle P;

XX
 DR WPI: 2005-021271/02.

XX
 DR N-PSDB; ADV66124.

XX
 PT New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.

XX
 PS Claim 12; SEQ ID NO 48; 227pp; English.

XX
 CC The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.

XX
 SQ Sequence 497 AA;

Query Match 90.4%; Score 47; DB 9; Length 497;
 Best Local Similarity 88.9%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOHNEYPYT 9
 |||||
 DB 473 QOHNEYPYT 481

RESULT 36

AD283427
 ID AD283427 standard; protein; 506 AA.

XX
 AC AD283427;

XX
 DT 14-JUL-2005 (first entry)

XX
 DE Delimmunized construct 3-1xanti-CD3.

XX
 KW neoplasm; inflammation; immune disorder; infection; allergy;
 KW graft versus host disease; Cytostatic; Antiinflammatory;

XX
 KW immunosuppressive; virucide; antibacterial; Antiallergic; Antiparasitic.

XX
 OS Synthetic.

XX
 PN WO2005040220-A1.

XX
 PD 06-MAY-2005.

XX
 PF 15-OCT-2004; 2004WO-BP011646.

XX 16-OCT-2003; 2003EP-00023581.
 PR (MICR-) MICROMET AG.
 XX
 PA Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
 PI Carr FU, Hamilton AA, Williams S;
 XX MPI: 2005-333494/34.
 DR N-PSDB; ADZ83426.
 XX
 XX New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.
 PT proliferative disease.
 XX
 PS Claim 20; SEQ ID NO 49; 639pp; English.
 XX
 CC The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of deimmunized construct 3-1xanti-CD3.
 XX
 SQ Sequence 506 AA;
 XX
 XX Query Match 90.4%; Score 47; DB 9; Length 506;
 XX Best Local Similarity 88.9%; Pred. No. 2.6;
 XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 OQHNEYPLT 9
 DB 108 OQHNEYPLT 116
 XX
 XX RESULT 37
 XX ADV66113
 XX ID ADV66113 standard; protein; 515 AA.
 XX AC ADV66113;
 XX DT 24-FEB-2005 (first entry)
 XX DE Anti-CD3-anti-EpCAM bispecific single chain antibody - SEQ ID 36.
 XX bispecific single chain antibody; epichelial cell adhesion molecule;
 XX EpCAM; CD3; tumor; cancer; cytostatic.
 XX OS Unidentified.
 XX OS WO2004106383-A1.
 XX PN 09-DEC-2004.
 XX PD 26-MAY-2004; 2004WO-EP005687.
 XX PF 31-MAY-2003; 2003EP-00012133.
 XX PR 31-MAY-2003; 2003EP-00012134.
 XX (MICR-) MICROMET AG.
 XX PA Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 XX PI

PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
 XX MPI: 2005-021271/02.
 DR N-PSDB; ADV66112.
 XX
 XX New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.
 XX
 PS Claim 12; SEQ ID NO 36; 227pp; English.
 XX
 CC The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a bispecific
 CC single chain antibody of the invention.
 XX
 SQ Sequence 515 AA;
 XX
 XX Query Match 90.4%; Score 47; DB 9; Length 515;
 XX Best Local Similarity 88.9%; Pred. No. 2.7;
 XX Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 OQHNEYPLT 9
 DB 108 OQHNEYPLT 116
 XX
 XX RESULT 38
 XX ADR03427
 XX ID ADR03427 standard; peptide; 9 AA.
 XX AC ADR03427;
 XX DT 21-OCT-2004 (first entry)
 XX DE Humanised MHM24 CDR-L3 mutant peptide, GIU93A1a.
 XX CD1a antibody; human immunodeficiency virus infection; HIV infection;
 XX rhinovirus infection; inflammatory skin disease; psoriasis;
 XX inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 XX adult respiratory distress syndrome; allergic disease; eczema; asthma;
 XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 XX SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 XX chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 XX skin hypersensitivity disorder; poison ivy; poison oak;
 XX B-cell malignancy; chronic lymphocytic leukemia; hairy cell leukaemia;
 XX graft versus host disease; cancer; gene therapy;
 XX murine anti-human CD1a monoclonal antibody; MHM24; variable light chain;
 XX VL; murine; human; fusion protein; complementarity determining region;
 XX CDR; mutant; mutein.
 XX
 XX Mus sp.
 XX OS Homo sapiens.
 XX OS Chimeric.
 XX PN US2004146507-A1.
 XX PD 29-JUL-2004.
 XX PF 03-DEC-2003; 2003US-00727737.
 XX PR 27-NOV-1996; 96US-0031945P.
 XX PR 20-NOV-1997; 97US-00975329.
 XX (GERTH) GENENTECH INC.
 XX PA Jardieu PM, Presta LG;
 XX PI

DR WPI; 2004-552640/53.
 XX New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 64; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD1a monoclonal antibody
 CC (MHM24) CDR-L3 mutant peptide. This sequence is used in the
 CC exemplification of the invention.
 CC
 XX Sequence 9 AA:
 SQ
 Query Match 88.5%; Score 46; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QQHNEPYLT 9
 Db 1 QQHNAVPLT 9
 RESULT 39
 AAR64819 standard; protein; 234 AA.
 ID AAR64819
 XX
 AC AAR64819;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-JUL-1995 (first entry)
 XX
 DE OMVU10 ScFv fragment.
 XX
 DE ScFv; single chain Fv; expression cassette; Aspergillus; Mucor;
 KM Neurospora; Penicillium; OMVU10; monoclonal antibody; OMVU10;
 KM Streptococcus; antibody engineering.
 XX
 OS Synthetic.
 XX
 FH Key
 FH Location/Qualifiers
 FT 28..32
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region
 FT 47..64
 FT /label= CDR11
 FT /note= "complementarity determining region 2"
 FT Region
 FT 96..103
 FT /label= CDR111
 FT /note= "complementarity determining region 3"
 FT Peptide
 FT 115..129
 FT /label= Linker
 FT 130..234
 FT /label= VL
 FT /note= "Mab OMVU10 VL"
 FT Region
 FT 154..163
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT 179..185

FT /label= CDR11
 FT /note= "complementarity determining region 2"
 FT Region 218..225
 FT /label= CDR111
 FT /note= "complementarity determining region 3"
 XX
 PN WO9429457-A2.
 XX
 PD 22-DEC-1994.
 XX
 PP 09-JUN-1994; 94WO-EP001906.
 XX
 PR 09-JUN-1993; 93EP-00201660.
 PR 09-JUN-1993; 93EP-00201661.
 PR 14-JUN-1993; 93EP-00201706.
 XX
 PA (UNITL) UNILEVER NV.
 PA (UNITL) UNILEVER PLC.
 PA (NEDE) NEDERLAND ORG. TNO.
 PI Frenken LGJ, Van Gorcom RFM, Hessing JGM, Van Den Hondel CAMJ;
 PI Musters W, Verbakel JMA, Verrips CT;
 XX WPI; 1995-036484/05.
 DR N-PSDB; AAQ76287.
 XX
 PT Prodn. of single chain Fv antibody fragments - as fusion proteins using a
 PT transformed mould of the genus Aspergillus, Mucor, Neurospora or
 PT Penicillium.
 XX
 PS Example 4; Page 30-31; 70pp; English.
 XX
 CC An ScFv fragment of OMVU10, a Mab raised against oral streptococci, was
 CC constructed by PCR amplification of OMVU10 heavy and light chain
 CC sequences, and expressed from pUR4457. The ScFv-encoding Pet1-XhoI
 CC fragment of pUR4457 is given in AAQ76287, and the encoded protein in
 CC AAR64819. (Updated on 25-MAR-2003 to correct PW field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 CC
 XX Sequence 234 AA:
 SQ
 Query Match 88.5%; Score 46; DB 2; Length 234;
 Best Local Similarity 88.9%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 QQHNEPYLT 9
 Db 218 QQHNEPYMT 226
 RESULT 40
 ADR03426 standard; peptide; 9 AA.
 ID ADR03426
 XX
 AC ADR03426;
 XX
 DT 21-OCT-2004 (first entry)
 DT
 XX
 DE Humanised MHM24 CDR-L3 mutant peptide, AsnL92Aa.
 XX
 KM CD1a antibody; human immunodeficiency virus infection; HIV infection;
 KM rhinovirus infection; inflammatory skin disease; psoriasis;
 KM inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KM adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KM autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KM SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KM tuberculosis; sarcoidosis; polymyositis;
 KM chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KM skin hypersensitivity disorder; poison ivy; poison oak;
 KM B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KM graft versus host disease; cancer; gene therapy;
 KM murine anti-human CD1a monoclonal antibody; MHM24; variable light chain;
 KM VL; murine; human; fusion protein; complementarity determining region;

XX	CDR ₁ mutant; mutein.
KW	
XX	
OS	Mus sp.
OS	Homo sapiens.
OS	Chimeric.
XX	
PN	US2004146507-A1.
XX	
PD	29-JUL-2004.
XX	
PF	03-DEC-2003; 2003US-00727737.
XX	
PR	27-NOV-1996; 96US-0031945P.
PR	20-NOV-1997; 97US-00975329.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Jardieu PM, Presta LG;
XX	
DR	WPI; 2004-552640/53.
XX	
XX	
PT	New antibody mutant of a species-dependent antibody, useful for treating
PT	and preventing infectious diseases, psoriasis, inflammatory bowel
PT	disease, allergic conditions, autoimmune diseases, or cancer.
XX	
PS	Example; SEQ ID NO 63; 54pp; English.
XX	
CC	The present invention relates to an antibody mutant of a species-
CC	dependent antibody with beneficial properties. The invention is useful
CC	for treating and preventing infectious diseases such as human
CC	immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC	disease such as psoriasis, inflammatory bowel diseases such as Crohn's
CC	disease and ulcerative colitis, adult respiratory distress syndrome,
CC	allergic diseases such as eczema and asthma, autoimmune diseases such as
CC	rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC	mellitus, Reynaud's syndrome, immunological diseases such as
CC	tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC	disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC	disorders such as poison ivy and poison oak, B-cell malignancies such as
CC	chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
CC	disease and cancer. The invention is also useful in gene therapy. The
CC	present sequence is humanised murine anti-human CD1a monoclonal antibody
CC	(MHM24) CDR-I3 mutant peptide. This sequence is used in the
CC	exemplification of the invention.
XX	
SO	Sequence 9 AA:
XX	
Query Match	84.6%; Score 44; DB 8; Length 9;
Best Local Similarity	88.9%; Pred. No. 26+06;
Matches	8; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY	1 OOHNEVPLT 9
Db	1 OOHAEVPLT 9
XX	
RESULT 41	
ADDR03428	
ID	ADDR03428 standard; peptide; 9 AA.
XX	
AC	ADDR03428;
XX	
DT	21-OCT-2004 (first entry)
XX	
DE	Humanised MHM24 CDR-I3 mutant peptide, TyrL94Ala.
XX	
KW	CD1a antibody; human immunodeficiency virus infection; HIV infection;
KW	rhinovirus infection; inflammatory skin disease; psoriasis;
KW	inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW	adult respiratory distress syndrome; allergic disease; eczema; asthma;
KW	autoimmune disease; Rheumatoid arthritis; systemic lupus erythematosus;
KW	SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
KW	tuberculosis; sarcoidosis; polymyositis;

KW	chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
KV	skin hypersensitivity disorder; poison ivy; poison oak;
KX	B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
KY	graft versus host disease; cancer; gene therapy;
KZ	murine anti-human CD11a monoclonal antibody; MRM24; variable light chain;
LK	VL; murine; human; fusion protein; complementarity determining region;
LM	CDR; mutant; mutein.
XX	
OS	Mus sp.
OS	Homo sapiens.
OS	Chimeric.
PN	US2004146507-A1.
PD	29-JUL-2004.
PF	03-DEC-2003; 2003US-00727737.
PR	27-NOV-1996; 96US-0031945P.
PR	20-NOV-1997; 97US-00975329.
PA	(GETH) GENENTECH INC.
P1	Jardieu PM, Presta LG:
PI	WPI; 2004-552640/53.
XX	
PT	New antibody mutant of a species-dependent antibody, useful for treating
PT	and preventing infectious diseases, psoriasis, inflammatory bowel
PT	disease, allergic conditions, autoimmune diseases, or cancer.
PS	Example; SEQ ID NO 65; 54pp; English.
XX	
CC	The present invention relates to an antibody mutant of a species-
CC	dependent antibody with beneficial properties. The invention is useful
CC	for treating and preventing infectious diseases such as human
CC	immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
CC	diseases such as psoriasis, inflammatory bowel diseases such as Crohn's
CC	disease and ulcerative colitis, adult respiratory distress syndrome,
CC	allergic diseases such as eczema and asthma, autoimmune diseases such as
CC	rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
CC	mellitus, Reynaud's syndrome, immunological diseases such as
CC	tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
CC	disease (COPD), CNS inflammatory disorder, skin hypersensitivity
CC	disorders such as poison ivy and poison oak, B-cell malignancies such as
CC	chronic lymphocytic leukaemia and hairy cell leukemia, graft versus host
CC	disease and cancer. The invention is also useful in gene therapy. The
CC	present sequence is humanised murine anti-human CD11a monoclonal antibody
CC	(MRM24) CDR-IJ mutant peptide. This sequence is used in the
CC	exemplification of the invention.
XX	
SO	Sequence 9 AA:
OY	Query Match 82.7%; Score 43; DB 8; Length 9;
OY	Best Local Similarity 88.9%; Pred. No. 2e+06; Indels 0; Gaps 0;
DB	Matches 8; Conservative 0; Mismatches 1;
OY	1 QOHNVEPLT 9
OY	
DB	1 QOHNDEAPLT 9
RESULT 42	
ID	ADW38453 standard; protein, 109 AA.
AC	ADW38453;
DT	24-MAR-2005 (first entry)
DE	CD11a light chain variable region #1.
KX	monoclonal antibody; CD11a; light-chain variable region;

KW heavy-chain variable region.
 XX
 OS Homo sapiens.
 XX CN1439651-A.
 PN
 XX 03-SEP-2003.
 PD
 XX 20-FEB-2002; 2002CN-00110866.
 PF
 XX 20-FEB-2002; 2002CN-00110866.
 PR
 XX 20-FEB-2002; 2002CN-00110866.
 PA (ZHON-) ZHONGXIN GUOJIAN PHARM CO LTD SHANGHAI.
 XX
 XX Wang H, Wang J;
 PI WPI; 2004-169719/17.
 XX N-PSDB; ADM38455.
 DR
 XX Recombinant human CD11a monoclonal antibody and its preparation and
 PT medicinal composition.
 PS
 XX Claim 1; Page 12; 16pp; Chinese.
 CC The present invention relates to a recombinant monoclonal antibody for
 CC human CD11a has the amino acid sequence shown by SEQ ID No.1 or SEQ ID
 CC No.5 in light-chain variable region and the amino acid sequence shown by
 CC SEQ ID No.2 or SEQ ID No.6 in heavy-chain variable region. Its
 CC bioactivity and the expression in host cell are greatly increased. The
 CC DNA molecule for coding the antibody, its preparation process and the
 CC medicinal composition containing it are also disclosed. The present
 CC sequence represents a light chain variable region of human CD11a.
 XX
 SQ Sequence 109 AA;

Query Match 82.7%; Score 43; DB 8; Length 109;
 Best Local Similarity 88.9%; Pred. No. 2.9;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QOHNEYPILT 9
 |||||
 Db 90 QOHNEYPILT 98

RESULT 43
 ADP47236
 ID ADP47236 standard; peptide; 9 AA.
 XX
 AC ADP47236;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human phospholipase A2-specific mAb light chain peptide #6.
 XX
 KW human; monoclonal antibody; phospholipase A2; PLA2;
 KW inflammatory disorder; degenerative disorder;
 KW joint inflammatory reaction; skin inflammatory reaction;
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 KW Alzheimer's disease; atherosclerosis; restenosis; light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO2004050850-A2.
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038234.
 XX
 PR 02-DEC-2002; 2002US-0430724P.
 PA (ABGE-) ABGENIX INC.
 PA (LEXI-) LEXICON GENETICS INC.
 XX

PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
 PI Jia X, Nocerini MR;
 XX
 DR WPI; 2004-461119/43.
 XX
 XX New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 PS
 XX Example 5; SEQ ID NO 151; 128pp; English.
 CC The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC amino acid sequence represents a human PLA2-specific monoclonal antibody
 CC light chain peptide.
 XX
 SQ Sequence 9 AA;

Query Match 80.8%; Score 42; DB 8; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 QHNEYPILT 9
 |||||
 Db 2 QHNEYPILT 9

RESULT 44
 ADR03425
 ID ADR03425 standard; peptide; 9 AA.
 XX
 AC ADR03425;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Humanised MEM24 CDR-L3 mutant peptide, HisE91A1A.

KW CD11a antibody; human immunodeficiency virus infection; HIV infection;
 KW rhinovirus infection; inflammatory skin disease; psoriasis;
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW adult respiratory distress syndrome; allergic disease; eczema; asthma;
 KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW SLE; diabetes mellitus; Reynaud's syndrome; immunological disease;
 KW tuberculosis; sarcoidosis; polymyositis;
 KW chronic obstructive pulmonary disease; COPD; CNS inflammatory disorder;
 KW skin hypersensitivity disorder; poison ivy; poison oak;
 KW B-cell malignancy; chronic lymphocytic leukaemia; hairy cell leukaemia;
 KW graft versus host disease; cancer; gene therapy;
 KW murine anti-human CD11a monoclonal antibody; MEM24; variable light chain;
 KW VL; murine; human; fusion protein; complementarity determining region;
 KW CDR; mutant; mutein.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US2004146507-A1.
 PD 29-JUL-2004.
 XX
 PF 03-DEC-2003; 2003US-00727737.
 XX
 PR 27-NOV-1996; 96US-0031945P.
 XX
 PR 20-NOV-1997; 97US-00975329.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PA Jardieu PM, Presta LG;
 PI

DR WPI; 2004-552640/53.
 XX New antibody mutant of a species-dependent antibody, useful for treating
 PT and preventing infectious diseases, psoriasis, inflammatory bowel
 PT disease, allergic conditions, autoimmune diseases, or cancer.
 XX
 PS Example; SEQ ID NO 62; 54pp; English.
 XX
 CC The present invention relates to an antibody mutant of a species-
 CC dependent antibody with beneficial properties. The invention is useful
 CC for treating and preventing infectious diseases such as human
 CC immunodeficiency virus (HIV) and rhinovirus infections, inflammatory skin
 CC disease such as psoriasis, inflammatory bowel diseases such as Crohn's
 CC disease and ulcerative colitis, adult respiratory distress syndrome,
 CC allergic diseases such as eczema and asthma, autoimmune diseases such as
 CC rheumatoid arthritis, systemic lupus erythematosus (SLE), diabetes
 CC mellitus, Reynaud's syndrome, immunological diseases such as
 CC tuberculosis, sarcoidosis, polymyositis and chronic obstructive pulmonary
 CC disease (COPD), CNS inflammatory disorder, skin hypersensitivity
 CC disorders such as poison ivy and poison oak, B-cell malignancies such as
 CC chronic lymphocytic leukaemia and hairy cell leukaemia, graft versus host
 CC disease and cancer. The invention is also useful in gene therapy. The
 CC present sequence is humanised murine anti-human CD13a monoclonal antibody
 CC (MHM24) CDR-L3 mutant peptide. This sequence is used in the
 CC exemplification of the invention.
 CC
 XX Sequence 9 AA;
 SQ
 Query Match 80.8%; Score 42; DB 8; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2e+06;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QOHNEYPPLT 9
 Db 1 QOHNEYPPLT 9
 XX
 RESULT 45
 ADX98316
 ID ADX98316 standard; peptide; 9 AA.
 AC ADX98316;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Human anti-HGF antibody light chain variable region CDR3 peptide -SEQ 88.
 XX
 KM antibody; cytosstatic; cancer; neoplasm; solid tumor;
 KM hepatocyte growth factor; HGF; light chain variable region.
 XX
 OS Homo sapiens.
 XX
 PN WO2005017107-A2.
 XX
 PD 24-FEB-2005.
 XX
 PF 16-JUL-2004; 2004WO-US018936.
 XX
 PR 18-JUL-2003; 2003US-0488681P.
 XX
 PA (AMGE-) AMGEN INC.
 PA (ABGE-) ABGENIX INC.
 XX
 PI Burgess TL, Coxon A, Green LL, Zhang K;
 XX
 DR WPI; 2005-182350/19.
 XX
 PT New polypeptide comprising a complementarity determining region (CDR)
 PT consisting of CDR1a, CDR2a, CDR3a, CDR1b, CDR2b or CDR3b and capable of
 PT binding hepatocyte growth factor, useful in preparing a composition for
 PT treating cancer.
 XX
 PS Claim 5; SEQ ID NO 88; 301pp; English.

XX
 CC The invention relates to a novel isolated polypeptide comprising at least
 CC one complementarity-determining region (CDR) consisting of CDR1a, CDR2a
 CC or CDR3a, or CDR1b, CDR2b or CDR3b. The polypeptide, in association with
 CC an antibody heavy or light chain, is capable of binding hepatocyte growth
 CC factor (HGF). HGF, also known as scatter factor (SF), has been identified
 CC as a potent mitogen for hepatocytes and also as a secretory protein of
 CC fibroblasts and smooth muscles that acts to induce motility of epithelial
 CC cells. The polypeptide demonstrates cytosstatic activity and may be useful
 CC in preparing a composition for treating cancer or a solid tumor. The
 CC current sequence is that of the human anti-HGF antibody light chain
 CC variable region CDR3 peptide -SEQ 88 of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 80.8%; Score 42; DB 9; Length 9;
 Best Local Similarity 87.5%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 QHNSYPLT 9
 Db 2 QHNSYPLT 9
 XX
 RESULT 46
 AEA45084
 ID AEA45084 standard; peptide; 9 AA.
 AC AEA45084;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Apolipoprotein E C-terminal domain related sequence, SEQ ID 282.
 XX
 KM Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
 KM Antiparkinsonian; Anticonvulsant; Respiratory-Gen.; Apolipoprotein E;
 KM Alzheimer's disease; amyloidosis; Parkinson's disease; Huntingtons chorea;
 KM Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
 KM Spongiform encephalopathy; Creutzfeldt Jakob disease;
 KM motor neurone disease; chronic obstructive pulmonary disease.
 XX
 OS Homo sapiens.
 XX
 PN GB2408508-A.
 XX
 PD 01-JUN-2005.
 XX
 PF 26-NOV-2004; 2004GB-00026043.
 XX
 PR 28-NOV-2003; 2003US-0525174P.
 XX
 PA (ASTR) ASTRAZENECA AB.
 PA (DYAX-) DYAX CORP.
 XX
 PI Nordstedt C, Goldschmidt T, Henderlix M, Hoet R, Hoogenboom H,
 PI Hulten S, Andersson CV, Lindquist J, Sunemark D, Leonov S;
 XX
 DR WPI; 2005-408785/42.
 XX
 PT New human antibody or antibody fragment which binds to a sequence of the
 PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
 PT manufacturing a medicament for treating or preventing an amyloid disorder
 PT e.g. Alzheimer's disease.
 XX
 PS Example 8; SEQ ID NO 282; 392pp; English.
 XX
 CC The present invention relates to a human antibody or antibody fragment,
 CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD);
 CC AEA44803) and also to human plaques. The antibody or its fragment is
 CC useful for manufacturing a medicament for treating or preventing an
 CC amyloid disorder such as Alzheimer's disease, primary systemic
 CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
 CC familial amyloid polyneuropathy I, familial amyloid polyneuropathy III,

CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
CC anopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
CC thyroid, Attrial amyloidosis, Familial Danish dementia (FDD), Downs
CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
CC disease, Gerstmann-Strausser-Scheinker Disease (GSS), Kuru, Parkinsons
CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
CC chronic obstructive pulmonary disease. The present sequence was used to
CC illustrate the invention.

XX Sequence 9 AA;

Query Match 80.8%; Score 42; DB 9; Length 9;
Best Local Similarity 87.5%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QHNEYPLT 9
||| |||
Db 2 QHNSYPLT 9

RESULT 47

ABG77141
ID ABG77141 standard; protein; 107 AA.

XX AC ABG77141;

XX DT 24-OCT-2002 (first entry)

XX DE Anti-IGF-IR antibody (4.9.2) variable region light chain protein.

XX KW Insulin-like growth factor I receptor; antibody; human; cytostatic;
XX KW osteopethtic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour;
XX KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
XX KW acromegaly; gigantism; psoriasis; atherosclerosis.

XX OS Homo sapiens.

XX PN WO200253596-A2.

XX PD 11-JUL-2002.

XX PF 20-DEC-2001; 2001WO-US051113.

XX PR 05-JAN-2001; 2001US-0259927P.

XX PA (PIZ) PRIZER INC.

XX PA (ABGE-) ABGENIX INC.

XX PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;

XX DR WPI; 2002-575410/61.

XX DR N-PSDB; ABS62703.

XX PT Novel humanized, chimeric monoclonal antibody that specifically binds to
XX PT insulin-like growth factor I (IGF-1) receptor useful for inhibiting
XX PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
XX PS Claim 9; Page 129; 172pp; English.

XX CC This invention relates to a novel humanised, chimeric or human monoclonal
XX CC antibody or its antigen binding portion that specifically binds to
XX CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the
XX CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
XX CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
XX CC phosphorylation. The antibodies of the invention are useful for
XX CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
XX CC subject. The antibody or its antigen-binding portion is also useful for
XX CC treating cancer in a human. The method for this further involves an anti
XX CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
XX CC antibodies may also be useful for increasing IGF-IR activity and thus

CC restoring IGF-IR activity in a condition characterised by low IGF-IR
CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
CC also useful for inducing apoptosis of specific cells in a patient, and to
CC treat non-cancerous sites or disease, e.g. acromegaly, gigantism,
CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
CC minimise the immunogenic and allergic responses intrinsic to mouse or
CC mouse-derived monoclonal antibodies and thus increase the efficacy
CC and safety of the administered antibodies. The present sequence
CC represents an anti-insulin-like growth factor I receptor antibody of the
CC invention

XX SQ Sequence 107 AA;

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 4.4; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 QHNEYPLT 9
||| |||
Db 90 QHNSYPLT 97

RESULT 48

ADC99785
ID ADC99785 standard; protein; 107 AA.

XX AC ADC99785;

XX DT 01-JAN-2004 (first entry)

XX DE Anti-human MUC18 monoclonal antibody light chain protein SEQ ID 14.

XX KW anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
XX KW cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
XX KW cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
XX KW lung cancer; human.

XX OS Homo sapiens.

XX PN WO2003057838-A2.

XX PD 17-JUL-2003.

XX PF 26-DEC-2002; 2002WO-US041581.

XX PR 28-DEC-2001; 2001US-0346299P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas J;

XX DR WPI; 2003-587113/55.

XX DR N-PSDB; ADC99787.

XX PT New human anti-MUC18 monoclonal antibodies, useful for treating a disease
XX PT or condition associated with expression of MUC18 in a patient, e.g.
XX PT tumors, cancers, and other malignancies.
XX PS Claim 3; SEQ ID NO 14; 78pp; English.

XX CC The invention relates to a novel isolated monoclonal antibody comprising
XX CC a heavy or light chain amino acid or a heavy or light chain variable
XX CC domain where the antibody binds to MUC18. The monoclonal antibody of the
XX CC invention demonstrates cytostatic activity and may be useful for treating
XX CC a disease or condition associated with the expression of MUC18 on the
XX CC cell surface such as tumours, specifically melanoma, oesophageal,
XX CC pancreatic or colorectal tumours, carcinomas, particularly cervical
XX CC carcinomas and cervical intraepithelial neoplasia and cancers including
XX CC colorectal, breast or lung cancer, as well as other malignancies. The
XX CC current sequence is that of the anti-human MUC18 monoclonal antibody
XX CC light chain protein of the invention.

XX SQ Sequence 107 AA;

Query Match 80.8%; Score 42; DB 7; Length 107;
 Best Local Similarity 87.5%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEYPPLT 9
 ||| |||
 90 QHNSYPLT 97

RESULT 49

ADP05389
 ID ADD05389 standard; protein; 107 AA.

XX ADD05389;

DT 01-JAN-2004 (first entry)

DE Anti-MUC18 antibody light chain variable region protein, SEQ ID NO 14.

XX monoclonaal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
 KM antigen; tumour metastasis; melanoma; metastatic; human; light chain.

XX Homo sapiens.

XX MO2003057006-A2.

PD 17-JUL-2003.

PF 26-DEC-2002; 2002MO-US041582.

XX 28-DEC-2001; 2001US-0346460P.

PA (ABGE-) ABGENIX INC.

PI Gudae J, Bar-Eli M;

DR WPI; 2003-577496/54.

DR N-PSDB; ADP05391.

PT Use of monoclonal antibodies against MUC18 antigen, for diagnosing and
 creating tumors, inhibiting tumor growth, inhibiting cell invasion
 associated with melanoma, or increasing survival of an animal having a
 metastatic tumor.

PS Claim 3; SEQ ID NO 14; 87bp; English.

XX The invention relates to a novel monoclonal antibody used for inhibiting
 CC tumour growth in an animal. The tumour inhibition process comprises
 CC selecting an animal in need of treatment for a tumour, providing a
 CC monoclonal antibody comprising a heavy chain amino acid, where the
 CC antibody consists of any one of 10 fully defined sequences of 117-123
 CC amino acids given in the specification, and where the monoclonal antibody
 CC binds MUC18, and contacting the tumour with the antibody resulting in
 CC inhibited proliferation of the cells. The monoclonal antibody has
 CC cytostatic and can be used in the production of a vaccine. The monoclonal
 CC antibodies against the MUC18 antigen are useful for diagnosing and
 CC treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or
 CC tumour metastasis), inhibiting cell invasion associated with melanoma, or
 CC increasing survival of an animal having a metastatic tumour. This
 CC sequence represents an anti-MUC18 antibody light chain, variable region,
 CC protein of the invention.

XX Sequence 107 AA;

Query Match 80.8%; Score 42; DB 7; Length 107;

Best Local Similarity 87.5%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEYPPLT 9
 ||| |||
 90 QHNSYPLT 97

RESULT 50

ADP09827
 ID ADP09827 standard; protein; 107 AA.

XX ADP09827;

DT 12-FEB-2004 (first entry)

DE Human anti-MUC18 monoclonal antibody light chain #4.

XX cell proliferation inhibition; MUC18 tumour antigen;
 KM anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
 KM carcinoma; cancer; malignancy; light chain; human.

XX Homo sapiens.

XX MO2003057837-A2.

PD 17-JUL-2003.

PF 26-DEC-2002; 2002MO-US041580.

XX 28-DEC-2001; 2001US-0346414P.

PA (ABGE-) ABGENIX INC.

PI Gudae J;

DR WPI; 2003-598367/56.

DR N-PSDB; ADP09829.

PT Inhibiting cell proliferation associated with expression of MUC18 tumor
 antigen, involves incubating and inhibiting cell by administering anti-
 MUC18 monoclonal antibody.

PS Claim 3; SEQ ID NO 14; 83bp; English.

XX The invention comprises a method for inhibiting cell proliferation
 CC associated with expression of MUC18 tumour antigen. The method involves
 CC administering anti-MUC18 monoclonal antibody. The method of the invention
 CC is useful for inhibiting cell (e.g. melanoma or tumour cell)
 CC proliferation associated with the expression of MUC18 tumour antigen, the
 CC method is preferably useful for inhibiting tumour metastasis. The method
 CC is useful for inhibiting cell proliferation in patients with tumours,
 CC carcinomas, cancer and other malignancies. The present amino acid
 CC sequence represents a light chain from an MUC18 tumour antigen-specific
 CC monoclonal antibody.

XX Sequence 107 AA;

Query Match 80.8%; Score 42; DB 7; Length 107;
 Best Local Similarity 87.5%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEYPPLT 9
 ||| |||
 90 QHNSYPLT 97

Search completed: January 17, 2006, 11:59:29
 Job time : 67.3182 secs

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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:48:18 ; Search time 8.45455 Seconds
(without alignments)
102.424 Million cell updates/sec

Title: US-10-665-658-15

Perfect score: 52

Sequence: 1 QOHNEYPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	103	2 H30502	Ig kappa chain V r
2	52	100.0	106	2 S26345	Ig light chain V r
3	48	92.3	98	2 PH1083	Ig light chain V r
4	46	88.5	127	2 S04574	Ig kappa chain pre
5	42	80.8	125	2 S40353	Ig kappa chain V-J
6	41	78.8	88	2 A37262	Ig kappa chain V r
7	41	78.8	98	2 PH1072	Ig light chain V r
8	41	78.8	249	2 S41374	single chain Fv an
9	39	75.0	107	2 I69017	anti-HIV1 envelope
10	38	73.1	112	2 H26317	Ig kappa chain V r
11	38	73.1	327	2 AH2608	transcription regu
12	38	73.1	327	2 G97390	arac family transc
13	37	71.2	125	2 S40349	Ig kappa chain V-U
14	37	71.2	248	2 AF2533	hypothetical prote
15	37	71.2	1302	2 AC2017	cobalamin biosynth
16	36	69.2	91	2 S37525	Ig kappa chain V r
17	36	69.2	91	2 S17630	Ig kappa chain V r
18	36	69.2	107	2 S36264	Ig lambda chain V
19	36	69.2	107	2 A28195	Ig kappa chain V r
20	36	69.2	108	1 K1H0BN	Ig kappa chain V-I
21	36	69.2	108	2 B44371	Ig kappa chain V r
22	36	69.2	108	2 PL0204	anti-DNA autoantib
23	36	69.2	117	2 S40362	Ig kappa chain - h
24	36	69.2	129	2 S40369	Ig kappa chain - h
25	36	69.2	129	2 B23966	Ig kappa chain pre
26	36	69.2	145	2 PL0014	Ig kappa chain pre
27	36	69.2	641	2 T30076	hypothetical prote
28	35	67.3	115	2 S63596	Ig kappa chain V r
29	35	67.3	125	2 S40333	Ig kappa chain V-J

30	67.3	270	2 F88035	protein M01D1.7 (i
31	67.3	290	2 G86155	hypothetical prote
32	67.3	320	2 A81799	abortive phage res
33	67.3	360	2 T27324	hypothetical prote
34	67.3	1092	2 S77546	cobn protein - Syn
35	67.3	1751	2 T50002	hypothetical prote
36	65.4	31	2 A24730	Ig kappa chain V r
37	65.4	93	2 S17642	Ig kappa chain V r
38	65.4	93	2 S17641	Ig kappa chain V r
39	65.4	93	2 S17643	Ig kappa chain V r
40	65.4	93	2 S17640	Ig kappa chain V r
41	65.4	93	2 S17623	Ig kappa chain V r
42	65.4	106	2 PS0070	Ig kappa chain V r
43	65.4	111	2 S09965	Ig kappa chain V-J
44	65.4	112	2 D26317	Ig kappa chain V r
45	65.4	112	2 I26317	Ig kappa chain V r
46	65.4	130	2 B23456	Ig kappa chain pre
47	65.4	132	2 S40334	Ig kappa chain - h
48	65.4	223	2 E90795	probable membrane
49	65.4	245	2 A85656	hypothetical prote
50	65.4	309	2 A90439	ABC transporter, A
51	65.4	318	2 AB2363	hypothetical prote
52	65.4	339	2 C86536	hypothetical prote
53	65.4	339	2 E72086	hypothetical prote
54	65.4	344	2 C81581	6-phospho-beta-gal
55	65.4	474	1 A29897	parasporal crystal
56	65.4	652	2 I39811	parasporal crystal
57	65.4	659	2 S10228	cell size regulati
58	65.4	659	2 S54725	regulatory protein
59	65.4	803	1 K8B7W6	metalloprotease, C
60	65.4	842	2 S60402	metalloprotease, C
61	65.4	942	2 B72015	insulinase family/
62	65.4	942	2 C86610	WD-40 repeat prote
63	63.5	23	2 S23637	hypothetical prote
64	63.5	23	2 C28195	Ig kappa chain V r
65	63.5	86	2 S45324	Ig kappa chain V r
66	63.5	95	2 S69898	Ig kappa chain V r
67	63.5	95	2 B49442	Ig light chain V r
68	63.5	96	2 B49442	Ig light chain V r
69	63.5	104	2 B43413	Ig kappa chain V r
70	63.5	105	2 S36266	Ig lambda chain V
71	63.5	108	2 S19674	Ig kappa chain V r
72	63.5	111	1 K7MS83	Ig kappa chain V r
73	63.5	112	2 PL0275	Ig kappa chain V r
74	63.5	112	2 E26317	Ig kappa chain V r
75	63.5	112	2 A26317	Ig kappa chain V r
76	63.5	112	2 PL0274	Ig kappa chain V r
77	63.5	112	2 F26317	Ig kappa chain V r
78	63.5	112	2 G26317	Ig kappa chain V r
79	63.5	112	2 B26317	Ig kappa chain V r
80	63.5	113	2 A49260	antitumor monoclon
81	63.5	117	2 S41809	Ig kappa chain V r
82	63.5	117	2 S41810	Ig kappa chain V r
83	63.5	138	2 A26471	Ig kappa chain pre
84	63.5	162	2 C72665	hypothetical prote
85	63.5	197	2 S29593	Ig kappa chain (WM
86	63.5	251	1 BVECB3	biotin biosynthesi
87	63.5	251	2 G90735	probable enzyme B1
88	63.5	251	2 H85585	hypothetical prote
89	63.5	340	2 B70461	aspartate-semialde
90	63.5	413	2 S28066	sexual differential
91	63.5	450	2 T25546	hypothetical prote
92	63.5	520	2 AD2383	Na+/H+-exchanging
93	63.5	562	2 C72278	hypothetical prote
94	63.5	776	2 S28258	androgen-regulated
95	63.5	1050	2 S54640	KCS1 protein - yea
96	63.5	1404	2 T119377	hypothetical prote
97	62.5	721	2 AH3417	lipa protein (limp
98	61.5	71	2 S08019	lysis protein - ph
99	61.5	91	2 G30538	Ig kappa chain V r
100	61.5	91	2 S37511	Ig kappa chain V r
101	61.5	98	2 S26342	Ig kappa chain V r
102	61.5	102	2 S29584	Ig kappa chain V r

103	32	61.5	106	2	B54378	176	31	59.6	495	2	S76967	hypothetical prote
104	32	61.5	107	2	S47183	177	31	59.6	499	2	S75722	Ms-protoporphyrin
105	32	61.5	107	2	S48195	178	31	59.6	524	2	A82580	polyvinylalcohol d
106	32	61.5	108	2	S29581	179	31	59.6	547	2	S44841	Ko6H7.1 protein -
107	32	61.5	112	1	KYMS16	180	31	59.6	609	2	T28896	hypothetical prote
108	32	61.5	112	1	C26317	181	31	59.6	624	2	T33868	hypothetical prote
109	32	61.5	113	1	KYMS51	182	31	59.6	672	2	H82143	methvl-accepting c
110	32	61.5	117	1	K1HUI1	183	31	59.6	712	2	E83067	glycogen phosphory
111	32	61.5	117	1	C21056	184	31	59.6	815	2	AB0996	unknown protein F5
112	32	61.5	117	2	B21056	185	31	59.6	884	2	D96730	hypothetical prote
113	32	61.5	128	1	KYMS11	186	31	59.6	954	2	G71496	hypothetical prote
114	32	61.5	131	2	S55027	187	31	59.6	1190	2	S47536	oxyesterol-binding
115	32	61.5	137	2	A83751	188	31	59.6	1228	2	AE2397	protoporphyrin IX
116	32	61.5	213	2	S75216	189	31	59.6	1239	1	VHMVEE	structural polypor
117	32	61.5	219	2	B98075	190	31	59.6	1240	1	VHMVEE	structural polypor
118	32	61.5	300	2	G91288	191	31	59.6	1241	2	S26373	genome polyprotein
119	32	61.5	300	2	B86130	192	31	59.6	1242	2	A56605	structural polypor
120	32	61.5	300	2	S56545	193	31	59.6	1242	2	S72350	probable retroelem
121	32	61.5	302	2	A32801	194	31	59.6	1402	2	F84480	hypothetical prote
122	32	61.5	334	2	AD2321	195	31	59.6	2055	2	T00093	1-phosphatidylinos
123	32	61.5	362	2	A39714	196	31	59.6	2473	1	S38040	peptide synthetase
124	32	61.5	448	2	A30341	197	31	59.6	2560	1	I40457	mycosubtilin synth
125	32	61.5	451	2	AF0437	198	31	59.6	5369	2	T44807	2-dehydro-3-deoxy-
126	32	61.5	451	2	S73433	199	31	58.7	368	1	JN0865	hypothetical 5K pr
127	32	61.5	468	2	E70839	200	30	57.7	42	2	JQ0232	hypothetical prote
128	32	61.5	487	2	AC0328	201	30	57.7	54	2	G82592	hypothetical prote
129	32	61.5	507	2	G89908	202	30	57.7	91	2	S37527	hypothetical prote
130	32	61.5	519	2	G71604	203	30	57.7	97	2	PH1085	hypothetical prote
131	32	61.5	567	2	AG2008	204	30	57.7	99	2	S29585	hypothetical prote
132	32	61.5	592	2	T16725	205	30	57.7	99	2	C85707	unknown protein en
133	32	61.5	630	2	S77148	206	30	57.7	100	2	H38601	hypothetical prote
134	32	61.5	764	2	E84516	207	30	57.7	110	2	PN0535	hypothetical prote
135	32	61.5	840	2	T01272	208	30	57.7	118	2	S40350	hypothetical prote
136	32	61.5	887	2	A54832	209	30	57.7	125	2	SA0350	hypothetical prote
137	32	61.5	1003	2	S09145	210	30	57.7	129	1	QCQV42	AD2 protein - roma
138	32	61.5	1025	2	C82886	211	30	57.7	130	2	A32513	hypothetical prote
139	32	61.5	1067	1	S62421	212	30	57.7	132	2	S05268	hypothetical prote
140	32	61.5	1081	2	S15040	213	30	57.7	140	2	S57063	probable membrane
141	32	61.5	1370	2	T18188	214	30	57.7	142	2	E97752	hypothetical prote
142	32	61.5	1669	2	T49244	215	30	57.7	152	2	S30751	hypothetical prote
143	32	61.5	3848	2	T174104	216	30	57.7	153	2	T12454	hypothetical prote
144	31.5	60.6	761	2	T41304	217	30	57.7	159	2	E75151	molybdenum cofacto
145	31	59.6	75	2	A34966	218	30	57.7	163	2	T23691	hypothetical prote
146	31	59.6	76	2	E64453	219	30	57.7	169	2	S40994	hypothetical prote
147	31	59.6	92	2	S38622	220	30	57.7	197	2	E70349	anthranilate synth
148	31	59.6	106	2	S03303	221	30	57.7	201	2	AC2717	anthranilate synth
149	31	59.6	108	1	K1HUKU	222	30	57.7	201	2	C75356	hypothetical prote
150	31	59.6	112	2	C81123	223	30	57.7	206	2	B84243	hypothetical prote
151	31	59.6	117	2	S42466	224	30	57.7	212	2	G82103	phosphoribosylgIyc
152	31	59.6	128	2	S40343	225	30	57.7	224	2	F97498	hypothetical prote
153	31	59.6	135	2	T40119	226	30	57.7	224	2	T33202	hypothetical prote
154	31	59.6	155	2	AD2253	227	30	57.7	252	2	D98028	hypothetical prote
155	31	59.6	180	2	C64035	228	30	57.7	252	2	B95162	hypothetical prote
156	31	59.6	181	2	AG1853	229	30	57.7	260	2	A38114	resolvasa red - Sa
157	31	59.6	212	2	AG0344	230	30	57.7	290	2	AB4011	transcription acti
158	31	59.6	212	2	F86769	231	30	57.7	295	2	D96648	hypothetical prote
159	31	59.6	219	2	H95210	232	30	57.7	297	2	AF0671	conserved hypotet
160	31	59.6	225	1	CYFGE	233	30	57.7	311	2	A56235	transcription acti
161	31	59.6	248	1	T16315	234	30	57.7	325	2	B88537	truncated ZK370.3
162	31	59.6	258	2	AF2204	235	30	57.7	329	2	B89916	aspartate semialde
163	31	59.6	281	1	D30191	236	30	57.7	338	2	T50268	1-aminocyclopropan
164	31	59.6	283	1	T10228	237	30	57.7	341	2	F69789	hypothetical prote
165	31	59.6	324	1	JC4280	238	30	57.7	342	2	S55675	Gal-beta-1,3galNac
166	31	59.6	334	2	T07722	239	30	57.7	345	2	B43731	achaeate-acute comp
167	31	59.6	351	2	AG1436	240	30	57.7	358	2	A89980	hypothetical prote
168	31	59.6	351	2	AH1078	241	30	57.7	370	2	S49008	fork head protein
169	31	59.6	351	2	P82257	242	30	57.7	378	2	A44443	basic helix-loop-h
170	31	59.6	450	2	T23111	243	30	57.7	383	1	C8ECZ	cell division prot
171	31	59.6	457	2	JC4541	244	30	57.7	383	2	AB0519	cell division prot
172	31	59.6	469	2	T35526	245	30	57.7	383	2	C90641	cell division prot
173	31	59.6	486	2	JC4028	246	30	57.7	383	2	C85492	cell division prot
174	31	59.6	490	2	T23112	247	30	57.7	383	2	G96629	hypothetical prote
175	31	59.6	490	2	T23112	248	30	57.7	386	1	JH0610	acid phosphatase (

249	30	57.7	436	2	T39837	MAD box transcript
250	30	57.7	456	2	S45137	fuelti tarazu segme
251	30	57.7	465	2	J06369	histidine-acid pho
252	30	57.7	468	2	A86233	hypothetical prote
253	30	57.7	481	2	F86208	protein F22G5.30.1
254	30	57.7	488	1	YESABE	erythromycin resis
255	30	57.7	500	2	A48767	glutamate decarbox
256	30	57.7	561	2	T01950	hypothetical prote
257	30	57.7	562	1	HMTV2	hemagglutinin prec
258	30	57.7	566	1	HMTVAT	conserved hypotet
259	30	57.7	614	2	AP0062	hypothetical prote
260	30	57.7	615	2	T41576	hypothetical prote
261	30	57.7	627	2	B71709	sucrose alpha-gluc
262	30	57.7	642	2	S11386	sodium transport p
263	30	57.7	650	2	A54065	DNA polymerase alp
264	30	57.7	653	2	S40962	asparagine-rich pr
265	30	57.7	669	2	S14535	hypothetical prote
266	30	57.7	681	2	T33381	hypothetical prote
267	30	57.7	731	2	T19721	protein K04H4.2b [
268	30	57.7	739	2	B88553	protein K04H4.2b [
269	30	57.7	758	2	S46625	finger protein YDL
270	30	57.7	802	2	T24293	hypothetical prote
271	30	57.7	803	1	OKRFP5	protein-tyrosine k
272	30	57.7	828	2	C88402	protein H05C05.1 [
273	30	57.7	862	2	A05028	tpoc protein homol
274	30	57.7	923	2	S44664	ZK370.3 protein -
275	30	57.7	949	2	T24294	hypothetical prote
276	30	57.7	950	2	T09076	hypothetical prote
277	30	57.7	991	2	B71315	conserved hypotet
278	30	57.7	1108	2	A55915	guanylate cyclase
279	30	57.7	1110	1	S55279	guanylate cyclase
280	30	57.7	1132	2	S37932	hypothetical prote
281	30	57.7	1180	2	S69205	stripe a/b protein
282	30	57.7	1216	2	T02146	coactomer complex a
283	30	57.7	1301	1	A41622	protein-tyrosine-p
284	30	57.7	1816	2	A84845	probable ABC trans
285	30	57.7	1978	2	S77257	hypothetical prote
286	30	57.7	4273	2	C69679	polypeptide synthas
287	30	57.7	4450	2	UX0340	gramicidin S synth
288	30	57.7	4452	1	YGBSG2	gramicidin S synth
289	30	57.7	6486	2	T31076	tyrocidine synthet
290	29.5	56.7	1785	2	T21558	hypothetical prote
291	29.5	56.7	1929	2	T21559	hypothetical prote
292	29	55.8	50	2	C82725	hypothetical prote
293	29	55.8	78	2	AD2028	hypothetical prote
294	29	55.8	81	2	AF1768	ribosomal protein
295	29	55.8	81	2	AD1393	ribosomal protein
296	29	55.8	84	2	C81037	hypothetical prote
297	29	55.8	94	2	S26339	Ig kappa chain V r
298	29	55.8	94	2	S26340	Ig light chain V r
299	29	55.8	96	2	AG1451	hypothetical prote
300	29	55.8	102	2	S19464	hypothetical prote
301	29	55.8	103	2	H72664	Ig kappa chain V r
302	29	55.8	105	2	S26338	Ig kappa chain V r
303	29	55.8	106	2	G27887	Ig kappa chain V r
304	29	55.8	107	2	S26343	Ig kappa chain V r
305	29	55.8	108	1	K1H0LY	Ig kappa chain V-I
306	29	55.8	108	2	S36279	Ig lambda chain V
307	29	55.8	109	1	K3HUPM	Ig kappa chain V-I
308	29	55.8	109	2	C82676	benzene 1,2-dioxyg
309	29	55.8	111	1	KWMS43	Ig kappa chain V r
310	29	55.8	111	2	D45722	anti-glycoprotein
311	29	55.8	117	2	S11700	Ig kappa chain pre
312	29	55.8	131	1	KWMSM6	Ig kappa chain pre
313	29	55.8	134	2	T43367	Ig kappa chain - h
314	29	55.8	143	2	S43028	probable oligosacc
315	29	55.8	144	2	T16896	hypothetical prote
316	29	55.8	144	2	PI0106	Ig kappa chain pre
317	29	55.8	147	2	H86696	hypothetical prote
318	29	55.8	153	1	QQVZF7	F7 protein - vaccl
319	29	55.8	153	2	T37361	diemetic vifron pro
320	29	55.8	153	2	D42513	J1R protein - vacc
321	29	55.8	159	2	D72160	M1R protein - vari
322	29	55.8	159	2	T28516	hypothetical prote
323	29	55.8	159	2	S33092	U1R protein - vari
324	29	55.8	160	2	F89965	hypothetical prote
325	29	55.8	161	2	T50307	hypothetical prote
326	29	55.8	163	2	S74362	anthranilate synth
327	29	55.8	165	2	H83496	conserved hypotet
328	29	55.8	170	2	T18836	hypothetical prote
329	29	55.8	173	2	T44619	hypothetical prote
330	29	55.8	184	1	A35441	alkyl hydroperoxid
331	29	55.8	189	2	A63639	hypothetical prote
332	29	55.8	195	2	A99240	anthranilate synth
333	29	55.8	195	2	B40635	anthranilate synth
334	29	55.8	196	2	D69088	anthranilate synth
335	29	55.8	205	2	T07871	mitraculin homolog
336	29	55.8	211	2	AC2560	hypothetical prote
337	29	55.8	212	2	AE1877	hypothetical prote
338	29	55.8	215	2	T39280	probable ribosomal
339	29	55.8	217	2	T08278	hypothetical prote
340	29	55.8	220	1	B5AG58	viR5 protein prec
341	29	55.8	220	1	B6AG55	viR5 protein prec
342	29	55.8	228	2	A13248	component of type
343	29	55.8	228	2	A75516	ABC transporter, A
344	29	55.8	242	2	D71542	probable ribose-5-
345	29	55.8	245	2	T40971	20s proteasome com
346	29	55.8	253	2	T19129	hypothetical prote
347	29	55.8	260	2	A41531	TGbeta-regulated
348	29	55.8	262	2	AB0178	probable short cha
349	29	55.8	263	2	A64676	shikimate 5-dehydr
350	29	55.8	266	2	A71841	shikimate 5-dehydr
351	29	55.8	269	2	T36639	probable substrate
352	29	55.8	270	2	G83965	required for forma
353	29	55.8	270	2	C75257	hypothetical prote
354	29	55.8	270	2	G71061	hypothetical prote
355	29	55.8	276	2	T23187	transcription anti
356	29	55.8	285	2	D69632	hypothetical prote
357	29	55.8	285	2	B82234	probable hemolysin
358	29	55.8	291	2	B82261	probable AraC-fam1
359	29	55.8	295	2	AG0848	carbonate dehydrat
360	29	55.8	307	2	A29993	hypothetical prote
361	29	55.8	316	2	D83233	hypothetical prote
362	29	55.8	318	2	A86750	hypothetical prote
363	29	55.8	320	2	S16649	dipeptide ABC tran
364	29	55.8	323	2	D90527	glycerol-3-phospha
365	29	55.8	326	2	A82973	hypothetical prote
366	29	55.8	336	2	AB2973	hypothetical prote
367	29	55.8	347	2	T15375	hypothetical prote
368	29	55.8	351	2	AC1990	hypothetical prote
369	29	55.8	353	2	A85263	probable cdc2 kina
370	29	55.8	358	2	T05125	protein kinase hom
371	29	55.8	358	2	S75659	gene At103 protein
372	29	55.8	362	2	S48270	hypothetical prote
373	29	55.8	363	2	T26385	hypothetical prote
374	29	55.8	372	2	T64223	bifunctional endo-
375	29	55.8	376	2	S64479	probable membrane
376	29	55.8	382	2	AG0188	histidinol-phospha
377	29	55.8	388	2	F87208	cystathionine [gam
378	29	55.8	400	2	AE2889	acriflavin resista
379	29	55.8	403	2	B95347	conserved hypotet
380	29	55.8	405	2	C90194	hypothetical prote
381	29	55.8	406	2	AB0111	hypothetical prote
382	29	55.8	409	2	E86017	probable monooxyge
383	29	55.8	409	2	E91171	probable beta-keto
384	29	55.8	410	2	B97665	membrane fusion pr
385	29	55.8	413	2	AC1392	glycine hydroxymet
386	29	55.8	413	2	AE1767	type II site-speci
387	29	55.8	416	2	S26836	hypothetical prote
388	29	55.8	426	2	T48056	conserved hypotet
389	29	55.8	427	2	F72389	phosphate-binding
390	29	55.8	429	2	C87183	glycerol-3-phospha
391	29	55.8	431	2	B97710	molybdopterin bios
392	29	55.8	435	2	E82439	dolichyl-di-phosph
393	29	55.8	437	2	T41728	nitrilacetate
394	29	55.8	440	2	AG1367	nitrilacetate

395	29	55.8	440	2	AH1736	468	29	55.8	1119	2	AD1822	1	lucine-rich-repea
396	29	55.8	440	2	A39613	469	29	55.8	1178	2	S57698	1	regulatory protein
397	29	55.8	447	2	C85085	470	29	55.8	1279	2	T18312	1	hypothetical prote
398	29	55.8	448	2	S20105	471	29	55.8	1284	2	T50993	1	hypothetical prote
399	29	55.8	460	2	T48137	472	29	55.8	1293	1	YGECP	1	enterobactin synth
400	29	55.8	461	2	T33747	473	29	55.8	1293	2	E85557	1	enterobactin synth
401	29	55.8	464	2	T17332	474	29	55.8	1293	2	A90707	1	enterobactin synth
402	29	55.8	466	2	T47941	475	29	55.8	1350	2	AF2005	2	RNA polymerase bet
403	29	55.8	496	2	T01962	476	29	55.8	1457	2	T14577	2	protein kinase yak
404	29	55.8	503	2	B81858	477	29	55.8	1601	2	AE2011	1	hypothetical prote
405	29	55.8	503	2	C81086	478	29	55.8	1642	2	T19130	1	hypothetical prote
406	29	55.8	507	2	T00682	479	29	55.8	1660	2	A84647	1	hypothetical prote
407	29	55.8	531	2	S41986	480	29	55.8	1679	2	T50091	2	yeast Ecm29 cell w
408	29	55.8	543	2	H84724	481	29	55.8	1711	2	AD1842	1	vitellogenin precu
409	29	55.8	544	2	A47726	482	29	55.8	1790	1	S27772	2	vitellogenin - Rip
410	29	55.8	552	2	C64310	483	29	55.8	1876	2	T28627	1	sodium channel pro
411	29	55.8	553	2	E27793	484	29	55.8	1976	2	T56555	2	genome polypotein
412	29	55.8	555	2	A43784	485	29	55.8	2116	1	ZIVNSY	1	hypothetical prote
413	29	55.8	555	2	S03261	486	29	55.8	2391	2	G89779	1	hypothetical prote
414	29	55.8	566	1	HMIVD8	487	29	55.8	2692	2	T23768	2	hypothetical prote
415	29	55.8	566	1	HMITV8	488	29	55.8	2957	2	T33152	2	homeoic protein z
416	29	55.8	570	2	T38148	489	29	55.8	3005	2	T45584	2	hypothetical prote
417	29	55.8	575	2	S39484	490	29	55.8	3071	2	T45584	2	breast cancer tumo
418	29	55.8	586	2	T29695	491	29	55.8	3328	2	T10835	2	breast cancer susc
419	29	55.8	617	2	D96978	492	29	55.8	3329	2	T42205	2	breast cancer tumo
420	29	55.8	621	2	S49020	493	29	55.8	3329	2	T30904	2	surfactin syntheta
421	29	55.8	630	1	W1WL35	494	29	55.8	3587	2	T14046	2	hypothetical prote
422	29	55.8	630	2	T03582	495	29	55.8	3724	2	T18427	2	hypothetical prote
423	29	55.8	631	2	T26232	496	29	54.8	509	2	A05183	1	hypothetical prote
424	29	55.8	631	2	T32761	497	29	28.5	509	2	S40613	2	maturase-like prot
425	29	55.8	637	2	S36523	498	29	28.5	548	2	AB2069	2	hypothetical prote
426	29	55.8	637	2	T50951	499	29	54.8	529	2	AB1798	2	RNA polymerase sig
427	29	55.8	644	2	C65072	500	29	28.5	642	2	G87338	2	Tomb-dependent rec
428	29	55.8	644	2	C85944	501	29	54.8	824	2	D82841	2	hypothetical prote
429	29	55.8	644	2	G91098	502	29	53.8	63	2	B38601	1	Ig kappa chain V r
430	29	55.8	649	2	T47609	503	29	53.8	65	2	B18962	2	Ig kappa chain V r
431	29	55.8	653	2	S67035	504	29	53.8	86	2	S16826	2	Ig kappa chain V r
432	29	55.8	657	2	S71946	505	29	53.8	87	2	F81321	1	hypothetical prote
433	29	55.8	664	2	C64747	506	29	53.8	103	2	F82775	1	hypothetical prote
434	29	55.8	677	2	T50022	507	29	53.8	91	2	S17628	1	Ig kappa chain V r
435	29	55.8	691	2	T29951	508	29	53.8	93	2	A38601	1	Ig kappa chain V r
436	29	55.8	696	2	G71620	509	29	53.8	97	2	F71853	1	hypothetical prote
437	29	55.8	728	2	D86278	510	29	53.8	106	2	PH1056	1	Ig kappa chain V r
438	29	55.8	730	2	T49736	511	29	53.8	107	2	PL0267	1	Ig kappa chain V r
439	29	55.8	735	2	S64504	512	29	53.8	107	2	C45722	1	anti-glycoprotein
440	29	55.8	745	1	A46833	513	29	53.8	107	2	S26344	1	Ig kappa chain V r
441	29	55.8	815	2	PHECGG	514	29	53.8	107	2	F30535	1	Ig kappa chain V r
442	29	55.8	815	2	B86009	515	29	53.8	107	2	D30535	1	Ig kappa chain V r
443	29	55.8	815	2	A98163	516	29	53.8	107	2	G30535	1	Ig kappa chain V r
444	29	55.8	848	2	S48473	517	29	53.8	107	2	B30535	1	Ig kappa chain V r
445	29	55.8	882	2	A81631	518	29	53.8	107	2	A42848	1	Ig light chain V r
446	29	55.8	883	2	AH1268	519	29	53.8	108	2	B30535	1	Ig kappa chain V r
447	29	55.8	892	1	FAH00A	520	29	53.8	108	2	S69902	1	Ig kappa chain (cl
448	29	55.8	900	2	E69631	521	29	53.8	108	2	B53399	1	protein [imported
449	29	55.8	901	2	JC6093	522	29	53.8	111	1	KWMS37	1	Ig kappa chain V r
450	29	55.8	906	2	G69531	523	29	53.8	111	1	KWMS37	1	Ig kappa chain V r
451	29	55.8	915	2	T21773	524	29	53.8	111	2	I38740	1	Ig kappa chain V r
452	29	55.8	924	2	B41359	525	29	53.8	111	2	S09966	1	Ig kappa chain V-J
453	29	55.8	924	2	S12746	526	29	53.8	111	2	A33936	1	Ig kappa chain V r
454	29	55.8	927	2	T21772	527	29	53.8	111	2	S70302	1	hypothetical prote
455	29	55.8	946	2	S48433	528	29	53.8	112	2	F30538	1	Ig kappa chain V r
456	29	55.8	980	2	D69974	529	29	53.8	113	1	KWMS7S	1	Ig kappa chain V r
457	29	55.8	1008	2	T12532	530	29	53.8	115	2	H71104	1	hypothetical prote
458	29	55.8	1013	2	S65195	531	29	53.8	117	2	S69301	1	hypothetical prote
459	29	55.8	1030	2	T18669	532	29	53.8	123	2	S40310	1	Ig kappa chain V-J
460	29	55.8	1071	2	S48378	533	29	53.8	125	2	S40316	1	Ig kappa chain - h
461	29	55.8	1085	2	S62516	534	29	53.8	128	2	AE2639	1	hypothetical prote
462	29	55.8	1087	2	T30330	535	29	53.8	128	2	F97421	1	hypothetical prote
463	29	55.8	1091	1	PM8YR2	536	29	53.8	129	2	S52789	1	Ig kappa chain V r
464	29	55.8	1091	2	S67852	537	29	53.8	129	2	D32513	1	Ig kappa chain pre
465	29	55.8	1091	2	S25007	538	29	53.8	136	2	T10795	1	acyl carrier prote
466	29	55.8	1094	2	C70612	539	29	53.8	142	2	C33910	1	bal homeoic prote
467	29	55.8	1106	2	T25065	540	29	53.8	157	2	S57451	1	cysteine proteinas

541	28	53.8	162	2	D82319	probable sprt prot	614	28	53.8	300	2	T38963	hypothetical prote
542	28	53.8	164	2	T32627	hypothetical prote	615	28	53.8	302	2	C97422	cher homolog (Apo4
543	28	53.8	165	2	T09252	seed storage prote	616	28	53.8	302	2	AB2640	chemotaxis methyl
544	28	53.8	169	2	D72765	hypothetical prote	617	28	53.8	302	2	S61836	cher protein - Rhl
545	28	53.8	172	2	S18871	2S-like storage pr	618	28	53.8	305	2	A55371	minor capsid prote
546	28	53.8	173	2	T08011	2S seed storage pr	619	28	53.8	305	2	T16121	hypothetical prote
547	28	53.8	177	1	A39414	flavodoxin - enter	620	28	53.8	305	2	T33524	hypothetical prote
548	28	53.8	177	1	F81442	hypothetical prote	621	28	53.8	306	2	H89929	conserved hypotet
549	28	53.8	180	2	AD0134	probable prophage	622	28	53.8	306	2	E64348	lysine-cRNA 11ga
550	28	53.8	185	2	S11242	mwfl0 protein - my	623	28	53.8	310	2	C64033	35.9K hypothetical
551	28	53.8	190	2	A85360	hypothetical prote	624	28	53.8	311	2	T02009	hypothetical prote
552	28	53.8	190	2	E82060	conserved hypotet	625	28	53.8	316	2	C63727	hypothetical prote
553	28	53.8	195	2	A88360	protein W02B8.1 l1	626	28	53.8	317	2	C62411	oligopeptide trans
554	28	53.8	198	2	A87545	Hipa-related prote	627	28	53.8	322	2	D96921	aldehyde and adduc
555	28	53.8	198	2	T19797	hypothetical prote	628	28	53.8	324	2	T39175	transcription regu
556	28	53.8	202	2	H44583	venom allergen ant	629	28	53.8	326	2	AF2132	probable aldo/keto
557	28	53.8	202	2	G44583	venom allergen ant	630	28	53.8	329	2	AG0519	calpainin, acidic
558	28	53.8	212	1	XRECGF	phosphoribosylglyc	631	28	53.8	330	2	A53742	hypothetical prote
559	28	53.8	212	2	AB0819	phosphoribosylglyc	632	28	53.8	331	2	S76765	arginase (EC 3.5.3
560	28	53.8	212	2	B91049	phosphoribosylglyc	633	28	53.8	333	1	W2BYR	hypothetical prote
561	28	53.8	212	2	P85893	phosphoribosylglyc	634	28	53.8	335	2	T26617	conserved hypotet
562	28	53.8	212	2	D69641	amidotransferase h	635	28	53.8	336	2	E87199	beta-galactoside a
563	28	53.8	212	2	D82431	CbbY family protei	636	28	53.8	337	2	S36824	mg1 repressor and
564	28	53.8	214	2	S48947	hypothetical prote	637	28	53.8	340	2	AC0781	figellar switch p
565	28	53.8	216	2	S35947	phosphoglycerate m	638	28	53.8	340	2	B55544	beta-galactoside a
566	28	53.8	216	2	S35947	card protein - Erw	639	28	53.8	340	2	I54229	Gal beta 1,3galNAc
567	28	53.8	224	2	T29312	hypothetical prote	640	28	53.8	343	2	A45073	hypothetical prote
568	28	53.8	224	2	D72704	Ig gamma chain (cl	641	28	53.8	343	2	AB2451	hypothetical prote
569	28	53.8	224	2	S03050	replication protei	642	28	53.8	345	2	S09858	hypothetical prote
570	28	53.8	229	2	S49494	pseudouridyate sy	643	28	53.8	346	2	C91009	mg1 repressor (mp
571	28	53.8	229	2	AG0785	16S pseudouridyat	644	28	53.8	346	2	E85853	mg1 repressor, gal
572	28	53.8	231	2	P64987	16S pseudouridyat	645	28	53.8	350	2	T45082	isorepressor galS
573	28	53.8	231	2	E85857	transcription regu	646	28	53.8	350	2	E75047	acyl carrier prote
574	28	53.8	231	2	C91013	probable membrane	647	28	53.8	352	2	S47707	probable acyl carr
575	28	53.8	231	2	AI3632	hypothetical prote	648	28	53.8	352	2	F83729	hypothetical prote
576	28	53.8	234	2	S58252	hypothetical prote	649	28	53.8	352	2	T52184	zinc transporter Z
577	28	53.8	234	2	T27454	hypothetical prote	650	28	53.8	355	2	H91173	hypothetical 38.8K
578	28	53.8	241	2	AB1836	protein thermoregula	651	28	53.8	355	2	H91173	probable membrane
579	28	53.8	241	2	AC4504	uracil-DNA glucosyl	652	28	53.8	355	2	H86019	probable lipase (l
580	28	53.8	248	2	T03140	conserved hypotet	653	28	53.8	355	2	E84716	conserved hypotet
581	28	53.8	252	2	B69497	ABC transporter, A	654	28	53.8	358	2	G90456	hypothetical prote
582	28	53.8	252	2	P96945	hypothetical prote	655	28	53.8	358	2	S75234	portin foma precurs
583	28	53.8	254	2	T26090	formate dehydrogen	656	28	53.8	368	2	S46436	hypothetical prote
584	28	53.8	261	2	AC1397	formate dehydrogen	657	28	53.8	371	2	T35036	acid phosphatase (
585	28	53.8	261	2	AC1397	formate dehydrogen	658	28	53.8	381	2	JH0152	conserved hypotet
586	28	53.8	263	2	I54780	interferon-gamma r	659	28	53.8	383	2	AB2948	hypothetical prote
587	28	53.8	263	2	A44229	hypothetical prote	660	28	53.8	383	2	H98334	hypothetical prote
588	28	53.8	266	2	T22185	hypothetical prote	661	28	53.8	388	2	C95102	hypothetical prote
589	28	53.8	266	2	T01752	hypothetical prote	662	28	53.8	388	2	E97970	hypothetical prote
590	28	53.8	267	2	T17657	hypothetical prote	663	28	53.8	388	2	T02316	hypothetical prote
591	28	53.8	270	2	T49636	hypothetical prote	664	28	53.8	391	2	T45399	iron-sulfur cofact
592	28	53.8	270	2	T49636	hypothetical prote	665	28	53.8	396	2	D83122	probable FAD-depen
593	28	53.8	271	2	G64025	inosine-5'-monopho	666	28	53.8	398	2	S73883	yeaf protein homol
594	28	53.8	272	2	A84223	5-keto-4-deoxyuron	667	28	53.8	399	1	S73883	hypothetical prote
595	28	53.8	276	2	F83920	hypothetical prote	668	28	53.8	399	2	T19115	beta-1,6-N-acetylgl
596	28	53.8	279	2	I64024	hypothetical prote	669	28	53.8	400	2	A46297	thiamin biosynthes
597	28	53.8	279	2	E90264	hypothetical prote	670	28	53.8	403	2	AH1273	probable aminotran
598	28	53.8	280	1	D69513	conserved hypotet	671	28	53.8	403	2	AI1636	transcobalamin I p
599	28	53.8	281	2	H95158	l1cd3 protein (lmp	672	28	53.8	410	2	F87122	hypothetical prote
600	28	53.8	282	2	H98024	l1cd1 homolog (lmp	673	28	53.8	416	2	S09334	hypothetical prote
601	28	53.8	282	2	D82520	hypothetical prote	674	28	53.8	419	2	T29266	hypothetical prote
602	28	53.8	282	2	B86841	hypothetical prote	675	28	53.8	420	2	S50652	hypothetical prote
603	28	53.8	283	2	A64899	hypothetical prote	676	28	53.8	422	2	H96595	unknown protein, 9
604	28	53.8	288	2	T37081	hypothetical prote	677	28	53.8	423	2	S77395	carboxyl-terminal
605	28	53.8	290	2	T46470	hypothetical prote	678	28	53.8	428	2	B70078	conserved hypotet
606	28	53.8	291	2	T05024	heat shock transcr	679	28	53.8	428	2	S07916	Rf4 protein - yeast
607	28	53.8	292	2	F97082	transcription regu	680	28	53.8	435	2	T39719	beta transducin -
608	28	53.8	293	2	C71940	homoserine kinase	681	28	53.8	436	2	JC7982	AMS1-like protein
609	28	53.8	293	2	B64651	homoserine kinase	682	28	53.8	443	2	E64640	hypothetical prote
610	28	53.8	295	2	S58850	transcription regu	683	28	53.8	446	2	S34570	beta-glucosidase (
611	28	53.8	297	2	AD2318	hypothetical prote	684	28	53.8	447	2	D86853	asparagine-tRNA 1i
612	28	53.8	300	2	B85021	hypothetical prote	685	28	53.8	449	2	H69862	Na+-transporting A
613	28	53.8	300	2	T16778	hypothetical prote	686	28	53.8	451	2	T16162	hypothetical prote

687	28	53.8	459	2	T17349	NADH2 dehydrogenas	760	28	53.8	638	2	S22491	acetylactate synth
688	28	53.8	459	2	T17184	NADH2 dehydrogenas	761	28	53.8	640	2	S62747	homeotic protein A
689	28	53.8	459	2	T17364	NADH2 dehydrogenas	762	28	53.8	648	2	S62290	soluble lytic mure
690	28	53.8	459	2	T17361	NADH2 dehydrogenas	763	28	53.8	651	2	S24609	cytoskeletal prote
691	28	53.8	459	2	T17163	NADH2 dehydrogenas	764	28	53.8	665	2	E75124	formate dehydrogen
692	28	53.8	459	2	T17166	NADH2 dehydrogenas	765	28	53.8	666	2	H69581	protein dim-1 [imp
693	28	53.8	459	2	T17172	NADH2 dehydrogenas	766	28	53.8	672	1	A29836	beta-galactosidase
694	28	53.8	459	2	T17144	NADH2 dehydrogenas	767	28	53.8	673	1	P82930	DNA ligase UUI21 [
695	28	53.8	459	2	T17169	NADH2 dehydrogenas	768	28	53.8	677	1	S09078	chromogranin B pre
696	28	53.8	459	2	T17175	NADH2 dehydrogenas	769	28	53.8	677	1	F64139	guanosine-3',5'-bi
697	28	53.8	459	2	T17178	NADH2 dehydrogenas	770	28	53.8	681	1	H82059	2',3'-cyclic-nucle
698	28	53.8	459	2	T17181	NADH2 dehydrogenas	771	28	53.8	687	2	S58778	probable membrane
699	28	53.8	459	2	A87201	conserved hypothet	772	28	53.8	693	2	AR2357	hypothetical prote
700	28	53.8	467	2	E89605	conserved hypothet	773	28	53.8	695	2	T37667	probable cytochrom
701	28	53.8	472	2	T48074	hypothetical prote	774	28	53.8	698	2	A84547	hypothetical prote
702	28	53.8	476	2	A44170	membrane-bound rib	775	28	53.8	701	2	S64599	probable membrane
703	28	53.8	478	2	T38014	hypothetical zinc	776	28	53.8	702	2	T16401	alpha-1,3-mannosyl
704	28	53.8	478	2	T12683	embryogenesis prot	777	28	53.8	731	2	B83904	hypothetical prote
705	28	53.8	480	2	AB0148	catalase [EC 1.11.	778	28	53.8	736	2	A27477	cell division cont
706	28	53.8	482	2	B83113	catalase PA4236 [i	779	28	53.8	737	2	T30795	hypothetical prote
707	28	53.8	485	2	T41714	hypothetical serin	780	28	53.8	737	2	T28481	hypothetical prote
708	28	53.8	486	2	H81377	exopolysphatase	781	28	53.8	737	2	A72156	C2I protein - Vari
709	28	53.8	496	2	T37477	catalase [EC 1.11.	782	28	53.8	737	2	F42508	E2I protein - vacc
710	28	53.8	497	2	T42443	catalase [EC 1.11.	783	28	53.8	737	2	E36841	E2I protein - vari
711	28	53.8	504	2	S00390	Ig gamma chain [Cl	784	28	53.8	745	1	S75354	probable copper-cr
712	28	53.8	504	2	A87386	conserved hypothet	785	28	53.8	747	1	E71429	probable FCA gamma
713	28	53.8	506	1	CS80	catalase [EC 1.11.	786	28	53.8	763	2	T27620	1,4-alpha-glucan b
714	28	53.8	506	1	A86169	catalase [EC 1.11.	787	28	53.8	764	2	AG1895	DNA excision repai
715	28	53.8	512	2	T27178	hypothetical prote	788	28	53.8	782	1	A35661	probable sulfatase
716	28	53.8	513	2	F96533	catalase [EC 1.11.	789	28	53.8	787	2	B70643	probable potassum
717	28	53.8	522	2	A75412	probable fucoyltr	790	28	53.8	802	2	T05596	desmocollin 2b pre
718	28	53.8	524	2	T27177	conserved hypothet	791	28	53.8	809	1	I0B0DD	probable serine/th
719	28	53.8	527	1	CSHU	catalase [EC 1.11.	792	28	53.8	814	2	T05537	hypothetical prote
720	28	53.8	527	1	CSRT	catalase [EC 1.11.	793	28	53.8	837	2	D84428	glycoprotein phosp
721	28	53.8	527	1	A36695	catalase [EC 1.11.	794	28	53.8	839	2	A56337	adenylate cyclase
722	28	53.8	530	2	JCS939	estrogen receptor	795	28	53.8	843	2	H82362	H82362
723	28	53.8	531	2	T01415	basic leucine zip	796	28	53.8	863	1	I0B0DC	desmocollin 2a pre
724	28	53.8	550	1	E28544	methyl coenzyme M	797	28	53.8	893	2	E95053	cell wall surfact
725	28	53.8	550	2	T37519	probable amino aci	798	28	53.8	957	2	S44748	C06G4.1 protein -
726	28	53.8	550	2	T45535	agag protein [limp	799	28	53.8	992	2	T08772	hypothetical prote
727	28	53.8	550	2	B69022	methyl coenzyme M	800	28	53.8	993	2	C55226	cyLM protein - Bnt
728	28	53.8	553	2	C69017	methyl coenzyme M	801	28	53.8	1014	2	AC1971	valyl-tRNA synthet
729	28	53.8	554	2	S43897	H+-transporting AT	802	28	53.8	1018	2	UC5799	alpha-D-mannosidas
730	28	53.8	556	2	A84364	hypothetical prote	803	28	53.8	1028	2	A56038	DNA-binding protei
731	28	53.8	557	2	B90037	methyl coenzyme M	804	28	53.8	1028	2	AD0052	probable multi-dru
732	28	53.8	557	2	T45150	hypothetical prote	805	28	53.8	1036	2	E84620	hypothetical prote
733	28	53.8	559	1	WMBS1	71K upper matrix P	806	28	53.8	1063	2	A33830	cation efflux synt
734	28	53.8	559	2	T08174	sesquiterpene cycl	807	28	53.8	1063	2	UC4700	cadmium, zinc, cob
735	28	53.8	571	2	T52164	nucleotide phospho	808	28	53.8	1067	2	D82436	transporter, AcFB/
736	28	53.8	578	2	T22311	hypothetical prote	809	28	53.8	1117	2	S38673	desmoglein 2 - hum
737	28	53.8	580	2	E84477	Mutator-like trans	810	28	53.8	1146	2	B35962	protein-tyrosine k
738	28	53.8	580	2	C84526	Mutator-like trans	811	28	53.8	1169	2	F97800	transcription-repa
739	28	53.8	580	2	T01862	hypothetical prote	812	28	53.8	1171	2	F97872	transcription-repa
740	28	53.8	585	1	S14732	H+-transporting tw	813	28	53.8	1174	2	T28701	probable polyketid
741	28	53.8	585	2	AG0955	conserved hypothet	814	28	53.8	1174	1	A43736	probable polyketid
742	28	53.8	585	2	AI1969	two-component sens	815	28	53.8	1182	2	A35962	creatine kinase (E
743	28	53.8	592	1	A30314	protein kinase C (816	28	53.8	1213	2	S16356	protein-tyrosine k
744	28	53.8	592	1	UC1480	protein kinase C (817	28	53.8	1224	1	ERHUAH	ovo protein - fruit
745	28	53.8	596	2	S61146	probable membrane	818	28	53.8	1258	2	F96753	Similar to downy m
746	28	53.8	597	2	A35928	hypothetical 86K P	819	28	53.8	1289	2	T31344	GP80 precursor - b
747	28	53.8	601	2	T29878	hypothetical prote	820	28	53.8	1360	2	F96596	hypothetical prote
748	28	53.8	601	2	D83238	hypothetical prote	821	28	53.8	1365	1	BVBVKS	killer toxin reas
749	28	53.8	606	2	T16449	hypothetical prote	822	28	53.8	1388	2	T47961	hypothetical prote
750	28	53.8	607	2	F84525	Mutator-like trans	823	28	53.8	1468	2	T18545	lyobactin synthet
751	28	53.8	613	2	A69203	phenylalanine-tRNA	824	28	53.8	1575	2	AD1512	peptidoglycan bou
752	28	53.8	616	2	E84463	Mutator-like trans	825	28	53.8	1583	2	AC1153	adhesin homolog 1m
753	28	53.8	617	2	T22175	hypothetical prote	826	28	53.8	1592	2	T22028	hypothetical prote
754	28	53.8	621	2	H70334	hypothetical prote	827	28	53.8	1649	2	T39938	hypothetical prote
755	28	53.8	622	1	A49344	cell wall assembly	828	28	53.8	1733	1	B45344	probable nuclear a
756	28	53.8	628	1	T08942	proton pump intera	829	28	53.8	1863	1	A58881	breast/ovarian can
757	28	53.8	633	2	F84483	Mutator-like trans	830	28	53.8	2098	2	T18397	protein CTRP - mal
758	28	53.8	638	2	S22490	acetylactate synth	831	28	53.8	2109	2	T31352	hypothetical prote
759	28	53.8	638	2	S22490	acetylactate synth	832	28	53.8	2109	2	T31352	hypothetical prote

833	28	53.8	2172	2	T00936	probable ATP-depen
834	28	53.8	2182	2	T28634	variant-specific s
835	28	53.8	2245	2	T27511	hypothetical prote
836	28	53.8	2322	2	T10542	hypothetical prote
837	28	53.8	2338	2	T25810	hypothetical prote
838	28	53.8	2492	1	A44213	nonstructural poly
839	28	53.8	2492	1	C44213	nonstructural poly
840	28	53.8	2492	1	NMWVTD	nonstructural poly
841	28	53.8	2588	2	T14342	NSI protein - mou
842	28	53.8	3672	2	T23433	hypothetical prote
843	28	53.8	3704	2	T37316	probable laminin a
844	28	53.8	4344	1	A53489	dyenin heavy chain
845	28	53.8	5147	1	IJFFTM	transcription-relat
846	27.5	52.9	335	2	AB2079	cinnamyl-alcohol d
847	27.5	52.9	357	2	S39509	diphosphate-fructo
848	27.5	52.9	405	2	A41169	fiber protein - hu
849	27.5	52.9	426	2	S39300	hypothetical prote
850	27.5	52.9	599	2	T21366	prolactin receptor
851	27.5	52.9	830	2	I50455	hypothetical prote
852	27.5	52.9	1030	2	T16114	glutamate synthase
853	27.5	52.9	3097	2	T28635	a 1-2 protein - in
854	27	51.9	47	2	S52540	Ig kappa chain V r
855	27	51.9	65	2	C38601	Ig light chain V r
856	27	51.9	67	2	PH1081	Ig light chain V r
857	27	51.9	69	2	PH1080	Ig light chain V r
858	27	51.9	84	2	S34099	Ig kappa chain V r
859	27	51.9	86	2	S16837	Ig kappa chain V r
860	27	51.9	86	2	S16839	Ig kappa chain V r
861	27	51.9	86	2	S16832	Ig kappa chain V r
862	27	51.9	86	2	S16827	Ig kappa chain V r
863	27	51.9	86	2	S16831	Ig kappa chain V r
864	27	51.9	86	2	S16828	Ig kappa chain V r
865	27	51.9	86	2	S16835	Ig kappa chain V r
866	27	51.9	87	2	S34097	Ig kappa chain V r
867	27	51.9	87	2	S16841	Ig kappa chain V r
868	27	51.9	87	2	S34098	Ig kappa chain V r
869	27	51.9	88	2	S34104	Ig kappa chain V r
870	27	51.9	90	2	I38601	Ig kappa chain V r
871	27	51.9	91	2	S17626	Ig kappa chain V r
872	27	51.9	92	2	S37509	Ig kappa chain V r
873	27	51.9	92	2	S37523	Ig kappa chain V r
874	27	51.9	93	2	H81994	hypothetical prote
875	27	51.9	95	2	PH0866	Ig kappa chain V r
876	27	51.9	97	2	H82765	hypothetical prote
877	27	51.9	98	2	I30608	Ig kappa chain V r
878	27	51.9	98	2	S19974	Ig kappa chain V r
879	27	51.9	102	2	S26346	Ig kappa chain V r
880	27	51.9	103	2	S13703	Ig kappa chain V r
881	27	51.9	104	2	S13700	Ig kappa chain V r
882	27	51.9	105	2	C30535	Ig kappa chain V r
883	27	51.9	107	2	S36269	Ig lambda chain V r
884	27	51.9	108	2	S34007	Ig kappa chain V r
885	27	51.9	108	2	S36277	Ig lambda chain V r
886	27	51.9	108	2	S30521	Ig kappa chain V r
887	27	51.9	108	2	T06898	hypothetical prote
888	27	51.9	111	1	KWMS08	Ig kappa chain V r
889	27	51.9	111	1	KWMS69	Ig kappa chain V r
890	27	51.9	112	2	B45060	hypothetical prote
891	27	51.9	114	2	F69782	Ig light chain V r
892	27	51.9	115	1	K3HUC1	Ig kappa chain pre
893	27	51.9	115	1	A30553	Ig kappa chain pre
894	27	51.9	118	2	PT0356	pancreatic ribonuc
895	27	51.9	119	1	NRST	Ig kappa chain V-J
896	27	51.9	124	1	S40348	Ig kappa chain V-J
897	27	51.9	125	2	S40344	Ig kappa chain V-J
898	27	51.9	126	2	A70815	hypothetical prote
899	27	51.9	128	2	S46372	Ig light chain var
900	27	51.9	128	2	PN0445	Ig kappa chain pre
901	27	51.9	128	2	S44155	hypothetical 14.5K
902	27	51.9	129	2	E90535	hypothetical prote
903	27	51.9	130	2	S40368	Ig kappa chain - h
904	27	51.9	132	2	S38646	Ig kappa chain V r
905	27	51.9	134	2	PC1214	Ig kappa chain pre
906	27	51.9	135	2	P86588	biopolymer transpo
907	27	51.9	135	2	C72037	ExoD/ToR family P
908	27	51.9	138	2	B95379	HYPOHETICAL MUCR
909	27	51.9	138	2	D82400	Tomb system transp
910	27	51.9	140	2	PL0013	Ig kappa chain pre
911	27	51.9	141	2	D82368	universal stress p
912	27	51.9	146	2	G83445	conserved hypotnet
913	27	51.9	152	2	AF2248	hypothetical prote
914	27	51.9	153	2	G97038	hypothetical prote
915	27	51.9	157	2	H89566	protein T08A9.5 (i
916	27	51.9	158	2	P85676	unknown protein en
917	27	51.9	158	2	P80817	probable phage rep
918	27	51.9	158	2	G64885	Ydr protein - Esc
919	27	51.9	159	2	H96925	protein containing
920	27	51.9	164	2	T29020	hypothetical prote
921	27	51.9	167	1	RDSODF	dihydrofolate redu
922	27	51.9	171	2	T32886	hypothetical prote
923	27	51.9	172	2	A75154	methylated-DNA-lpr
924	27	51.9	172	2	B81412	inorganic diphosph
925	27	51.9	176	2	BK0226	atrachin 21K chain
926	27	51.9	177	1	R5HSLS	ribosomal protein
927	27	51.9	187	2	T30679	probable DNA-dirc
928	27	51.9	187	2	AG0248	probable lipoprote
929	27	51.9	187	2	B81903	hypothetical prote
930	27	51.9	190	2	E95420	hypothetical prote
931	27	51.9	193	2	E83300	probable transcrip
932	27	51.9	193	2	AB1831	hypothetical prote
933	27	51.9	196	2	AB3194	hypothetical prote
934	27	51.9	196	2	B96980	uncharacterized co
935	27	51.9	197	2	P84257	hypothetical prote
936	27	51.9	199	2	H69449	phosphoribosyl ant
937	27	51.9	200	2	C75411	hypothetical prote
938	27	51.9	201	2	T15145	hypothetical prote
939	27	51.9	203	2	T02416	probable SET-domai
940	27	51.9	204	2	B42301	anthranilate synth
941	27	51.9	206	2	H75258	probable 3-demethy
942	27	51.9	211	2	B71341	conserved hypotnet
943	27	51.9	217	2	T04292	hypothetical prote
944	27	51.9	218	2	C81118	hypothetical prote
945	27	51.9	221	2	T29468	hypothetical prote
946	27	51.9	222	2	H83528	phosphoribosylamin
947	27	51.9	222	2	AE0276	dehydrobiotin synth
948	27	51.9	224	2	S09764	hypothetical prote
949	27	51.9	225	2	A33654	heat shock protein
950	27	51.9	227	2	E97719	ribonuclease III (
951	27	51.9	227	2	T22144	hypothetical prote
952	27	51.9	227	2	D85904	uracil-DNA-glycosy
953	27	51.9	229	2	T44315	hypothetical prote
954	27	51.9	229	2	S70956	otns protein - Vib
955	27	51.9	235	2	A64695	conserved hypotnet
956	27	51.9	235	2	D71808	hypothetical prote
957	27	51.9	236	2	H69492	hypothetical prote
958	27	51.9	238	2	F72533	hypothetical prote
959	27	51.9	239	2	T02984	myo-related protei
960	27	51.9	240	2	T24239	hypothetical prote
961	27	51.9	244	2	G96507	hypothetical prote
962	27	51.9	246	2	E72422	transcription regu
963	27	51.9	248	2	H84682	hypothetical prote
964	27	51.9	248	2	T01880	hypothetical prote
965	27	51.9	249	2	F69002	conserved hypotnet
966	27	51.9	250	2	D89771	hypothetical prote
967	27	51.9	251	2	E96637	hypothetical prote
968	27	51.9	252	2	AE2001	hypothetical prote
969	27	51.9	253	2	AG2362	hypothetical prote
970	27	51.9	253	2	A38201	transcription fact
971	27	51.9	254	2	F83497	hypothetical prote
972	27	51.9	255	2	T35883	transcription regu
973	27	51.9	261	2	E70723	probable wblz2 pro
974	27	51.9	265	2	A41116	transcription fact
975	27	51.9	266	2	A12762	conserved hypotnet
976	27	51.9	267	1	DCUMOP	oxotidine-5'-phosp
977	27	51.9	267	1	B84491	probable replicati
978	27	51.9	267	2	E95066	cell filamentation

979 27 51.9 267 2 P97933 hypothetical prote
 980 27 51.9 269 2 S48978 hypothetical prote
 981 27 51.9 269 2 T20670 hypothetical prote
 982 27 51.9 271 2 H97543 hypothetical prote
 983 27 51.9 272 2 T34184 hypothetical prote
 984 27 51.9 273 2 S07014 hypothetical prote
 985 27 51.9 273 2 S60751 homeotic protein s
 986 27 51.9 275 1 G69963 lipoprotein SpoIII
 987 27 51.9 277 2 T17400 hypothetical prote
 988 27 51.9 281 1 H64058 transcription init
 989 27 51.9 286 1 A34599 DNA-binding protei
 990 27 51.9 286 2 B97195 transcription regu
 991 27 51.9 288 2 S26495 transcription fact
 992 27 51.9 294 2 T34048 hypothetical prote
 993 27 51.9 295 2 S61644 hypothetical prote
 994 27 51.9 295 2 E84862 hypothetical prote
 995 27 51.9 296 2 S74253 homeotic protein s
 996 27 51.9 300 2 AC2245 hypothetical prote
 997 27 51.9 304 2 B23431 hypothetical prote
 998 27 51.9 306 2 E72598 probable ABC-trans
 999 27 51.9 307 2 E95934 probable enzyme, C
 1000 27 51.9 309 2 AG2860 transcription regu

ALIGNMENTS

RESULT 1

H30502 Ig kappa chain V region (D42) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Nov-1988 #sequence _revision 03-Aug-1992 #text _change 21-Jan-2000

C:Accession: H30502

R:Elit, D.; Webster, D.M.; Rees, A.R.

J. Immunol. 141, 1745-1753, 1988

A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic

A:Reference number: A30502; MUID:88315787; PMID:2457627

A:Accession: H30502

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-103 <EIL>

A:Cross-references: UNIPARC:UPI0000114D4; GB:M21912; NID:G197077; PIDN:AAA38910.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 52; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 0.0091;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEYPIT 9
 |||||
 DB 86 OOHNEYPIT 94

RESULT 2

S26345 Ig light chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence _revision 19-Mar-1998 #text _change 20-Jun-2000

C:Accession: S26345; S78447

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26345

A:Molecule type: mRNA

A:Cross-references: UNIPARC:UPI0000176981; EMBL:X59177

R:Caton, A.J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S78447

A:Accession: S78447

A:Molecule type: mRNA
 A:Residues: 1-96, 'S', '98-106 <CAT>
 A:Cross-references: UNIPARC:UPI0000115F72; EMBL:X59177; NID:952307; PIDN:CAA41887.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 52; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 0.0093;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEYPIT 9
 |||||
 DB 89 OOHNEYPIT 97

RESULT 3

PH1083 Ig light chain V region (clone 111.67) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence _revision 30-Sep-1993 #text _change 21-Jan-2000

C:Accession: PH1083

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B ce

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1083

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-98 <TIL>

A:Cross-references: UNIPARC:UPI0000176ABF

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 92.3%; Score 48; DB 2; Length 98;
 Best Local Similarity 88.9%; Pred. No. 0.049;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEYPIT 9
 |||||
 DB 89 OOHNEYPIT 97

RESULT 4

S04574 Ig kappa chain precursor V region (MRL-RF24L) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 04-Dec-1992 #sequence _revision 04-Dec-1992 #text _change 21-Jan-2000

C:Accession: S04574

R:Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th

Bur, J. Immunol. 17, 91-95, 1987

A:Title: Molecular analysis of the murine lupus-associated anti-self response: involve

A:Reference number: S04573; MUID:87133856; PMID:3102255

A:Accession: S04574

A:Molecule type: mRNA

A:Cross-references: UNIPARC:UPI0000115DF; EMBL:X14621; NID:952404; PIDN:CAA32774.1; PID

A>Note: The authors translated the codon TAT for residue 30 as Thr

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-127/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 88.5%; Score 46; DB 2; Length 127;
 Best Local Similarity 88.9%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEYPIT 9
 |||||
 DB 109 OOHNEYPIT 117

RESULT 5

S40353
 Ig kappa chain V-J-C region - human
 C:Species: Homo sapiens (man)
 C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40353
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891; PMID:8258341
 A:Accession: S40353
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-125 <KLE>
 A:Cross-references: UNIPARC:UPI0000176CAE; EMBL:X72463
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 P:30-104/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 42; DB 2; Length 125;
 Best Local Similarity 87.5%; Pred. No. 0.86;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNEYPLT 9
 ||| |||
 DB 104 QQYNSYPLT 111

RESULT 6

A37262
 Ig kappa chain V region (H2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Aug-1991 #sequence_revision 03-Apr-1992 #text_change 31-Dec-2004
 C:Accession: A37262
 R:Goshorn, S.C.; Retzel, B.; Jemerson, R.
 J. Biol. Chem. 266, 2134-2142, 1991
 A:Title: Common structural features among monoclonal antibodies binding the same antigen
 A:Reference number: A38601; MUID:91115823; PMID:170327
 A:Accession: A37262
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-88 <GOS>
 A:Cross-references: UNIPROT:Q8V1D0; UNIPARC:UPI0000176D7C; GB:M57987
 C:Superfamily: immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin

Query Match 78.8%; Score 41; DB 2; Length 88;
 Best Local Similarity 77.8%; Pred. No. 0.93;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHNEYPLT 9
 ||| |||
 DB 69 QQYNSYPLT 77

RESULT 7

PH1072
 Ig light chain V region (clone 83-cl) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
 C:Accession: PH1072
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1072
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 1-98 <TTL>
 A:Cross-references: UNIPROT:Q8V1D0; UNIPARC:UPI0000176ABC
 A:Experimental source: B cell, strain NZB x NZW.F1

C:Superfamily: immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 41; DB 2; Length 98;
 Best Local Similarity 77.8%; Pred. No. 1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHNEYPLT 9
 ||| |||
 DB 89 QQYNSYPLT 97

RESULT 8

S41374
 single chain Fv antibody - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
 C:Accession: S41374
 R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
 submitted to the EMBL Data Library, January 1994
 A:Description: Construction and functional characterization of a single chain Fv antibod
 A:Reference number: S41374
 A:Accession: S41374
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-249 <ART>
 A:Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

Query Match 78.8%; Score 41; DB 2; Length 249;
 Best Local Similarity 87.5%; Pred. No. 2.7;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNEYPLT 9
 ||| |||
 DB 229 QHREYPLT 236

RESULT 9

I69017
 anti-HIV envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (f
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
 C:Accession: I69017
 R:Chin, L.T.; Duenas, M.; Levy, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.
 Immunol. Lett. 44, 25-30, 1995
 A:Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed
 A:Reference number: I54563; MUID:95237884; PMID:7721339
 A:Accession: I69017
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-107 <RES>
 A:Cross-references: UNIPARC:UPI0000113P9C; GB:S77140; NID:G913352; PIDN:AA834102.1; PID
 C:Genetics:
 A:Gene: Ig Vkappa
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 39; DB 2; Length 107;
 Best Local Similarity 66.7%; Pred. No. 2.7;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QHNEYPLT 9
 ||| |||
 DB 89 QQYNSYPLT 97

RESULT 10

H26317
 Ig kappa chain V region (H28-A2) (H28-A2) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
 C:Accession: H26317

R:Catron, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Molecule type: DNA
A:Accession: H26317
A:Residues: 1-112 <CAT>
A:Cross-references: UNIPARC:UPI0000176A0E
A:Experimental source: strain Balb/c
A>Note: This sequence was determined from the germ-line gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 38; DB 2; Length 112;
Best Local Similarity 87.5%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 OQHNEYP 9
Db 95 OQHNEYP 102

RESULT 11
AH2608
transcription regulator, Arac family Atu0264 [imported] - Agrobacterium tumefaciens (str
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AH2608
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Giliat, W.; Grant, C.; Guenther, D.; Kuyavian, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Bidle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH2608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <KUR>
A:Cross-references: UNIPROT:Q8UM9; UNIPARC:UPI00000D175B; GB:AE008688; PIDN:AAL41286.1;
C:Genetics:
A:Gene: Atu0264
A:Map position: circular chromosome

Query Match 73.1%; Score 38; DB 2; Length 327;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OQHNEYP 7
Db 312 OQHNEYP 318

RESULT 12
G97390
arac family transcription regulator (AU121600) [imported] - Agrobacterium tumefaciens (s
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97390
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2333-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G97390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <KUR>
A:Cross-references: UNIPROT:Q8UM9; UNIPARC:UPI00000D175B; GB:AE007869; PIDN:AAK86080.1;

C:Genetics:
A:Gene: AGR C 453
A:Map position: circular chromosome

Query Match 73.1%; Score 38; DB 2; Length 327;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OQHNEYP 7
Db 312 OQHNEYP 318

RESULT 13
S40349
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S40349
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40349
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: UNIPARC:UPI000016163; EMBL:X72459; NID:9441386; PIDN:CAAS1127.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 71.2%; Score 37; DB 2; Length 125;
Best Local Similarity 77.8%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 OQHNEYP 9
Db 106 OQHNEYP 114

RESULT 14
AF2533
hypothetical protein alr7553 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120be
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2533
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasaomoto, S.; Watanabe, A.; Iriugu
Nakasaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2533
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <KUR>
A:Cross-references: UNIPROT:Q8ZSF7; UNIPARC:UPI00000CCD76; GB:AP003602; PIDN:BAH77196.1;
C:Genetics:
A:Gene: alr7553
A:Genome: plasmid

Query Match 71.2%; Score 37; DB 2; Length 248;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OQHNEYP 8
Db 64 OQHNEYP 71

RESULT 15

AC2017
cobalamin biosynthetic protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC2017
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Kanehisa, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA:Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1302 <KIR>
A:Cross-references: UNIPROT:Q8YWC4; UNIPARC:UPI00000CCB192; GB:BA000019; PIDN:BA078055.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: CobN
C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase

Query Match 71.2%; Score 37; DB 2; Length 1302;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OOHNEYPYT 9
||:||||
Db 924 Q8YWC4PPT 932

RESULT 16
S37525
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37525
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37525
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <KIR>
A:Cross-references: UNIPARC:UPI0000116583; EMBL:Z26619; NID:G405692; PIDN:CAA81372.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 69.2%; Score 36; DB 2; Length 91;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEYPYT 9
||:||||
Db 72 QOYNNWPLT 80

RESULT 17
S17630
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17630
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17630
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-91 <CLA>
A:Cross-references: UNIPARC:UPI00001767F7
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:8-81/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 36; DB 2; Length 91;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEYPYT 9
||:||||
Db 80 QOYNSYPT 88

RESULT 18
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36264
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36264
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: UNIPARC:UPI0000118DF4; EMBL:Z18845; NID:G33426; PIDN:CAA79297.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 36; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEYPYT 9
||:||||
Db 89 QOYNSYPT 97

RESULT 19
A28195
Ig kappa chain V region (anti-haloperidol antibody A) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000
C:Accession: A28195
R:Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A:Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid
A:Reference number: A28195; MUID:88153717; PMID:3267217
A:Accession: A28195
A:Molecule type: mRNA
A:Residues: 1-107 <SHR>
A:Cross-references: UNIPARC:UPI0000114D69; GB:M19766; NID:G197039; PIDN:AAA8891.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 36; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OOHNEYPYT 9
||:||||
Db 89 QOYNSYPT 97

RESULT 20
K1HUN
Ig kappa chain V-I region (Ban) - human
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A01878

R:Duillet, F.E.; O'Connor, T.P.; Benson, M.D.
Mol. Immunol. 23, 73-78, 1986
A:Title: Polymorphism in a kappa I primary (AL) amyloid protein (BAN).
A:Reference number: A01878; MUID:86174817; PMID:3083240
A:Accession: A01878
A:Molecule type: Protein
A:Residues: 1-108 <DMU>
A:Cross-references: UNIPROT:P04430; UNIPARC:UPI000012EL50
C:Genetics:
A:Gene: GDB:IGKVL
A:Cross-references: GDB:I36264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-107/Region: framework 4
F:23-88/Disulfide bonds: #status predicted

Query Match 69.2%; Score 36; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OOHNEPYLT 9
DB 89 QOYNSTPYT 97
||:|:|:|
||:|:|:|

RESULT 21
B44371
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Apr-1993 #sequence_revision 30-Apr-1993 #text_change 21-Jan-2000
C:Accession: B44371
R:Ayala, M.; Duenas, M.; Santos, A.; Vazquez, J.; Menendez, A.; Silva, A.; Gavilondo, J.
Biotechniques 13, 790-799, 1992
A:Title: Bacterial single-chain antibody fragments, specific for carcinoembryonic antigen
A:Reference number: A44371; MUID:93040204; PMID:1418981
A:Accession: B44371
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <AYA>
A:Cross-references: UNIPARC:UPI0000176EB2; GB:S49457; NID:G259513; PIDD:AA824087.1; PID:
A:Note: This sequence is inconsistent with the nucleotide translation
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 36; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEPYLT 8
DB 89 QOYNSTPYT 96
||:|:|:|
||:|:|:|

RESULT 22
PL0204
anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PL0204
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N

A:Reference number: PL0198; MUID:90309768; PMID:2114528
A:Accession: PL0204
A:Molecule type: mRNA
A:Residues: 1-108 <SMI>
A:Cross-references: UNIPARC:UPI0000113787; GB:X53644; NID:G50198; PIDD:CAA37695.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>
F:24-34/Region: complementarity-determining 1
F:50-56/Region: complementarity-determining 2
F:89-97/Region: complementarity-determining 3
F:96-108/Region: JH region

Query Match 69.2%; Score 36; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OOHNEPYLT 9
DB 89 QOYNSTPYT 97
||:|:|:|
||:|:|:|

RESULT 23
S40362
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40362
R:Klein, R.; Jenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40362
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <KLE>
A:Cross-references: UNIPARC:UPI0000176CA3; EMBL:X72472; NID:G441412; PID:G441413
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 36; DB 2; Length 117;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEPYLT 9
DB 99 QOYNWPLYT 107
||:|:|:|
||:|:|:|

RESULT 24
S40369
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40369
R:Klein, R.; Jenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40369
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLB>
A:Cross-references: UNIPARC:UPI0000116177; EMBL:X72479; NID:G441426; PIDD:CAA51147.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 36; DB 2; Length 129;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OOHNEPYLT 9

Db 110 QOQNSVPLT 118

RESULT 25

B23986
Ig kappa chain precursor V region (IR2) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Sep-1987 #sequence_revision 17-Sep-1987 #text_change 21-Jan-2000
C:Accession: B23986
R:Hellman, L.; Engstrom, A.; Bennich, H.; Petersson, U.
Gene 40, 107-114, 1985
A:Title: Structure and expression of kappa-chain genes in two Igg-producing rat immunocy
A:Reference number: A91541; MUID:86137406; PMID:3005117
A:Accession: B23986
A:Molecule type: mRNA
A:Residues: 1-129 <HEL>
A:Cross-references: UNIPARC:UPI000017679F
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 69.2%; Score 36; DB 2; Length 129;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QOQNEVPLT 9
Db 112 QYNEVPYT 119

RESULT 26

PL0014
Ig kappa chain precursor V region (P6-3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0014
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: PL0011; MUID:88142863; PMID:3125424
A:Accession: PL0014
A:Molecule type: mRNA
A:Residues: 1-145 <CHE>
A:Cross-references: UNIPARC:UPI00001767A7
A:Experimental source: cell line P6-3
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcho
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <Sig>
F:21-134/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F:36-116/Domain: immunoglobulin homology <IMM>
F:44-60/Region: complementarity-determining 1
F:76-82/Region: complementarity-determining 2
F:115-123/Region: complementarity-determining 3
F:135-145/Domain: constant region (fragment) #status predicted <COR>

Query Match 69.2%; Score 36; DB 2; Length 145;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQNEVPLT 9
Db 115 QOQDYSTPL 123

RESULT 27

T30076
hypothetical protein C06G1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T30076
R:Wu, X.; Le, T.

submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C06G1.
A:Reference number: Z20731
A:Accession: T30076
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-641 <WDX>
A:Cross-references: UNIPARC:UPI000017B747; EMBL:U41014; PIDN:AAA62305.1; CBSP:C06G1.4
C:Genetics:
A:Gene: CBSP:C06G1.4
A:Introns: 61/1; 112/1; 385/1; 415/3; 587/3

Query Match 69.2%; Score 36; DB 2; Length 641;
Best Local Similarity 62.5%; Pred. No. 64;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQNEVPL 8
Db 156 QOQOQYPM 163

RESULT 28

S63596
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S63596
R:Verdaguer, N.; Mateu, M.G.; Bravo, J.; Domingo, E.; Fita, I.
U. Mol. Biol. 256, 364-376, 1996
A:Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutra
A:Reference number: S63596; MUID:96174482; PMID:8594203
A:Accession: S63596
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-115 <VER>
A:Cross-references: UNIPARC:UPI00001154DD; GB:S81196; NID:G1336821; PIDN:AAA36171.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 35; DB 2; Length 115;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQNEVPLT 9
Db 93 QOQNEVPLT 101

RESULT 29

S40333
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40333
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40332; MUID:94080891; PMID:8258341
A:Accession: S40333
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLB>
A:Cross-references: UNIPARC:UPI0000116153; EMBL:X72443; NID:G441354; PIDN:CAA51111.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-108/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 35; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQNEVPLT 9

Db 107 QOQNSYFMT 115

RESULT 30

P88035
protein M01D1.7 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: P88035
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: P88035
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-270 <STO>
A:Cross-references: UNIPROT:O17228; UNIPARC:UPI0000078EA7; GB:chr_II; PIDN:AB70993.1; PI
C:Genetics:
A:Gene: M01D1.7
A:Map position: 2

Query Match 67.3%; Score 35; DB 2; Length 270;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QOHNEYP 7
|||
Db 85 EHNEYP 90

RESULT 31

G86155
Hypothetical protein T14P4.13 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86155
R:Rothologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Comn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G86155
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <STO>
A:Cross-references: UNIPROT:Q9FWX9; UNIPARC:UPI00000A60B7; GB:AE005172; NID:G9972379; PI
C:Genetics:
A:Map position: 1

Query Match 67.3%; Score 35; DB 2; Length 290;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP 8
|||
Db 87 QOHNEYP 94

RESULT 32

AE1799
abortive phage resistance mechanism [Lactococcus lactis] homolog lin2940 [imported] - Li
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1799

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fahl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mai
ok, C.; Schluteter, T.; Simoes, N.; Tlertiz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1799
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <GLA>
A:Cross-references: UNIPROT:Q926V0; UNIPARC:UPI00000CCA13; GB:AL592022; PIDN:CAC98165.1;
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin2940

Query Match 67.3%; Score 35; DB 2; Length 320;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP 8
|||
Db 298 QOHNEYP 305

RESULT 33

T27324
Hypothetical protein Y6B3B.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27324
R:White, S.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20345
A:Accession: T27324
A:Status: preliminary; translated from GB/EMBL/DBU
A:Molecule type: DNA
A:Residues: 1-360 <WIL>
A:Cross-references: UNIPROT:Q9XWE9; UNIPARC:UPI0000081279; EMBL:AL032655; PIDN:CAA21723...
A:Experimental source: clone Y6B3B
C:Genetics:
A:Gene: CESP:Y6B3B.10
A:Map position: 1
A:Introns: 24/3; 58/1; 88/3; 143/1; 205/2; 310/3

Query Match 67.3%; Score 35; DB 2; Length 360;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP 7
|||
Db 92 QOHNEYP 98

RESULT 34

S77546
cobN protein - Synecchocystis sp. (strain PCC 6803)
N:Alternate names: protein slr1211
C:Species: Synecchocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S77546
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O.K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S77546
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1092 <KAN>

A:Cross-references: UNIPROT:P73362; UNIPARC:UPI00000D3453; EMBL:D90905; GB:AB001339; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: COBN
C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase

Query Match 67.3%; Score 35; DB 2; Length 1092;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 OQHNEYPPT 9
|||
Db 715 QDHGEYPT 723

RESULT 35

T50002
hypothetical protein F12B17.280 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T50002

R:Byvan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000

A:Reference number: 225026

A:Accession: T50002

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1751 <BBY>

A:Cross-references: UNIPROT:Q9LX92; UNIPARC:UPI00000AB93F; EMBL:AL353995; GSPDB:GN00063;

A:Experimental source: cultivar Columbia; BAC clone F12B17

C:Genetics:

A:Gene: ATSP:F12B17.280

A:Map position: 5
A:introns: 323/3; 778/3; 1369/1; 1741/2

Query Match 67.3%; Score 35; DB 2; Length 1751;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 OQHNEYPPT 7
|||
Db 49 QOHSQYP 55

RESULT 36

A24730
Ig kappa chain V region (GM131) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 30-May-1997

C:Accession: A24730

R:Morin, J.W.; Black, A.; Wu, M.; Beychok, S.

Proc. Natl. Acad. Sci. U.S.A. 82; 7025-7029, 1985

A:Title: cDNA of the immunoglobulin kappa chain of an Epstein-Barr virus-transformed hum

A:Reference number: A24730; MUID:86016827; PMID:2413453

A:Accession: A24730

A:Molecule type: mRNA

A:Residues: 1-31 <MOR>

A:Cross-references: UNIPARC:UPI0000176DDC

C:Comment: The J segment (residues 19-31) does not correspond to any of the five human g

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 65.4%; Score 34; DB 2; Length 31;
Best Local Similarity 66.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 OQHNEYPPT 9
|||
Db 12 QOHDHPLPT 20

RESULT 37

S17642

Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S17642

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17642

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-93 <CLA>

A:Cross-references: UNIPARC:UPI0000176803

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 93;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 OQHNEYPPT 9
|||
Db 82 QOHSQYPPT 90

RESULT 38

S17641
Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S17641

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17641

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-93 <CLA>

A:Cross-references: UNIPARC:UPI0000176802

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 93;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 OQHNEYPPT 9
|||
Db 82 QOHSQYPPT 90

RESULT 39

S17643
Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S17643

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A:Title: Making antibody fragments using phage display libraries.

A:Reference number: S17230; MUID:91326098; PMID:1907718

A:Accession: S17643

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-93 <CLA>

A:Cross-references: UNIPARC:UPI0000176804

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 93;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP LT 9
||: ||||
Db 82 QOYSGYPLT 90

RESULT 40

S17640
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17640
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17640
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
A:Cross-references: UNIPARC:UPI0000176801
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-83/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 93;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP LT 9
||: ||||
Db 82 QOYSGYPLT 90

RESULT 41

S17623
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17623
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17623
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
A:Cross-references: UNIPARC:UPI000017678F
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-83/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 93;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP LT 9
||: ||||
Db 82 QOYSGYPLT 90

RESULT 42

PS0070
Ig kappa chain V region (38C13 V6.1) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: PS0070
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989

A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement
A:Reference number: A92781; MUID:89310348; PMID:2501443
A:Accession: PS0070
A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-106 <LEV>
A:Cross-references: UNIPARC:UPI00001767C8
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 106;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOHNEYP LT 9
||: ||||
Db 88 QOQSSYPLT 96

RESULT 43

S09965
Ig kappa chain V-J region (106-10E) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 21-Jan-2000
C:Accession: S09965
R:Reininger, L.; Shibata, T.; Ozaki, S.; Shitai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A:Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
A:Reference number: S09965; MUID:90269328; PMID:2347362
A:Accession: S09965
A:Molecule type: mRNA
A:Residues: 1-111 <REI>
A:Cross-references: UNIPARC:UPI0000115864; EMBL:X51853; NID:955394; PIDN:CAA36146.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 111;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP LT 7
||: ||||
Db 93 QOSNEYP 99

RESULT 44

D26317
Ig kappa chain V region (H37-84) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: D26317
R:Caon, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a de
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: D26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Cross-references: UNIPARC:UPI0000176A18
A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germ-line gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus he
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 OHNEYP LT 9

Db 95 QHLEXPFT 102

RESULT 45

Ig kappa chain V region (H158-89H4) - mouse
A:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: I26317
R:Gatton, A.J.; Brownlee, G.G.; Straudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: I26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Cross-references: UNIPARC:UPI0000176A0D
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germ-line gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 112;

Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QHNEYPFT 9

Db 95 QHLEXPFT 102

RESULT 46

Ig kappa chain precursor V region - mouse
A:Species: Mus musculus (house mouse)
C:Date: 26-Oct-1989 #sequence_revision 26-Oct-1989 #text_change 21-Jan-2000
C:Accession: B32456
R:Dombrink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.
J. Biol. Chem. 264, 4513-4522, 1989
A:Title: Variable region primary structures of a high affinity anti-fluorescein immunogl
A:Reference number: A32456; MUID:89174706; PMID:2494173
A:Accession: B32456
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <DOM>
A:Cross-references: UNIPARC:UPI00001148B9; GB:J04610; NID:G556313; PIDN:AAA50296.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-113/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 130;

Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPFT 9

Db 112 QOYSGYPLT 120

RESULT 47

Ig kappa chain - human
S40334
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40334
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40334

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-132 <KLS>

A:Cross-references: UNIPARC:UPI0000176CA9; EMBL:X72444

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 34; DB 2; Length 132;

Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QOHNEYPFT 9

Db 110 QOFNSYPT 118

RESULT 48

probable membrane protein [imported] - Escherichia coli (strain O157:H7, substrain R1MD
E90795
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E90795
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhtara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E90795
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-223 <HAY>
A:Cross-references: UNIPROT:O8X9T2; UNIPARC:UPI0000165414; GB:BA000007; PIDN:BA034756.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECA1333

Query Match 65.4%; Score 34; DB 2; Length 223;

Best Local Similarity 50.0%; Pred. No. 51;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYPFT 8

Db 119 EKHNYPT 126

RESULT 49

hypothetical protein Z1594 [imported] - Escherichia coli (strain O157:H7, substrain EDL5
A85656
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A85656; H85604
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Llim, A.; Diallanca, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85656
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <STO>
A:Cross-references: UNIPROT:O8X9T2; UNIPARC:UPI00000D07A8; GB:AE005174; NID:G12514474; F
A:Experimental source: strain O157:H7, substrain EDL933
A:Accession: H85604
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <STO>
A:Cross-references: UNIPARC:UPI00000D07A8; GB:AE005174; NID:G12513957; PIDN:AA05300.1;
C:Genetics:
A:Gene: Z1594; Z1155

Query Match

65.4%; Score 34; DB 2; Length 245;

Best Local Similarity 50.0%; Pred. No. 56;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 OQHNEYPL 8
::||:|:
Db 141 EKHNYCPI 148

RESULT 50

A90439
ABC transporter, ATP binding protein SSO2647 [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 31-Dec-2004
C:Accession: A90439
R,She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: A90439
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-309 <KUR>
A:Cross-references: UNIPROT:Q9VH6; UNIPARC:UPI00000647E3; GB:AE006641; NID:G13815959; E
C:Genetics:
A:Gene: SSO2647

Query Match 65.4%; Score 34; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 NEYPLT 9
|||||
Db 236 NEYPLT 241

Search completed: January 17, 2006, 12:06:24
Job time : 16.4545 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:47:28 ; Search time 50.7273 Seconds
(without alignments)
125.174 Million cell updates/sec

Title: US-10-665-658-15
Perfect score: 52
Sequence: 1 QOHNEYPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	78.8	171	2	Q4HU43_GIBBE
2	40	76.9	236	2	Q6GMX9_HUMAN
3	39	75.0	645	2	Q756M7_ASHGO
4	39	75.0	707	2	Q95R07_DROME
5	38	73.1	327	2	Q8UTM9_AGRIS
6	38	73.1	1695	2	Q548F8_DICDI
7	37	71.2	248	2	Q82SF7_ANASP
8	37	71.2	507	2	Q601Z7_MYCHY
9	37	71.2	990	2	Q7UXL8_RHOBA
10	37	71.2	1302	2	Q8YWC4_ANASP
11	37	71.2	5729	2	Q81622_PLAF7
12	36	69.2	108	1	KXIV_HUMAN
13	36	69.2	108	2	Q8V1J0_MOUSE
14	36	69.2	147	2	Q8CBK2_MOUSE
15	36	69.2	212	2	Q8G1P0_LACTC
16	36	69.2	212	2	Q7N3F6_PHOIT
17	36	69.2	238	2	Q58E04_MOUSE
18	36	69.2	240	2	Q65ZC9_HUMAN
19	36	69.2	244	2	Q65ZC8_HUMAN
20	36	69.2	355	2	Q96ZJ3_SULTO
21	36	69.2	395	2	Q7PYD2_ANOGA
22	36	69.2	477	2	Q5IGN5_ENTHI
23	36	69.2	477	2	Q9FH77_ARATH
24	36	69.2	571	2	Q17740_CAEEL
25	36	69.2	803	1	PDE4D_RAT
26	36	69.2	809	1	PDE4D_HUMAN
27	36	69.2	841	1	CHS1_BHYBL
28	36	69.2	851	1	Q750F1_ASHGO
29	36	69.2	986	2	Q86M45_DICDI
30	36	69.2	1042	2	Q4MMV7_ASPFU
31	36	69.2	1053	2	Q54QM6_DICDI

32	36	69.2	1059	2	Q8C5X1_MOUSE	Q8C5X1 mus musculu
33	36	69.2	1059	2	Q6PAL5_MOUSE	Q6PAL5 mus musculu
34	36	69.2	1070	1	Y0355_HUMAN	Q15053 homo sapien
35	36	69.2	1070	2	Q5REB5_PONPY	Q5REB5 pongo pygma
36	36	69.2	1070	2	Q4R3A1_MACPA	Q4R3A1 macaca fasc
37	36	69.2	1133	2	Q54MU4_DICDI	Q54MU4 dictyosteli
38	36	69.2	1162	2	Q6DA45_BRNCT	Q6DA45 erwina car
39	36	69.2	1373	2	Q9VTS4_DROME	Q9VTS4 drosophila
40	35	67.3	111	1	RV3K_MOUSE	Q16663 mus musculu
41	35	67.3	123	2	Q92614_LISTIN	Q92614 listeria in
42	35	67.3	210	2	Q5HER4_EHRRW	Q5HER4 ehrlichia r
43	35	67.3	211	2	Q5FHC6_EHRRG	Q5FHC6 ehrlichia r
44	35	67.3	211	2	Q5FE34_EHRRW	Q5FE34 ehrlichia r
45	35	67.3	234	2	Q4KM66_RAT	Q4KM66 rattus norv
46	35	67.3	237	2	Q659Y8_MOUSE	Q659Y8 mus musculu
47	35	67.3	270	2	Q17228_CAEEL	Q17228 caenorhabdi
48	35	67.3	290	2	Q9FWX9_ARATH	Q9FWX9 arabidopsis
49	35	67.3	290	2	Q8R6G2_FUSNN	Q8R6G2 fusobacteri
50	35	67.3	294	2	Q5AXF7_EMENT	Q5AXF7 aspergilli
51	35	67.3	320	2	Q926V0_LISTIN	Q926V0 listeria in
52	35	67.3	360	2	Q61AT1_CAEER	Q61AT1 caenorhabdi
53	35	67.3	360	2	Q9XME9_CAEEL	Q9XME9 caenorhabdi
54	35	67.3	378	2	Q52368_MAGGR	Q52368 magnaporthe
55	35	67.3	592	2	Q90WS9_BRARR	Q90WS9 brachydanio
56	35	67.3	592	2	Q98SM8_BRARR	Q98SM8 brachydanio
57	35	67.3	592	2	Q5PR29_BRARR	Q5PR29 brachydanio
58	35	67.3	608	2	Q7R9Z2_PLAYO	Q7R9Z2 plasmodium
59	35	67.3	614	2	Q4YW78_PLABE	Q4YW78 plasmodium
60	35	67.3	636	2	Q5J406_SALCH	Q5J406 salmonella
61	35	67.3	647	2	Q751M9_ASHGO	Q751M9 ashbya goes
62	35	67.3	943	2	Q8UKS4_VYIRU	Q8UKS4 heliothis z
63	35	67.3	949	2	Q4P4Y1_USTWA	Q4P4Y1 uceliagro ma
64	35	67.3	958	2	Q4N210_THEPA	Q4N210 theileria p
65	35	67.3	1014	2	Q924B7_9ZZZZ	Q924B7 plasmid col
66	35	67.3	1014	2	Q79VU6_SALTY	Q79VU6 salmonella
67	35	67.3	1014	2	Q9R2G9_9ZZZZ	Q9R2G9 plasmid r64
68	35	67.3	1014	2	Q4FIT5_EBNTA	Q4FIT5 salmonella
69	35	67.3	1088	2	Q5VTN5_HALWA	Q5VTN5 halocaula
70	35	67.3	1092	2	P73362_SYNY3	P73362 synecocyst
71	35	67.3	1105	2	Q7S1V1_NEUCR	Q7S1V1 neurospora
72	35	67.3	1435	2	Q7PMX7_ANOGA	Q7PMX7 anopheles g
73	35	67.3	1751	2	Q9LX92_ARATH	Q9LX92 arabidopsis
74	35	67.3	1913	2	Q5TLA5_LEUMA	Q5TLA5 leucophaea
75	35	67.3	1913	2	Q9GR96_LEUMA	Q9GR96 leucophaea
76	34	65.4	98	2	Q6F7P2_ACTAD	Q6F7P2 actinobact
77	34	65.4	112	2	Q8K1P2_MOUSE	Q8K1P2 mus musculu
78	34	65.4	125	1	SMG_DROYA	P60320 drosophila
79	34	65.4	197	2	Q4L4D1_STRAH	Q4L4D1 straphylococ
80	34	65.4	200	2	Q90Z59_BRARR	Q90Z59 brachydanio
81	34	65.4	208	2	Q81PA3_DROME	Q81PA3 drosophila
82	34	65.4	223	2	Q7AFH0_ECO57	Q7AFH0 escherichia
83	34	65.4	225	2	Q8X9T2_ECO57	Q8X9T2 escherichia
84	34	65.4	245	2	Q8CU06_OCRIF	Q8CU06 oceanobacil
85	34	65.4	257	2	Q7NUY4_GLOVI	Q7NUY4 gloeobacter
86	34	65.4	262	2	Q50V46_ENTHI	Q50V46 entamoeba h
87	34	65.4	262	2	Q7XDC4_ORYSA	Q7XDC4 oryza sativ
88	34	65.4	267	2	Q9FMH2_ORYSA	Q9FMH2 oryza sativ
89	34	65.4	275	2	Q624R8_CAEER	Q624R8 caenorhabdi
90	34	65.4	284	2	Q7VU69_BORPE	Q7VU69 bordetella
91	34	65.4	284	2	Q7M4P8_BORPE	Q7M4P8 bordetella
92	34	65.4	284	2	Q7W374_BORBR	Q7W374 bordetella
93	34	65.4	300	2	Q5XFW9_RAT	Q5XFW9 rattus norv
94	34	65.4	301	1	TSGA2_MOUSE	Q8V1G3 mus musculu
95	34	65.4	309	2	TSGA2_HUMAN	Q8V1G3 mus musculu
96	34	65.4	309	1	Q97VH6_SULTO	Q97VH6 sulfolobus
97	34	65.4	318	2	Q7S887_NEUCR	Q7S887 neurospora
98	34	65.4	318	2	Q8YNV3_ANASP	Q8YNV3 anabaena sp
99	34	65.4	320	2	Q6G4E2_BARRB	Q6G4E2 bartonella
100	34	65.4	334	2	Q4VIC2_BACCC	Q4VIC2 bacillus ce
101	34	65.4	336	2	Q6N8X0_RHOPA	Q6N8X0 rhodospheudo
102	34	65.4	336	2	Q6ABL8_PROAC	Q6ABL8 propionibac
103	34	65.4	339	2	Q9Z8H8_CHLPP	Q9Z8H8 chlamydia p
104	34	65.4	344	2	Q9K286_CHLPP	Q9K286 chlamydia p

105	34	65.4	356	2	Q41Q10_GIBZE	Q41Q10_gibberella	178	33	63.5	204	2	Q922D2_MOUSE	Q922d2_mus musculus
106	34	65.4	365	2	Q4UM4_XANCP	Q4um4_xanthomonas	179	33	63.5	221	2	Q6MR13_BDEBA	Q6mr13_bdellovibrio
107	34	65.4	365	2	Q8P5B8_XANCP	Q8p5b8_xanthomonas	180	33	63.5	234	2	Q5XKG4_MOUSE	Q5xkg4_mus musculus
108	34	65.4	373	2	Q4RU06_TETNG	Q4rue6_tetradon n	181	33	63.5	240	2	Q52L64_MOUSE	Q52l64_mus musculus
109	34	65.4	400	2	Q5EVG5_9TROC	Q5evg5_otkopleura	182	33	63.5	251	1	BIOC_ETOLI	P12999 escherichia
110	34	65.4	411	2	Q9NSJ2_CAEEL	Q9nsj2_caenorhabdi	183	33	63.5	251	2	Q9APN9_9BACT	Q9apn9_uncultured
111	34	65.4	413	2	Q87H90_VIBPA	Q87h90_vibrio para	184	33	63.5	251	2	Q83544_SHITL	Q83544_shigella fl
112	34	65.4	425	2	Q5QVS9_VIBPA	Q5qvs9_vibrio para	185	33	63.5	251	2	Q8X822_ECOS7	Q8x822_escherichia
113	34	65.4	428	2	Q5QVS9_IDILO	Q5qvs9_idiomarina	186	33	63.5	257	2	Q5VMU2_ORYSA	Q5vmu2_oryza sativ
114	34	65.4	429	2	Q7MU72_PORGI	Q7mu72_porphyrion	187	33	63.5	257	2	Q5LA09_BACPA	Q5la09_bacteroides
115	34	65.4	429	2	Q71MX1_9ILIL	Q71mx1_porchanthra	188	33	63.5	261	2	Q6C7P4_YARLI	Q6c7p4_yarrowia 11
116	34	65.4	474	1	LACG_LACCA	P14696 lactobacill	189	33	63.5	263	2	Q6BRT2_DEBNA	Q6brt2_debaryomyce
117	34	65.4	511	2	Q9VXG3_DROME	Q9vxg3_drosophila	190	33	63.5	266	2	Q53RD8_HUMAN	Q53rd8_homo sapien
118	34	65.4	516	2	Q61605_ORYSA	Q61605_oryza sativ	191	33	63.5	269	2	Q6YP29_ONYPR	Q6yp29_onion yello
119	34	65.4	538	2	Q967D0_GEOCY	Q967d0_geodia cydo	192	33	63.5	271	2	Q64Q08_BACPR	Q64q08_bacteroides
120	34	65.4	549	2	Q6FS82_CANGA	Q6fs82_candida gla	193	33	63.5	291	1	Q53B8_HUMAN	Q53b8_homo sapien
121	34	65.4	550	2	Q8TOW5_METAC	Q8tows_methanosarc	194	33	63.5	291	1	Q5RBKE_PONPY	Q5rbke_pongo pygma
122	34	65.4	555	2	Q27J35_TRYCR	Q27j35_trypanosoma	195	33	63.5	292	2	Q4Y4V6_PLACH	Q4y4v6_plasmodium
123	34	65.4	555	2	Q96971_9TRYR	Q96971_trypanosoma	196	33	63.5	295	1	CB102_LACPL	Q88xv1_lactobacill
124	34	65.4	564	2	Q643Z0_CRIFA	Q643z0_citridia f	197	33	63.5	304	2	Q7Y5V4_9CAUD	Q7y5v4_bacterioph
125	34	65.4	581	2	Q51RH5_MAGGR	Q51rh5_magnaporthe	198	33	63.5	305	2	Q5A258_EMENI	Q5a258_aspergillus
126	34	65.4	594	2	Q4FWS5_LEIMA	Q4fws5_leishmania	199	33	63.5	305	2	Q6AYB0_RAT	Q6ayb0_rattus norv
127	34	65.4	595	2	Q6CTA4_KULUA	Q6cta4_kuylveromyc	200	33	63.5	333	2	Q74IC7_LACJO	Q74ic7_lactobacill
128	34	65.4	622	2	Q6BNU5_DEBNA	Q6bnu5_debaryomyce	201	33	63.5	340	1	DHAS_AOUAB	Q67716_aquifex aeo
129	34	65.4	624	2	Q7XVM5_ORYSA	Q7xvm5_oryza sativ	202	33	63.5	340	1	Q85BE1_9CAUD	Q85be1_enterobacte
130	34	65.4	630	2	Q8MTA4_DROME	Q8mta4_drosophila	203	33	63.5	342	2	Q7Y0K5_GINBI	Q7y0k5_gingyo bilo
131	34	65.4	652	1	CR3BA_BACTO	Q6n117 bacillus th	204	33	63.5	348	2	Q5SHZ4_CRYNE	Q5shz4_cryptococcu
132	34	65.4	659	1	CR3BA_BACTO	P17669 bacillus th	205	33	63.5	348	2	Q5K7H8_CRYNE	Q5k7h8_cryptococcu
133	34	65.4	690	1	ART1_YEAST	P22149 saccharomyc	206	33	63.5	362	2	Q4MWS0_BACCE	Q4mw0_bacillus ce
134	34	65.4	690	1	Q06993_YEAST	Q06993_saccharomyc	207	33	63.5	362	2	Q6HNZ8_BACCK	Q6hnz8_bacillus th
135	34	65.4	711	2	Q6CMA5_KULUA	Q6cma5_kuylveromyc	208	33	63.5	362	2	Q73J34_BACCL	Q73j34_bacillus ce
136	34	65.4	749	2	Q8W614_9CAUD	Q8w614_sinorhizobi	209	33	63.5	362	2	Q81HK1_BACCR	Q81hk1_bacillus ce
137	34	65.4	753	2	Q8EG86_SHEON	Q8eg86_shewanella	210	33	63.5	362	2	Q81US3_BACAN	Q81us3_bacillus an
138	34	65.4	776	2	Q6V7P2_9CAUD	Q6v7p2_burkholderi	211	33	63.5	362	2	Q63FPM3_BACCE	Q63fpm3_bacillus ce
139	34	65.4	802	2	Q41OK1_GIBZE	Q41ok1_gibberella	212	33	63.5	363	2	Q60932_METCA	Q60932_methylococc
140	34	65.4	803	1	SW16_YEAST	P09399 saccharomyc	213	33	63.5	368	2	Q8DI88_SYNEL	Q8di88_synechococc
141	34	65.4	813	2	Q5GSO2_WOLTR	Q5gsq2_wolbachia s	214	33	63.5	389	2	Q8C135_MOUSE	Q8c135_mus musculu
142	34	65.4	816	2	Q4BMO_TETNG	Q4bmo_tetradon n	215	33	63.5	405	2	Q9VQ12_DROME	Q9vq12_drosophila
143	34	65.4	842	1	CLAA_YEAST	P48562 saccharomyc	216	33	63.5	413	1	ESCI_SCHPO	Q04635_schizosacch
144	34	65.4	942	2	Q926TV_CHLPN	Q926tv_chlamydia p	217	33	63.5	414	2	Q6C7D1_YARLI	Q6c7d1_yarrowia 11
145	34	65.4	999	1	SMG_DROME	Q23972 drosophila	218	33	63.5	422	2	Q9D8T1_MOUSE	Q9d8t1_mus musculu
146	34	65.4	1097	1	KIFID_RAT	Q35787 reticul norv	219	33	63.5	430	2	Q51G44_ENTHI	Q51g44_entamoeba h
147	34	65.4	1152	2	Q81255_PLAF7	Q81255_plasmodium	220	33	63.5	439	2	Q54QK6_DICDI	Q54qk6_dicytyoselli
148	34	65.4	1249	2	Q7Q5T1_ANOGA	Q7q5t1_anopheles g	221	33	63.5	439	2	Q7REZ6_PLAYO	Q7rez6_plasmodiell
149	34	65.4	1393	2	Q52GM4_MAGGR	Q52gm4_magnaporthe	222	33	63.5	449	2	Q6VOK4_CAYCU	Q6vok4_mycobacteri
150	34	65.4	1396	2	Q4RP37_TETNG	Q4rp37_tetradon n	223	33	63.5	450	2	Q02136_CAEEL	Q02136_caenorhabdi
151	34	65.4	1428	2	Q8BI61_SHEON	Q8bi61_shewanella	224	33	63.5	456	2	Q4J9X8_SULAC	Q4j9x8_sulfolobus
152	34	65.4	1436	2	Q96ZU5_SULTO	Q96zj5_sulfolobus	225	33	63.5	460	2	Q5B447_EMENI	Q5b447_aspergillus
153	34	65.4	1444	2	Q7PDKO_PLAYO	Q7pdko_plasmodium	226	33	63.5	462	2	Q4WUW4_ASFPU	Q4wu4_aspergillus
154	34	65.4	1643	2	Q7YVGI_CRYPV	Q7yygi_cryptospori	227	33	63.5	480	2	Q7ZUN4_BRARE	Q7zun4_brachydanio
155	34	65.4	1654	2	Q5CXK5_CRYPV	Q5cxk5_cryptospori	228	33	63.5	493	2	Q8BJ67_MOUSE	Q8bj67_mus musculu
156	34	65.4	1655	2	Q5CND5_CRYHO	Q5cnd5_cryptospori	229	33	63.5	520	2	Q4ZMP9_PSESY	Q4zmp9_pseudomonas
157	34	65.4	1683	1	Y1214_ANASP	Q8rv57 arabidopsis	230	33	63.5	520	2	Q8BA52_PSESM	Q8ba52_pseudomonas
158	34	65.4	1702	2	Q7PSJ9_ANOGA	Q7psj9_anopheles sp	231	33	63.5	520	2	Q8YNE6_ANASP	Q8yne6_anabena sp
159	34	65.4	1703	2	Q8WHX1_PSLINU	Q8whx1_psillocum nu	232	33	63.5	522	2	Q88QUL_PSEPK	Q88qul_pseudomonas
160	34	65.4	1973	2	Q5CGH7_CRYHO	Q5cgh7_cryptospori	233	33	63.5	526	2	Q874W7_KLUBE	Q874w7_kuylveromyc
161	34	65.4	2105	2	Q5CHMS_CRYHO	Q5chms_cryptospori	234	33	63.5	533	2	Q7SKP2_BRARE	Q7skp2_brachydanio
162	34	65.4	2308	2	Q9VPI7_DROME	Q9vp17_drosophila	235	33	63.5	536	2	Q4S113_TETNG	Q4s113_tetradon n
163	34	65.4	2615	2	Q5TVF6_ANOGA	Q5tvf6_anopheles g	236	33	63.5	545	2	Q6OWY7_CABER	Q6ow7_caeenorhabdi
164	34	65.4	6384	2	Q74OD1_MYCPA	Q74od1_mycobacteri	237	33	63.5	559	2	Q8KXG9_HUMAN	Q8kx9_homo sapien
165	34	65.4	11696	2	Q5CV09_CRYPV	Q5cv09_cryptospori	238	33	63.5	562	2	Q9XOV3_THEMA	Q9xov3_thermotoga
166	34	64.4	524	2	Q6CYG2_KULUA	Q6cyg2_kuylveromyc	239	33	63.5	595	2	Q54W00_DICDI	Q54w00_dicytyoselli
167	33.5	64.4	759	2	Q5DVG0_9CREN	Q5dvg0_sulfolobus	240	33	63.5	625	2	Q6BI61_DEBNA	Q6bi61_debaryomyce
168	33	63.5	86	2	Q8S8N1_ARATH	Q8s8n1_arabidopsis	241	33	63.5	639	2	Q4PH32_USTMA	Q4ph32_ustilago ma
169	33	63.5	88	2	Q9SS32_DROME	Q9ss32_drosophila	242	33	63.5	658	2	Q7LGR2_YEAST	Q7lgr2_saccharomyc
170	33	63.5	111	1	KVJN_MOUSE	P01666 mus musculu	243	33	63.5	663	2	Q68DQ3_HUMAN	Q68dq3_homo sapien
171	33	63.5	112	2	Q6LEMH_MOUSE	Q6lehm8 mus musculu	244	33	63.5	670	2	Q9NS54_LACBL	Q9ns54_caenorhabdi
172	33	63.5	152	2	Q762I8_KLEPN	Q762i8_klebsiella	245	33	63.5	683	2	Q88S94_CAEEL	Q88s94_lactobacill
173	33	63.5	155	2	Q4XK43_PLACH	Q4xk43_plasmodium	246	33	63.5	685	2	Q7RIQ9_GIALA	Q7riq9_giardia lam
174	33	63.5	162	2	Q9YE24_AARPE	Q9ye24_aetopyrum p	247	33	63.5	693	2	Q5U1A6_DROME	Q5u1a6_drosophila
175	33	63.5	167	2	Q7Z8G2_9GARG	Q7z8g2_cortinariu	248	33	63.5	713	2	Q7RG19_PLAYO	Q7rg19_plasmodium
176	33	63.5	178	2	Q8S1V8_ORYSA	Q8s1v8_oryza sativ	249	33	63.5	719	2	Q8DIY5_STRAS	Q8diy5_streptococc
177	33	63.5	199	2	Q5WK30_BACSK	Q5wk30_bacillus cl	250	33	63.5	719	2	Q8E3Z8_STRAS	Q8e3z8_streptococc

251	33	63.5	723	2	Q54W06	DICDI	Q54W06	dictyosteli	324	32	61.5	142	2	Q4SCK2	TEITNG	Q4ack2	tetradodon n
252	33	63.5	754	1	ADAM7	HUMAN	Q9nah9	homo saplen	325	32	61.5	153	2	Q4ZNT9	PEESY	Q4znt9	pseudomonas
253	33	63.5	765	2	Q50YB3	ENTH1	Q50yb3	entamoeba h	326	32	61.5	153	2	Q87WT3	PEESY	Q87wt3	pseudomonas
254	33	63.5	766	1	GIGB	STNEL	Q8dlb8	synecococc	327	32	61.5	157	2	Q4YDF6	PLABE	Q4ydf6	plasmodium
255	33	63.5	776	1	ADAM7	MACPA	Q28875	macera fasc	328	32	61.5	158	2	Q50ZU2	ENTH1	Q50zu2	entamoeba h
256	33	63.5	818	2	Q41928	GIBZE	Q41928	glibdrellia	329	32	61.5	164	2	Q9SR12	ARATH	Q9sr12	arabidopsis
257	33	63.5	830	2	Q91VH0	MOUSE	Q91vh0	mus musculu	330	32	61.5	166	2	Q9FSR9	BCOLI	Q9fsr9	escherichia
258	33	63.5	840	2	Q5U0Y6	DROME	Q5u0y6	drosophila	331	32	61.5	168	2	Q9FSR3	SALCH	Q9fsr3	salmonella
259	33	63.5	926	2	Q9W3G1	DROME	Q9w3g1	drosophila	332	32	61.5	171	2	Q01640	DRGR	Q01640	drosophila
260	33	63.5	944	2	Q6R187	DEBNA	Q6r187	debaromyce	333	32	61.5	182	2	Q6S974	APILI	Q6s974	apls mellif
261	33	63.5	949	2	Q54EB3	DICDI	Q54eb3	dictyosteli	334	32	61.5	194	2	Q6YS20	ORYSA	Q6ys20	oryza sativ
262	33	63.5	990	2	Q6AJB0	DESPS	Q6ajb0	desulfohalo	335	32	61.5	200	2	Q7R2Y0	GRALA	Q7r2y0	giardia lam
263	33	63.5	1008	2	Q523U0	MAGR	Q523u0	magnaporthe	336	32	61.5	202	2	Q7UCIS	SHIFL	Q7ucis	shigella fl
264	33	63.5	1050	2	Q12494	YEAST	Q12494	saccharomyc	337	32	61.5	204	2	Q59J05	CANAL	Q59j05	candida alb
265	33	63.5	1052	2	Q6Z4F1	ORYSA	Q6z4f1	oryza sativ	338	32	61.5	208	2	Q7QAB8	ANOGA	Q7qab8	anopheles g
266	33	63.5	1058	2	Q6ZU10	HUMAN	Q6zu10	homo saplen	339	32	61.5	213	2	Q8FNV1	COREF	Q8fnv1	coxynebacce
267	33	63.5	1100	2	Q7OTZ0	GITAL	Q7otz0	giardia lam	340	32	61.5	213	2	P73104	SYNY3	P73104	synecocyst
268	33	63.5	1122	2	Q7WYAI	9GAMM	Q7wyai	sheanella	341	32	61.5	219	2	Q8DDN1	STRR6	Q8ddn1	streptococc
269	33	63.5	1190	2	Q8TVN7	METKA	Q8tvn7	methanopyru	342	32	61.5	221	2	Q5L6V5	CHILAB	Q5l6v5	chlamydophi
270	33	63.5	1205	2	Q74ZU3	ASHGO	Q74zu3	asbhyia goos	343	32	61.5	230	2	Q5M8L8	XENTR	Q5m8l8	xenopus tro
271	33	63.5	1220	2	Q4P897	USTMA	Q4p897	usciilago ma	344	32	61.5	234	2	Q647W6	9ARCH	Q647w6	uncultured
272	33	63.5	1298	2	Q8G981	OSGAG	Q8g981	oscillatori	345	32	61.5	236	2	Q7Z3Y4	HUMAN	Q7z3y4	homo saplen
273	33	63.5	1299	2	Q847C8	NODSP	Q847c8	nodularia s	346	32	61.5	236	2	Q5WNP8	CABBR	Q5wnp8	caenorhabdi
274	33	63.5	1310	2	Q4QE82	LEIWA	Q4qe82	leishmania	347	32	61.5	243	2	Q521P5	MOUSE	Q521p5	mus musculu
275	33	63.5	1404	2	Q45251	CABEL	Q45251	caenorhabdi	348	32	61.5	243	2	Q08858	KUEPN	Q08858	klebsiella
276	33	63.5	1444	1	C1084	HUMAN	Q5vxu9	homo saplen	349	32	61.5	250	1	M4AB8	HUMAN	Q5vy19	homo saplen
277	33	63.5	1463	2	Q7TF56	PRRSV	Q7tf56	prtrsv hb-2(350	32	61.5	252	2	Q6FPY6	CANGA	Q6fpy6	candida gla
278	33	63.5	1514	2	Q5SSC1	CRYNE	Q5sscl	cryptococcu	351	32	61.5	252	2	Q9BL05	LEIMA	Q9bl05	leishmania
279	33	63.5	1514	2	Q5XGR8	CRYNE	Q5xgr8	cryptococcu	352	32	61.5	255	2	Q5LGA2	BACFN	Q5lga2	bacteroides
280	33	63.5	1536	2	Q474H8	TEITNG	Q474h8	tetradodon n	353	32	61.5	259	2	Q7N925	PHOIL	Q7n925	photorhabdu
281	33	63.5	1673	2	Q9V019	DROME	Q9v019	drosophila	354	32	61.5	276	2	Q4H4F3	BACCI	Q4h4f3	bacillus ci
282	33	63.5	1849	2	Q86WGS	HUMAN	Q86wgs	homo saplen	355	32	61.5	275	2	Q9THQ1	9POAL	Q9thq1	dyckia sp.
283	33	63.5	2011	2	Q9RA19	VIRMA	Q9ra19	vibrio mari	356	32	61.5	281	2	Q9TKM4	9POAL	Q9tkm4	ananas anan
284	33	63.5	2102	2	Q559T8	DICDI	Q559t8	dictyosteli	357	32	61.5	276	2	Q67R99	SYMTH	Q67r99	synbiobacce
285	33	63.5	2154	2	Q8F6C2	ECOL6	Q8f6c2	escherichia	358	32	61.5	287	2	Q50XG3	ENTH1	Q50xg3	entamoeba h
286	33	63.5	2254	2	Q75J05	DICDI	Q75j05	dictyosteli	359	32	61.5	300	1	F1M4H	BCOLI	Q87634	escherichia
287	33	63.5	2254	2	Q8MXN1	DICDI	Q8mxn1	dictyosteli	360	32	61.5	300	2	Q6UKU5	BCOLI	Q6uku5	escherichia
288	33	63.5	2516	2	Q553C0	DICDI	Q553c0	dictyosteli	361	32	61.5	300	2	Q6UKU5	BCOLI	Q6uku5	escherichia
289	33	63.5	3302	2	Q70TY5	GITAL	Q70ty5	giardia lam	362	32	61.5	300	2	Q6UKU7	BCOLI	Q6uku7	escherichia
290	33	63.5	3848	2	Q81DR0	PLAF7	Q81dr0	plasmodium	363	32	61.5	300	2	Q6UKU8	BCOLI	Q6uku8	escherichia
291	33	63.5	6675	2	Q4KCD8	PSERS	Q4kcd8	pseudomonas	364	32	61.5	300	2	Q6UKU8	BCOLI	Q6uku8	escherichia
292	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	365	32	61.5	300	2	Q6UKV4	BCOLI	Q6ukv4	escherichia
293	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	366	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
294	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	367	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
295	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	368	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
296	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	369	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
297	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	370	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
298	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	371	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
299	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	372	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
300	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	373	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
301	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	374	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
302	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	375	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
303	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	376	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
304	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	377	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
305	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	378	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
306	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	379	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
307	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	380	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
308	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	381	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
309	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	382	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
310	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	383	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
311	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	384	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
312	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	385	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
313	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	386	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
314	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	387	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
315	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	388	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
316	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	389	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
317	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	390	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
318	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	391	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
319	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	392	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
320	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	393	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
321	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	394	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
322	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	395	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia
323	33	63.5	9498	2	Q42T75	PSERS	Q42t75	pseudomonas	396	32	61.5	300	2	Q6UKV6	BCOLI	Q6ukv6	escherichia

397	32	61.5	313	2	Q41ZN3_AZOV1	Q41zn3 azotobacter	470	32	61.5	630	2	F73661_SYNY3	F73661 synechocyst
398	32	61.5	318	2	Q4PE24_USTMA	Q4pe24 uetiliago ma	471	32	61.5	644	2	Q6BH80_DEBNA	Q6bh80 debaromyce
399	32	61.5	318	2	Q4SSV5_TETNG	Q4ssv5 tetricodon n	472	32	61.5	655	2	Q4WY11_ASFPU	Q4wy11 aspergillus
400	32	61.5	328	2	Q7VNM3_HAEEDU	Q7vnm3 haemophilus	473	32	61.5	726	2	Q521G7_MAGGR	Q521g7 magnaporthe
401	32	61.5	329	2	Q4P9Z5_USTMA	Q4p9z5 uetiliago ma	474	32	61.5	747	2	P79160_CALJA	P79160 callitrix
402	32	61.5	329	2	Q61M05_CAEBR	Q61m05 caenorhabdi	475	32	61.5	753	2	Q96Z69_SULTO	Q96z69 sulfobius
403	32	61.5	334	2	Q8YPR9_ANASP	Q8ypr9 anabaena sp	476	32	61.5	764	2	Q9Z067_ARATH	Q9z067 arabidopsis
404	32	61.5	342	2	Q4YB74_PLABE	Q4yb74 plasmodium	477	32	61.5	779	2	Q9MR93_PODAN	Q9mr93 podopora a
405	32	61.5	347	2	Q81LFO_SHEFL	Q81lfo shigella fl	478	32	61.5	785	2	Q4UA29_THEAN	Q4ua29 thellexia a
406	32	61.5	348	2	Q6M068_BREBA	Q6m068 belliovibri	479	32	61.5	815	2	Q8W2T2_ORYSA	Q8w2t2 cryza sativ
407	32	61.5	353	2	Q8H3V0_ORYSA	Q8h3v0 oryza sativ	480	32	61.5	840	2	Q64557_ARATH	Q64557 arabidopsis
408	32	61.5	357	2	Q61AF7_CAEBR	Q61af7 caenorhabdi	481	32	61.5	855	2	Q4P3C5_USTMA	Q4p3c5 ustia
409	32	61.5	361	2	Q5BK19_XENTR	Q5bk19 xenopus tro	482	32	61.5	864	2	Q5CPA3_CRYHO	Q5cpa3 crytopospori
410	32	61.5	362	1	Q4KLM1_XENLA	Q4klm1 xenopus lae	483	32	61.5	869	2	Q8FGB3_ECOL6	Q8fgb3 escherichia
411	32	61.5	362	1	RDCL_CANPA	RDCL canis famli	484	32	61.5	878	2	Q5JUP3_ORYSA	Q5jup3 oryza sativ
412	32	61.5	362	1	RDCL_HUMAN	P25106 homo sapien	485	32	61.5	887	1	QUAI_DROME	Q233969 drosophila
413	32	61.5	362	1	RDCL_MOUSE	P56485 mus musculu	486	32	61.5	887	2	Q540V4_DROME	Q540v4 drosophila
414	32	61.5	362	1	RDCL_RAT	P58039 rattus norv	487	32	61.5	888	2	Q8IN17_DROME	Q8in17 drosophila
415	32	61.5	362	2	Q5JRV4_HUMAN	Q5jrv4 homo sapien	488	32	61.5	920	2	Q5CLZ3_CRYHO	Q5clz3 crytopospori
416	32	61.5	362	2	Q9JLZ0_RAT	Q9j1z0 rattus norv	489	32	61.5	921	2	Q7YZ56_CRYPV	P60755 mus musculu
417	32	61.5	369	2	Q8RRH3_FUSNN	Q8rrh3 fusobacteri	490	32	61.5	949	1	MAMC1_MOUSE	P60756 rattus norv
418	32	61.5	370	2	Q8QPR6_XENLA	Q8qpr6 xenopus lae	491	32	61.5	949	1	MAMC1_RAT	Q51YK4 magnaporthe
419	32	61.5	371	2	Q6XYZ0_SPIKU	Q6xyz0 spiroplasma	492	32	61.5	979	2	Q51YK4_MAGGR	Q5p411 ureaplasma
420	32	61.5	378	2	Q5JUP2_ORYSA	Q5jup2 oryza sativ	493	32	61.5	1025	2	Q9P011_UREPA	Q9p011 ureaplasma
421	32	61.5	388	2	Q7QXJ3_GIALA	Q7qxj3 giardia lam	494	32	61.5	1067	1	LONM_SCHPO	Q09766 schistosach
422	32	61.5	388	2	Q51FU0_ENTHI	Q51fu0 entamoeba h	495	32	61.5	1069	2	Q4WM29_ASFPU	Q4wm29 aspergillus
423	32	61.5	411	2	Q7J3P10_TREDE	Q7j3p10 treponema d	496	32	61.5	1077	2	Q8EKF3_SHEON	Q8ekf3 shewanella
424	32	61.5	419	2	Q7USHS_SYNPX	Q7ushs synechococc	497	32	61.5	1081	1	PDR6_YEAST	P32767 saccharomyc
425	32	61.5	425	2	Q7JPS3_TREDE	Q7jps3 treponema d	498	32	61.5	1096	2	Q7R3Z3_GIALA	Q7r3z3 giardia lam
426	32	61.5	448	2	Q8CLT1_YERPE	Q8clt1 yerstinia pe	499	32	61.5	1100	2	Q8V189_MOUSE	Q8v189 mus musculu
427	32	61.5	448	2	Q8ZB32_YERPE	Q8zb32 yerstinia pe	500	32	61.5	1100	2	Q5SX62_MOUSE	Q5sx62 mus musculu
428	32	61.5	448	2	Q664Y7_YERPS	Q664y7 yerstinia ps	501	32	61.5	1120	2	Q8FPG5_ECOL6	Q8fgp5 escherichia
429	32	61.5	450	2	Q7RNV0_PLAYO	Q7rny0 plasmodium	502	32	61.5	1120	2	Q6A011_MOUSE	Q6a011 mus musculu
430	32	61.5	450	2	Y047_MYCPN	P75067 mycoplasma	503	32	61.5	1145	1	PCD19_MOUSE	Q80E3 mus musculu
431	32	61.5	452	1	Q5B2H7_EMENTI	Q5b2h7 aspergillus	504	32	61.5	1148	1	PCD19_HUMAN	Q8tab3 homo sapien
432	32	61.5	452	2	Q5QXHS_IDILO	Q5qxhs idiomarina	505	32	61.5	1175	2	Q7MX74_PORGI	Q7mx74 porphyromon
433	32	61.5	455	2	Q914S2_STPAU	Q914s2 stephylococ	506	32	61.5	1176	2	Q5UK69_ORYSA	Q5uk69 oryza sativ
434	32	61.5	458	2	Q6GNZ1_PHOAZ	Q6gnz1 photorhabdu	507	32	61.5	1200	2	Q97277_PLAF7	Q97277 plasmodium
435	32	61.5	458	2	Q7N8R0_PHOIL	Q7n8r0 photochabdu	508	32	61.5	1223	2	Q6BT08_DEBNA	Q6bt08 debaromyce
436	32	61.5	466	2	Q61Y14_CAEBR	Q61y14 caenorhabdi	509	32	61.5	1256	2	Q7XIK7_ORYSA	Q7xik7 oryza sativ
437	32	61.5	466	2	Q9PFG1_ARATH	Q9pfgr1 arabidopsis	510	32	61.5	1283	2	Q7QAK4_ANOGA	Q7qak4 anopheles g
438	32	61.5	466	2	Q4KF41_PSEFS	Q4kf41 pseudomonas	511	32	61.5	1292	2	Q4N6Z0_THEPA	Q4n6z0 thellexia p
439	32	61.5	468	2	Q7GDAD_MYCTU	Q7gdad mycobacteri	512	32	61.5	1323	2	Q7QW8_PLAYO	Q7qw8 plasmodium
440	32	61.5	468	2	Q7JG04_MYCTU	Q7jg04 mycobacteri	513	32	61.5	1351	2	P90744_CAEEL	P90744 caenorhabdi
441	32	61.5	468	2	Q7J2P9_MYCBO	Q7j2p9 mycobacteri	514	32	61.5	1370	2	Q7R422_GIALA	Q7r422 giardia lam
442	32	61.5	473	2	Q5HG86_STPAC	Q5hg86 stephylococ	515	32	61.5	1424	2	Q4L3C8_STAH7	Q4l3c8 staphylococ
443	32	61.5	487	2	Q66788_YERPS	Q66788 yerstinia ps	516	32	61.5	1506	2	Q8KCO8_CHUTE	Q8kco8 chlorobium
444	32	61.5	487	2	Q8ZD93_YERPE	Q8zd93 yerstinia pe	517	32	61.5	1510	2	Q8KCO8_CHUTE	Q8kco8 dictyosceli
445	32	61.5	491	2	Q8GFP6_CITFR	Q8gfp6 citricobacter	518	32	61.5	1534	2	Q5SDR9_DICDI	Q5sdr9 dictyosceli
446	32	61.5	491	2	Q7VK71_HEILHP	Q7vk71 helicobacte	519	32	61.5	1669	2	Q9LXK4_ARATH	Q9lxx4 arabidopsis
447	32	61.5	496	2	Q4IV30_AZOV1	Q4iv30 azotobacter	520	32	61.5	1873	2	Q6NTNS_XENLA	Q6ntns xenopus lae
448	32	61.5	502	1	CAPA_PIG	Q66839 sus scrofa	521	32	61.5	2294	2	Q4RUIZ3_TETNG	Q4ruiz3 tetricodon n
449	32	61.5	505	2	Q914S1_STPAU	Q914s1 stephylococ	522	32	61.5	2294	2	Q4RPG4_TETNG	Q4rpg4 tetricodon n
450	32	61.5	505	2	Q8NWX5_STPAU	Q8nwx5 stephylococ	523	32	61.5	3232	2	Q94Z05_CIAPU	Q94z05 claviiceps p
451	32	61.5	505	2	Q6GH72_STPAR	Q6gh72 stephylococ	524	32	61.5	3328	2	Q6ZAK2_BURMA	Q6zak2 burkholderi
452	32	61.5	505	2	Q6G9M4_STPAS	Q6g9m4 stephylococ	525	32	61.5	3665	2	Q7UQ60_RHOBA	Q7uq60 rhodospirell
453	32	61.5	506	2	Q96GUP4_ASPNG	Q96gup4 aspergillus	526	32	61.5	3848	2	Q76737_DICDI	Q76737 dictyosceli
454	32	61.5	507	2	Q7AS72_STPAN	Q7as72 stephylococ	527	32	61.5	4671	2	Q9VH97_DROME	Q9vh97 drosophila
455	32	61.5	507	2	Q9JUE2_STPAU	Q9jue2 stephylococ	528	32	61.5	6094	2	Q63J72_BURPS	Q63j72 burkholderi
456	32	61.5	511	2	Q6OXE2_CAEBR	Q6oxe2 caenorhabdi	529	32	60.6	382	2	Q4U6R2_SUTAC	Q4u6r2 sulfobius
457	32	61.5	513	2	Q819W0_APTLI	Q819w0 apis mellif	530	32	60.6	761	2	Q59784_SCHPO	Q59784 schizosach
458	32	61.5	519	1	GPWI_COXBU	Q83bh2 coxiella bu	531	32	60.6	852	2	Q5ANP5_CANAL	Q5anp5 candida alb
459	32	61.5	519	1	Q96Z59_PLAF7	Q96z59 plasmodium	532	32	61.5	872	2	Q66Q70_9HIV1	Q66q70 human immun
460	32	61.5	521	2	Q7YJL3_9ASPA	Q7yj13 hamorchia v	533	32	60.6	882	2	Q90024_9HIV1	Q90024 human immun
461	32	61.5	557	2	Q9PLK3_ARATH	Q9plk3 arabidopsis	534	32	60.6	1236	2	Q4QG71_LEIMA	Q4qg71 leishmania
462	32	61.5	558	2	Q5A1C1_CANAL	Q5a1c1 candida alb	535	32	59.6	66	2	Q541Y6_DICDI	Q541y6 dictyosceli
463	32	61.5	561	2	Q5A1C1_CANAL	Q5a1c1 candida alb	536	32	59.6	76	1	Y1230_MERYA	Q86z7 methanococc
464	32	61.5	567	2	Q8YWI2_ANASP	Q8ywj2 anabaena sp	537	32	59.6	81	2	Q8H5W8_ORYSA	Q8h5w8 oryza sativ
465	32	61.5	570	1	SMA4_CAEBR	P45697 caenorhabdi	538	32	59.6	81	2	Q7O435_9HIV1	Q7o435 human immun
466	32	61.5	583	2	Q5XUW6_LEGFL	Q5xuw6 legionella	539	32	59.6	101	2	Q7UXO4_RHOBA	Q7uxo4 rhodospirell
467	32	61.5	584	2	Q5X3H5_LEGFL	Q5x3h5 legionella	540	32	59.6	104	2	Q5O3Z9_ECOLI	Q5o3z9 escherichia
468	32	61.5	595	2	Q7Z275_BRARE	Q7z275 brachydanto	541	32	59.6	108	1	KVIL_HUMAN	Q6ze70 synechocyst
469	32	61.5	612	2	Q5QY69_IDILO	Q5qy69 idiomarina	542	32	59.6	111	2	Q6ZE70_SYNY3	

543	31	59.6	112	2	Q9JRI7_NEIMA	Q9JRI7_neissexia m	616	31	59.6	273	2	Q76UN7_BEEV	Q76UN7_eastern equ
544	31	59.6	112	2	Q7D10_NEIMB	Q7D10_neissexia m	617	31	59.6	273	2	Q76UN8_BEEV	Q76UN8_eastern equ
545	31	59.6	112	2	Q8K1F3_MOUSE	Q8K1F3_mus musculus	618	31	59.6	273	2	Q76UN9_BEEV	Q76UN9_eastern equ
546	31	59.6	114	2	Q5ZHK9_CHICK	Q5ZHK9_gallus galli	619	31	59.6	273	2	Q76UP0_BEEV	Q76UP0_eastern equ
547	31	59.6	121	2	Q4K793_PSERP	Q4K793_pseudomonas	620	31	59.6	273	2	Q88840_BEEV	Q88840_eastern equ
548	31	59.6	129	2	Q9BRT6_HUMAN	Q9BRT6_homo sapien	621	31	59.6	273	2	Q88841_BEEV	Q88841_eastern equ
549	31	59.6	131	1	M050_ARATH	P93277 arabidopsis	622	31	59.6	273	2	Q88842_BEEV	Q88842_eastern equ
550	31	59.6	134	1	Q9WHJ0_GRETR	Q9WHJ0_walleye epi	623	31	59.6	273	2	Q88843_BEEV	Q88843_eastern equ
551	31	59.6	135	2	Q74807_SCHPO	Q74807_schizosacch	624	31	59.6	273	2	Q88844_BEEV	Q88844_eastern equ
552	31	59.6	136	2	Q5TNM7_ANOGA	Q5TNM7_anopheles g	625	31	59.6	273	2	Q88845_BEEV	Q88845_eastern equ
553	31	59.6	137	2	Q7QMT6_ANOGA	Q7QMT6_anopheles g	626	31	59.6	273	2	Q88846_BEEV	Q88846_eastern equ
554	31	59.6	142	2	Q5UQ39_MIMIV	Q5UQ39_mimivirus.	627	31	59.6	273	2	Q88847_BEEV	Q88847_eastern equ
555	31	59.6	145	2	Q6BPM5_DEBHA	Q6BPM5_debaryomyce	628	31	59.6	273	2	Q88848_BEEV	Q88848_eastern equ
556	31	59.6	147	2	Q9B0G2_9CAUD	Q9B0G2_staphylococ	629	31	59.6	273	2	Q88849_BEEV	Q88849_eastern equ
557	31	59.6	148	2	Q6D4F0_ERMCT	Q6D4F0_erynia car	630	31	59.6	273	2	Q88850_BEEV	Q88850_eastern equ
558	31	59.6	155	2	Q8YR71_ANASP	Q8YR71_anabaena sp	631	31	59.6	273	2	Q88851_BEEV	Q88851_eastern equ
559	31	59.6	156	2	Q6BZ54_DEBHA	Q6BZ54_debaryomyce	632	31	59.6	273	2	Q90212_BEEV	Q90212_eastern equ
560	31	59.6	169	2	Q5BZFI_SCHUA	Q5BZFI_schistosoma	633	31	59.6	276	2	Q7XYM4_ORYSA	Q7XYM4_oryza sativ
561	31	59.6	171	2	Q8XQ10_RALSO	Q8XQ10_ralstonia s	634	31	59.6	278	2	Q85097_POTV	Q85097_peanut molt
562	31	59.6	181	2	Q8YZT1_ANASP	Q8YZT1_anabaena sp	635	31	59.6	278	2	Q85098_POTV	Q85098_peanut molt
563	31	59.6	182	2	Q7UUI1_RHOBA	Q7UUI1_rhodopirell	636	31	59.6	278	2	Q85099_POTV	Q85099_peanut molt
564	31	59.6	184	2	Q5XPK4_CHEIB	Q5XPK4_chelion labr	637	31	59.6	278	2	Q85100_POTV	Q85100_peanut molt
565	31	59.6	186	2	Q5AUB0_CANAL	Q5AUB0_candida alb	638	31	59.6	278	2	Q85101_POTV	Q85101_peanut molt
566	31	59.6	186	2	Q5AUN9_CANAL	Q5AUN9_candida alb	639	31	59.6	279	2	Q9CZD0_MOUSE	Q9CZD0_mus musculus
567	31	59.6	191	2	Q7SKG9_9HIV1	Q7SKG9_human immun	640	31	59.6	279	2	Q5UJ72_BRABE	Q5UJ72_brachydanio
568	31	59.6	195	2	Q4MKO9_BACCE	Q4MKO9_bacillus ce	641	31	59.6	281	1	DEGV_BACSV	P32436 bacillus su
569	31	59.6	195	2	Q7JBR1_BACCI	Q7JBR1_bacillus ce	642	31	59.6	283	2	Q9SW52_ARATH	Q9SW52_arabidopsis
570	31	59.6	195	2	Q81TM2_BACCN	Q81TM2_bacillus an	643	31	59.6	299	2	Q5W256_9ENTR	Q5W256_serratia sp
571	31	59.6	195	2	Q63ED1_BACCC	Q63ED1_bacillus ce	644	31	59.6	304	2	Q67PNE_SYMTW	Q67PNE_symbiodace
572	31	59.6	195	2	Q81G69_BACCR	Q81G69_bacillus ce	645	31	59.6	305	2	Q51WK7_MAGGR	Q51WK7_magnaporthe
573	31	59.6	195	2	Q6HLU8_BACHK	Q6HLU8_bacillu th	646	31	59.6	314	2	Q22623_VACCO	Q22623_vaccinium c
574	31	59.6	207	2	Q51HM3_MAGGR	Q51HM3_magnaporthe	647	31	59.6	314	2	Q8DCC4_VIBVU	Q8DCC4_vibrio vuln
575	31	59.6	209	2	Q4XBE2_PLACH	Q4XBE2_plasmodium	648	31	59.6	315	1	Q6A8C6_PROAC	Q6A8C6_propionibac
576	31	59.6	212	2	Q4WCE4_ASPTU	Q4WCE4_aspergillus	649	31	59.6	315	1	PYRB_XANAC	Q51720_xanthomonas
577	31	59.6	212	2	Q9CGD9_LACIA	Q9CGD9_lactococcus	650	31	59.6	315	1	PYRB_XANOR	Q51720_xanthomonas
578	31	59.6	212	2	Q8DBC3_VIBVU	Q8DBC3_vibrio vuln	651	31	59.6	315	2	Q9N3F7_CAEEL	Q9N3F7_caenorhabdi
579	31	59.6	212	2	Q8ZCX7_YERPE	Q8ZCX7_yersinia pe	652	31	59.6	315	2	Q8DRC9_SYNEL	Q8DRC9_synchrococc
580	31	59.6	212	2	Q668B4_YERPS	Q668B4_yersinia ps	653	31	59.6	317	1	YMX1_CAEEL	Q94509_caenorhabdi
581	31	59.6	213	2	Q8DXM4_STRAS	Q8DXM4_streptococc	654	31	59.6	317	2	Q5DGT4_SCHJA	Q5DGT4_schistosoma
582	31	59.6	213	2	Q8B394_STRAS	Q8B394_streptococc	655	31	59.6	318	2	Q5M8J0_XENTR	Q5M8J0_xenopus tiro
583	31	59.6	215	2	Q4FR42_9GAMM	Q4FR42_psychrobact	656	31	59.6	319	2	Q84844_9POTV	Q84844_peanut molt
584	31	59.6	217	2	Q8LOS2_STRSU	Q8LOS2_streptococc	657	31	59.6	320	2	Q66TDE_HUMAN	Q66TDE_homo sapien
585	31	59.6	219	2	Q663G3_PLAFA	Q663G3_plasmodium	658	31	59.6	320	2	Q5XGH3_XENTR	Q5XGH3_xenopus tiro
586	31	59.6	219	2	Q97P36_STRPN	Q97P36_streptococc	659	31	59.6	321	2	Q6NLP9_ARATH	Q6NLP9_arabidopsis
587	31	59.6	224	2	Q7MTK0_VIBRY	Q7MTK0_vibrio vuln	660	31	59.6	322	2	Q7QFH6_ANOGA	Q7QFH6_anopheles g
588	31	59.6	222	1	RNP3_METMP	P60781_methanococc	661	31	59.6	322	1	CRO_RANCA	P17264 rana catesb
589	31	59.6	222	2	Q83VR0_9PROT	Q83VR0_methyllobaci	662	31	59.6	323	1	CRO_RANTR	P02532 rana tempor
590	31	59.6	233	2	Q8E450_STRAS	Q8E450_streptococc	663	31	59.6	326	2	Q6EP22_ORYSA	Q6EP22_oryza sativ
591	31	59.6	233	2	Q8DYJ3_STRAS	Q8DYJ3_streptococc	664	31	59.6	328	2	Q6DJG6_XENIA	Q6DJG6_xenopus lae
592	31	59.6	236	2	Q65XD1_ORYSA	Q65XD1_oryza sativ	665	31	59.6	329	2	Q8RBI4_THETN	Q8RBI4_thermoanaer
593	31	59.6	241	2	Q4Y933_PLAAB	Q4Y933_plasmodium	666	31	59.6	332	2	Q8PUY3_METMA	Q8PUY3_methanosarc
594	31	59.6	241	2	Q7NGE8_GLOVI	Q7NGE8_gloeobacter	667	31	59.6	332	2	Q8T224_TRYCAN	Q8T224_trypanosoma
595	31	59.6	245	1	TRMB_ACTAD	Q61CN6_actinobact	668	31	59.6	334	2	Q9UPQ8_HUMAN	Q9UPQ8_homo sapien
596	31	59.6	246	2	Q51TN9_MAGGR	Q51TN9_magnaporthe	669	31	59.6	334	2	Q9EST0_ARATH	Q9EST0_arabidopsis
597	31	59.6	246	2	Q70I38_LOTJA	Q70I38_lotus japon	670	31	59.6	337	2	Q4JAU1_SULAC	Q4JAU1_sulfolobus
598	31	59.6	248	2	Q97008_LEIMA	Q97008_leishmania	671	31	59.6	337	2	Q75I15_ORYSA	Q75I15_oryza sativ
599	31	59.6	249	2	Q93MB1_ANASP	Q93MB1_anabaena sp	672	31	59.6	338	1	PYRB_PROMA	Q7V666_prochlorococ
600	31	59.6	251	2	Q6A2S7_VIBRU	Q6A2S7_vibrio vuln	673	31	59.6	338	2	Q7TSS6_MOUSE	Q7TSS6_mus musculus
601	31	59.6	252	2	Q937E7_NOSPU	Q937E7_noscoec punc	674	31	59.6	350	2	Q7WH15_VIBRY	Q7WH15_vibrio vuln
602	31	59.6	258	2	Q8YSA0_ANASP	Q8YSA0_anabaena sp	675	31	59.6	351	2	Q72SD3_LISME	Q72SD3_listeria mo
603	31	59.6	259	2	Q62MY4_BURMA	Q62MY4_burholderi	676	31	59.6	351	2	Q8YAT2_LISMO	Q8YAT2_listeria mo
604	31	59.6	259	2	Q63Y09_BURPS	Q63Y09_burholderi	677	31	59.6	354	1	Q92F53_LISIN	Q92F53_listeria in
605	31	59.6	260	2	Q6IAS0_HUMAN	Q6IAS0_homo sapien	678	31	59.6	354	2	Q5UP25_9PROT	Q5UP25_uncultured
606	31	59.6	265	2	Q7PY94_ANOGA	Q7PY94_anopheles g	679	31	59.6	355	2	Q31884_9ERIC	Q31884_bomplandia
607	31	59.6	266	2	Q6W383_9CREN	Q6W383_uncultured	680	31	59.6	358	2	Q8SMU7_9ERIC	Q8SMU7_lilanthus d
608	31	59.6	266	2	Q8Y2Q1_RALSO	Q8Y2Q1_ralstonia s	681	31	59.6	358	2	Q9THY3_9ERIC	Q9THY3_cobaea scan
609	31	59.6	273	2	Q76UN0_BEEV	Q76UN0_eastern equ	682	31	59.6	360	2	Q7SB96_NEUCR	Q7SB96_neurospora
610	31	59.6	273	2	Q76UN1_BEEV	Q76UN1_eastern equ	683	31	59.6	363	2	Q8XYM4_RALSO	Q8XYM4_ralstonia s
611	31	59.6	273	2	Q76UN2_BEEV	Q76UN2_eastern equ	684	31	59.6	365	2	Q7N2R6_PHOLI	Q7N2R6_photobactd
612	31	59.6	273	2	Q76UN3_BEEV	Q76UN3_eastern equ	685	31	59.6	369	2	Q61AY3_CAEER	Q61AY3_caenorhabdi
613	31	59.6	273	2	Q76UN4_BEEV	Q76UN4_eastern equ	686	31	59.6	371	2	Q7QW75_GIALA	Q7QW75_giardia lam
614	31	59.6	273	2	Q76UN5_BEEV	Q76UN5_eastern equ	687	31	59.6	372	2	Q51FR6_ENTHI	Q51FR6_entamoeba h
615	31	59.6	273	2	Q76UN6_BEEV	Q76UN6_eastern equ	688	31	59.6	372	2	Q5QZNS_IDITLO	Q5QZNS_idiomarina

689	31	59.6	773	2	Q4SBP5_TETNG	Q4ebp5 tetraodon n	762	31	59.6	531	1	TILS_CANBP	Q7vrc9 candidatus
690	31	59.6	375	2	Q8MPW5_CABEL	Q8mpw5 caenorhabdi	763	31	59.6	540	2	Q7O8C8_ANOGA	Q7vrc8 anopheles g
691	31	59.6	377	2	Q4SYE9_TETNG	Q4sy9 tetraodon n	764	31	59.6	544	2	Q7MT75_WOLSU	Q7mt75 wolinnella s
692	31	59.6	378	2	Q8CUM7_DICDI	Q8cum7 dictyostei	765	31	59.6	546	2	Q4LU62_9BURK	Q4lu62 burkholderi
693	31	59.6	380	2	Q8MPW4_CABEL	Q8mpw4 caenorhabdi	766	31	59.6	559	2	Q6D198_ERWCT	Q6d198 erwina car
694	31	59.6	381	2	Q752D0_ASHGO	Q752d0 ashbya gos	767	31	59.6	560	2	Q6R531_9INFA	Q6r531 influenza a
695	31	59.6	394	2	Q59242_CANAL	Q59242 candida alb	768	31	59.6	561	2	Q91ID6_9REOV	Q91id6 lymantria d
696	31	59.6	394	2	Q59242_CANAL	Q59242 candida alb	769	31	59.6	571	2	Q4SIX1_TETNG	Q4six1 tetraodon n
697	31	59.6	394	2	Q86DC7_CABEL	Q86dc7 caenorhabdi	770	31	59.6	573	2	Q4MXU0_ASPFU	Q4mxu0 aspergillus
698	31	59.6	395	2	Q5R8R6_VIBF1	Q5r8r6 vibrio fisc	771	31	59.6	573	2	Q8E530_OCEH1	Q8e530 oceanobacil
699	31	59.6	395	2	Q6TRYQ_MIOTA	Q6tryq micipitecus	772	31	59.6	579	2	Q9H5H7_HUMAN	Q9h5h7 homo sapien
700	31	59.6	397	2	Q5E3N4_VIBF1	Q5e3n4 vibrio fisc	773	31	59.6	579	2	Q7Z636_HUMAN	Q7z636 homo sapien
701	31	59.6	397	2	Q6R4Q3_VIBF1	Q6r4q3 vibrio fisc	774	31	59.6	587	2	Q525T5_MAGGR	Q525t5 magnaporthe
702	31	59.6	397	2	Q8D9D7_VIBVU	Q8d9d7 vibrio vuln	775	31	59.6	588	2	Q4XU50_PLACH	Q4xu50 plasmodium
703	31	59.6	397	2	Q9KTD9_VIBCV	Q9ktd9 vibrio chol	776	31	59.6	592	2	Q59UT0_CANAL	Q59uto candida alb
704	31	59.6	397	2	Q7MLQ2_VIBVY	Q7mlq2 vibrio vuln	777	31	59.6	598	2	Q4VIB4_BACC2	Q4vib4 bacillus ce
705	31	59.6	404	2	Q8MPW8_CABEL	Q8mpw8 caenorhabdi	778	31	59.6	599	2	Q4RV96_TETNG	Q4rv96 tetraodon n
706	31	59.6	407	2	Q4K497_PSEF5	Q4k497 pseudomonas	779	31	59.6	603	2	Q95QA7_CABEL	Q95qa7 caenorhabdi
707	31	59.6	411	2	Q5AG10_CANAL	Q5ag10 candida alb	780	31	59.6	609	2	Q51U64_MAGGR	Q51u64 magnaporthe
708	31	59.6	411	2	Q67MD2_SYWTH	Q67md2 symbiodace	781	31	59.6	612	2	Q84XA4_VIGUN	Q84xa4 vigna ungui
709	31	59.6	412	2	Q61SK3_CABRA	Q61sk3 caenorhabdi	782	31	59.6	620	2	Q8T069_DROME	Q8t069 drosophila
710	31	59.6	412	2	Q5IC53_9BETA	Q5ic53 murid herpe	783	31	59.6	624	2	Q9TYO8_CABEL	Q9tyo8 caenorhabdi
711	31	59.6	414	2	Q8D9D5_VIBVU	Q8d9d5 vibrio vuln	784	31	59.6	631	2	Q5T012_HUMAN	Q5t012 homo sapien
712	31	59.6	416	2	Q4UIG9_VIBVY	Q4uig9 vibrio vuln	785	31	59.6	631	2	Q6PB77_MOUSE	Q6pb77 mus musculu
713	31	59.6	416	2	Q4UIS3_THEAN	Q4uis3 theileria a	786	31	59.6	635	2	Q54ND5_DICDI	Q54nd5 dictyostei
714	31	59.6	423	2	Q5ARV9_EMENTI	Q5arv9 aspergillus	787	31	59.6	636	2	Q6CL90_KLULA	Q6cl90 kluyveromyc
715	31	59.6	427	2	Q91YXN_ARATH	Q91yxn arabidopsis	788	31	59.6	636	2	Q5XKC7_HUMAN	Q5xkc7 homo sapien
716	31	59.6	431	2	Q5TNP1_ANOGA	Q5ctf1 anopheles g	789	31	59.6	638	1	Q8IKR0_VYIRU	Q8ikr0 heliothis z
717	31	59.6	433	2	Q5TNL5_ANOGA	Q5tnl5 anopheles g	790	31	59.6	644	2	Q6C843_YARLI	Q6c843 yarrowia sta
718	31	59.6	438	2	Q4LGL2_9BURK	Q4lgl2 burkholderi	791	31	59.6	645	2	Q8D689_VIBVU	Q8d689 vibrio vuln
719	31	59.6	439	2	Q6UQ72_ORYZA	Q6uq72 oryza sativ	792	31	59.6	646	2	Q872C1_NEUCR	Q872c1 neurospora
720	31	59.6	446	2	Q5B7W6_EMENTI	Q5b7w6 aspergillus	793	31	59.6	651	2	Q520A5_MAGGR	Q520a5 magnaporthe
721	31	59.6	447	2	Q8MPW7_CABEL	Q8mpw7 caenorhabdi	794	31	59.6	651	2	Q8T0A2_DROME	Q8t0a2 drosophila
722	31	59.6	449	2	Q5UF12_PYRKO	Q5uf12 pyrococcus	795	31	59.6	653	2	Q4SPF7_TETNG	Q4spf7 tetraodon n
723	31	59.6	452	2	Q6BLH5_DEBHA	Q6blh5 debaromyce	796	31	59.6	656	2	Q8MPW9_CABEL	Q8mpw9 caenorhabdi
724	31	59.6	452	2	Q8WZM6_TRHIA	Q8wzm6 trichoderma	797	31	59.6	657	2	Q95QAE_CABEL	Q95qa6 caenorhabdi
725	31	59.6	453	2	Q6CS61_KLULA	Q6cs61 kluyveromyc	798	31	59.6	663	2	Q7VJ82_HELHU	Q7vj82 helicobacte
726	31	59.6	454	2	Q8ZQ54_SALTU	Q8zq54 salmonella	799	31	59.6	666	2	Q7VFB0_DROME	Q7vfb0 drosophila
727	31	59.6	457	2	Q54453_STPMU	Q54453 streptococc	800	31	59.6	668	2	Q4V534_HAEIN	P44242 haemophilus
728	31	59.6	462	2	Q8H6S4_PONTR	Q8h6s4 poncirus tr	801	31	59.6	670	2	Q4QKP6_HAE18	Q4qkp6 haemophilus
729	31	59.6	466	2	Q6OS42_CABRA	Q6os42 caenorhabdi	802	31	59.6	672	2	Q4Q879_LBIMA	Q4q879 leishmania
730	31	59.6	468	2	Q90WM5_FUGRU	Q90wm5 fugu rubrip	803	31	59.6	672	2	Q9KQVO_VIBCH	Q9kqvo vibrio chol
731	31	59.6	469	2	Q5N0Z4_SYNP6	Q5n0z4 synecococc	804	31	59.6	676	2	Q4HY29_GIBZE	Q4hy29 gibberella
732	31	59.6	469	2	Q9X8Q3_STRCO	Q9x8q3 streptococ	805	31	59.6	682	2	Q56135_9PROTV	Q56135 watermelon
733	31	59.6	471	2	Q8TXP4_METKA	Q8txp4 methanopyru	806	31	59.6	683	2	Q4ID39_GIBZE	Q4id39 gibberella
734	31	59.6	476	2	Q8MPW6_CABEL	Q8mpw6 caenorhabdi	807	31	59.6	683	2	Q9JG47_VYIRU	Q9jg47 tev-like mi
735	31	59.6	477	2	Q54Y13_DICDI	Q54y13 dictyostei	808	31	59.6	683	2	Q9JG64_VYIRU	Q9jg64 tev-like mi
736	31	59.6	477	2	Q5E8U0_VIBF1	Q5e8u0 vibrio fisc	809	31	59.6	688	2	Q5JQ64_VYIRU	Q5jq64 entamoeba h
737	31	59.6	477	2	Q5R162_BRABE	Q5r162 brachydanto	810	31	59.6	689	2	Q5OSQ6_ENTHI	Q5osq6 entamoeba h
738	31	59.6	480	2	Q4MWL8_ASPFU	Q4mw18 aspergillus	811	31	59.6	697	2	Q8Q0K8_METMA	Q8q0k8 methanosarc
739	31	59.6	482	2	Q5IAS7_PETMA	Q5ias7 petromyzon	812	31	59.6	697	2	Q6LVP9_PROPR	Q6lvp9 photobacter
740	31	59.6	486	2	Q91576_XENLA	Q91576 xenopus lae	813	31	59.6	703	2	Q4NC51_9MICC	Q4nc51 atrophobla
741	31	59.6	488	2	Q5N221_AZOSE	Q5n221 azotarcus sp	814	31	59.6	704	2	Q4V464_DROME	Q4v464 drosophila
742	31	59.6	490	1	SMG1_CABEL	Q9u1d4 caenorhabdi	815	31	59.6	706	2	Q95QAE_CABEL	Q95qa8 caenorhabdi
743	31	59.6	490	2	Q8PEV8_XANAC	Q8pev8 xanthomonas	816	31	59.6	708	2	Q61610_CABER	Q61610 caenorhabdi
744	31	59.6	491	2	Q9FMR7_ARATH	Q9fmr7 arabidopsis	817	31	59.6	710	2	Q8TKV5_METAC	Q8tkv5 methanosarc
745	31	59.6	492	2	Q8IYEA_HUMAN	Q8iye4 homo sapien	818	31	59.6	712	2	Q9HVP8_PSEAB	Q9hvf8 pseudomonas
746	31	59.6	492	2	Q5MQD6_9INFA	Q5mqd6 influenza a	819	31	59.6	716	2	Q8MPX0_CABEL	Q8mpx0 caenorhabdi
747	31	59.6	492	2	Q8B2W2_9INFA	Q8b2w2 influenza a	820	31	59.6	717	2	Q6LME2_PROPR	Q6lme2 photobacter
748	31	59.6	493	2	Q4IC01_GIBZE	Q4ic01 gibberella	821	31	59.6	720	2	Q7XHP5_ORYSA	Q7xhp5 oryza sativ
749	31	59.6	495	2	Q55897_SYNVJ3	Q55897 synecocycat	822	31	59.6	722	2	Q7MDP0_VIBVY	Q7mdp0 vibrio vuln
750	31	59.6	498	2	Q6F921_ACTAD	Q6f921 acinetobact	823	31	59.6	726	2	Q9V952_DROME	Q9v952 drosophila
751	31	59.6	499	1	BCH9_STNY3	Q55773 synecocycat	824	31	59.6	729	2	Q5NBJ3_ORYSA	Q5nbj3 oryza sativ
752	31	59.6	509	2	Q8MSC9_DROME	Q8msc9 drosophila	825	31	59.6	732	2	Q6L148_CABRA	Q6l148 caenorhabdi
753	31	59.6	510	2	Q5AG44_CANAL	Q5ag44 candida alb	826	31	59.6	748	2	Q4IQ78_GIBZE	Q4iq78 gibberella
754	31	59.6	514	2	Q7SB11_NEUCR	Q7sb11 neurospora	827	31	59.6	749	2	Q4QET9_LBIMA	Q4qet9 leishmania
755	31	59.6	518	1	ELI2_ARATH	Q6z124 homo sapien	828	31	59.6	757	2	Q5APD8_DICDI	Q5apd8 dictyostei
756	31	59.6	521	2	Q6ZT24_HUMAN	Q6z124 homo sapien	829	31	59.6	783	2	Q9FBV4_STRCO	Q9fbv4 streptococ
757	31	59.6	522	2	Q4WGC1_ASPFU	Q4wgc1 aspergillus	830	31	59.6	785	2	Q5BAQ7_EMENTI	Q5baq7 aspergillus
758	31	59.6	524	2	Q5AVQ7_EMENTI	Q5avq7 aspergillus	831	31	59.6	785	2	Q54WA7_DICDI	Q54wa7 dictyostei
759	31	59.6	524	2	Q9PB85_XYLFA	Q9pb85 xyella fas	832	31	59.6	795	2	Q9Y1J5_DICDI	Q9y1j5 dictyostei
760	31	59.6	527	2	Q5XW25_9PERO	Q5xw25 oplegnathus	833	31	59.6	798	2	Q6FMQ9_CANGA	Q6fmq9 candida gla
761	31	59.6	530	2	Q9RQO3_MYCCA	Q9rqg3 mycoplasma	834	31	59.6	814	2	Q4RFH4_TETNG	Q4rfh4 tetraodon n

835	31	59.6	815	2	Q571U2_SALCH	Q571U2_salmoneila	908	31	59.6	1395	2	Q52A60_MAGCR	Q52A60_magnaporthe
836	31	59.6	815	2	Q5PM10_SALPA	Q5PM10_salmoneila	909	31	59.6	1402	2	Q5SL4_ARATH	Q5SL4_atribopsis
837	31	59.6	815	2	Q8Z231_SALPA	Q8Z231_salmoneila	910	31	59.6	1404	2	Q7RFP2_PLAYO	Q7RFP2_plasmidium
838	31	59.6	815	2	Q8ZIG7_SALTYA	Q8ZIG7_salmoneila	911	31	59.6	1416	2	Q9C435_MAGCR	Q9C435_magnaporthe
839	31	59.6	819	2	Q54CG3_DICDI	Q54CG3_dicystostei	912	31	59.6	1436	2	Q4PG07_USTMA	Q4PG07_ustilago ma
840	31	59.6	838	2	Q9CAK9_ARATH	Q9CAK9_atribopsis	913	31	59.6	1478	2	Q6ZOA5_MOUSE	Q6ZOA5_mus musculus
841	31	59.6	840	2	Q84B27_SPIKU	Q84B27_splittiplasma	914	31	59.6	1485	2	Q5ZD73_MAGCR	Q5ZD73_magnaporthe
842	31	59.6	842	2	Q4X0X4_ASPEU	Q4X0X4_aspergillus	915	31	59.6	1537	2	Q55F55_DICDI	Q55F55_dicystostei
843	31	59.6	856	2	Q61X16_CABBR	Q61X16_caenorhabdi	916	31	59.6	1563	1	RIM_CABBL	RIM_caenorhabdi
844	31	59.6	865	2	Q54R59_DICDI	Q54R59_dicystostei	917	31	59.6	1600	2	Q7S8J4_NEUCR	Q7S8J4_neutropora
845	31	59.6	873	2	Q5SGF7_DICDI	Q5SGF7_dicystostei	918	31	59.6	1610	2	Q813U2_PLAF7	Q813U2_plasmidium
846	31	59.6	879	2	Q6CX10_KLULA	Q6CX10_kluyveromyc	919	31	59.6	1744	2	Q9C3Z2_COCHR	Q9C3Z2_cochliobol
847	31	59.6	884	2	Q9CAB4_ARATH	Q9CAB4_atribodopsis	920	31	59.6	1978	2	Q7RHK6_PLAYO	Q7RHK6_plasmidium
848	31	59.6	886	2	Q8NZY6_HUMAN	Q8NZY6_homo sapien	921	31	59.6	2055	2	Q7Y055_HUMAN	Q7Y055_homo sapien
849	31	59.6	903	2	Q81I40_PLAF7	Q81I40_plasmidium	922	31	59.6	2061	2	Q4YZG4_PLABE	Q4YZG4_plasmidium
850	31	59.6	925	2	Q96JG7_PLAF7	Q96JG7_plasmidium	923	31	59.6	2102	2	Q5T011_HUMAN	Q5T011_homo sapien
851	31	59.6	939	2	Q9VH85_DROME	Q9VH85_drosophila	924	31	59.6	2136	2	Q83N66_TROM8	Q83N66_tropheryma
852	31	59.6	952	2	Q7YU88_DROME	Q7YU88_drosophila	925	31	59.6	2147	2	Q83FPH_TROMT	Q83FPH_tropheryma
853	31	59.6	954	2	Q84594_CHLTR	Q84594_chlamydia t	926	31	59.6	2159	2	Q7KVD8_DROME	Q7KVD8_drosophila
854	31	59.6	959	2	Q7XGT4_ORYSA	Q7XGT4_oryza sativ	927	31	59.6	2307	2	Q9AG79_9ACTO	Q9AG79_streptomyce
855	31	59.6	959	2	Q93VY2_ORYSA	Q93VY2_oryza sativ	928	31	59.6	2308	2	Q83NU3_TROM8	Q83NU3_tropheryma
856	31	59.6	980	2	Q51V42_MAGCR	Q51V42_magnaporthe	929	31	59.6	2312	2	Q83GX5_TROMT	Q83GX5_tropheryma
857	31	59.6	988	2	Q8GQM4_ACTCA	Q8GQM4_acinetobact	930	31	59.6	2383	2	Q4RM12_TRTNG	Q4RM12_tetradodon n
858	31	59.6	1034	2	Q9W3X2_DROME	Q9W3X2_drosophila	931	31	59.6	2473	1	TOR2_YEAST	TOR2_yeast
859	31	59.6	1066	2	Q4N4P9_THSPA	Q4N4P9_chelilleria p	932	31	59.6	2560	1	PBS2_BACSU	PBS2_bacillus su
860	31	59.6	1078	2	Q5VRT7_ORYSA	Q5VRT7_oryza sativ	933	31	59.6	2571	2	Q87704_BACSU	Q87704_bacillus su
861	31	59.6	1080	2	Q6N7M5_CORDI	Q6N7M5_corynebacte	934	31	59.6	2628	2	Q88F78_PSEPK	Q88F78_pseudomonas
862	31	59.6	1089	2	Q89QZ5_BRALJ	Q89QZ5_bradynrhizob	935	31	59.6	2649	2	Q9W0T2_DROME	Q9W0T2_drosophila
863	31	59.6	1091	2	Q5KWA7_GEOKA	Q5KWA7_geobacillus	936	31	59.6	2669	2	Q95VIB8_DROME	Q95VIB8_drosophila
864	31	59.6	1110	2	Q83C98_COXBU	Q83C98_coxiella bu	937	31	59.6	2859	2	Q9W0T1_DROME	Q9W0T1_drosophila
865	31	59.6	1128	2	Q54R95_DICDI	Q54R95_dicystostei	938	31	59.6	2859	2	Q7NVV9_CHRVO	Q7NVV9_chromobacte
866	31	59.6	1145	2	Q51HD7_MAGCR	Q51HD7_magnaporthe	939	31	59.6	2900	2	Q81ZB0_PLAF7	Q81ZB0_plasmidium
867	31	59.6	1152	2	Q74J45_LACIO	Q74J45_lactobacilli	940	31	59.6	3099	1	POLG_PEMVA	POLG_pemva
868	31	59.6	1172	2	Q4TSV7_GSPBN	Q4TSV7_erythrobact	941	31	59.6	3569	2	Q81BVB_PLAF7	Q81BVB_plasmidium
869	31	59.6	1188	1	QSH1_YEAST	P35845_saccharomyc	942	31	59.6	3583	2	Q9V3N4_DROME	Q9V3N4_drosophila
870	31	59.6	1188	2	Q86ZC4_YEAST	Q86ZC4_saccharomyc	943	31	59.6	3584	2	Q9U999_DROME	Q9U999_drosophila
871	31	59.6	1190	2	Q4MA12_ASPEU	Q4MA12_aspergillus	944	31	59.6	3612	2	Q7QVU2_GIALA	Q7QVU2_giardia lam
872	31	59.6	1219	2	Q4RX15_TRTNG	Q4RX15_tetradodon n	945	31	59.6	3680	2	Q5D1S7_PSEAB	Q5D1S7_pseudomonas
873	31	59.6	1220	2	Q6ZKB6_BURMA	Q6ZKB6_burholderi	946	31	59.6	3680	2	Q5D1U0_PSEAB	Q5D1U0_pseudomonas
874	31	59.6	1227	2	Q7R188_PLAYO	Q7R188_plasmidium	947	31	59.6	3902	2	Q4SC60_TRTNG	Q4SC60_tetradodon n
875	31	59.6	1228	2	Q8Y1N7_ANASP	Q8Y1N7_anabaena sp	948	31	59.6	4336	2	Q4ZV34_PSEBY	Q4ZV34_pseudomonas
876	31	59.6	1239	1	POLS_BEEV	P08768_eastern equ	949	31	59.6	4336	2	Q864F8_PSEBM	Q864F8_pseudomonas
877	31	59.6	1240	1	POLS_BEEV3	P27284_eastern equ	950	31	59.6	4379	2	Q9R4H4_9NOSO	Q9R4H4_nostoc sp.
878	31	59.6	1241	2	Q5OUQ8_IDILIO	Q5OUQ8_idiomarina	951	31	59.6	4901	2	Q4KES9_PSEBF	Q4KES9_pseudomonas
879	31	59.6	1241	2	Q66579_BEEV	Q66579_eastern equ	952	31	59.6	5369	2	Q9R9J0_BACSU	Q9R9J0_bacillus su
880	31	59.6	1242	2	Q88795_BEEV	Q88795_eastern equ	953	30.5	58.7	315	2	Q6ZDVI_ORYSA	Q6ZDVI_oryza sativ
881	31	59.6	1242	2	Q88792_BEEV	Q88792_eastern equ	954	30.5	58.7	368	1	Q8S606_ORYSA	Q8S606_oryza sativ
882	31	59.6	1242	2	Q88790_BEEV	Q88790_eastern equ	955	30.5	58.7	835	2	Q7SE57_ASHGO	Q7SE57_ashgoc
883	31	59.6	1242	2	Q88794_BEEV	Q88794_eastern equ	956	30.5	58.7	42	2	Q69VCO_ORYSA	Q69VCO_oryza sativ
884	31	59.6	1242	2	Q88796_BEEV	Q88796_eastern equ	957	30	57.7	42	2	Q32761_ORYSA	Q32761_oryza sativ
885	31	59.6	1242	2	Q88797_BEEV	Q88797_eastern equ	958	30	57.7	42	2	Q4RB55_TRTNG	Q4RB55_tetradodon n
886	31	59.6	1242	2	Q88797_BEEV	Q88797_eastern equ	959	30	57.7	54	2	Q9PBH7_XYRFA	Q9PBH7_xyella fae
887	31	59.6	1242	2	Q9PZX5_BEEV	Q9PZX5_eastern equ	960	30	57.7	57	2	Q5BMY9_9CAUD	Q5BMY9_cyanophaga
888	31	59.6	1242	2	Q9PZX5_BEEV	Q9PZX5_eastern equ	961	30	57.7	68	2	Q5C2T4_SCHUR	Q5C2T4_schistosoma
889	31	59.6	1242	2	Q08359_BEEV	Q08359_eastern equ	962	30	57.7	72	2	Q7S938_NEUCR	Q7S938_neutropora
890	31	59.6	1242	2	Q88799_BEEV	Q88799_eastern equ	963	30	57.7	74	2	Q81OH4_BACAN	Q81OH4_bacillus an
891	31	59.6	1242	2	Q9PZM9_BEEV	Q9PZM9_eastern equ	964	30	57.7	80	2	Q8GV93_9ASPA	Q8GV93_galanthus p
892	31	59.6	1242	2	Q9PZX4_BEEV	Q9PZX4_eastern equ	965	30	57.7	88	2	Q9VFG8_DROME	Q9VFG8_drosophila
893	31	59.6	1242	2	Q9PZX0_BEEV	Q9PZX0_eastern equ	966	30	57.7	93	2	Q6CV31_KLULA	Q6CV31_kluyveromyc
894	31	59.6	1242	2	Q9PZX3_BEEV	Q9PZX3_eastern equ	967	30	57.7	95	2	Q5F779_NEIGI	Q5F779_neisseria g
895	31	59.6	1242	2	Q9PZX6_BEEV	Q9PZX6_eastern equ	968	30	57.7	111	1	Q9DHDO_YLDV	Q9DHDO_yaba-like d
896	31	59.6	1242	2	Q88798_BEEV	Q88798_eastern equ	969	30	57.7	111	2	Q6YK55_BRANA	Q6YK55_brasica na
897	31	59.6	1242	2	Q9PZX1_BEEV	Q9PZX1_eastern equ	970	30	57.7	113	2	Q4LM71_9BURK	Q4LM71_burholderi
898	31	59.6	1242	2	Q9PZX1_BEEV	Q9PZX1_eastern equ	971	30	57.7	102	2	Q61MW3_CABBR	Q61MW3_caenorhabdi
899	31	59.6	1242	2	Q88678_BEEV	Q88678_eastern equ	972	30	57.7	102	2	Q7Y5L8_GVCL	Q7Y5L8_cryptophleb
900	31	59.6	1242	2	Q4QXJ9_BEEV	Q4QXJ9_eastern equ	973	30	57.7	111	1	KVJ3_MOUSE	KVJ3_mus musculu
901	31	59.6	1242	2	Q4QXJ7_BEEV	Q4QXJ7_eastern equ	974	30	57.7	111	2	Q9DHDO_YLDV	Q9DHDO_yaba-like d
902	31	59.6	1259	2	Q4POV7_USTMA	Q4POV7_ustilago ma	975	30	57.7	113	2	Q6YK55_BRANA	Q6YK55_brasica na
903	31	59.6	1281	2	Q63U48_BURPS	Q63U48_burholderi	976	30	57.7	113	2	Q4LM71_9BURK	Q4LM71_burholderi
904	31	59.6	1307	2	Q58WQ5_9BACT	Q58WQ5_uncultured	977	30	57.7	114	2	Q8K1F1_MOUSE	Q8K1F1_mus musculu
905	31	59.6	1309	2	Q5MD35_9DELT	Q5MD35_cyctobacter	978	30	57.7	115	2	Q65HS4_BACLD	Q65HS4_bacillus li
906	31	59.6	1330	2	Q6CHC3_YARLI	Q6CHC3_yarrowia li	979	30	57.7	118	2	Q7ADP1_ECO57	Q7ADP1_escherichia
907	31	59.6	1339	2	Q54QRO_DICDI	Q54QRO_dicystostei	980	30	57.7	118	2		

981	30	57.7	118	2	Q8XE2 ECO57	Q8XE2 escherichia
982	30	57.7	121	2	Q8FR59 CORF	Q8FR59 corynabacte
983	30	57.7	122	2	Q8PV9 METMA	Q8PV9 methanosarc
984	30	57.7	123	2	Q7ZY35 XENLA	Q7ZY35 xenopus lae
985	30	57.7	123	2	Q6NVR5 XENTR	Q6NVR5 xenopus tro
986	30	57.7	127	2	Q8SD45 9CAUD	Q8SD45 pseudomonas
987	30	57.7	128	2	Q5CRH2 CRYPV	Q5CRH2 cryptospori
988	30	57.7	128	2	Q5CHY3 CRYHO	Q5CHY3 cryptospori
989	30	57.7	129	1	VAL2 TGMV	P03562 tomato sold
990	30	57.7	130	2	Q9D945 MOUSE	Q9D945 mus muscu
991	30	57.7	131	1	CNI09 HUMAN	Q8NE14 homo sapien
992	30	57.7	131	2	Q67044 9INFA	Q67044 influenza a
993	30	57.7	131	2	Q67045 9INFA	Q67045 influenza a
994	30	57.7	131	2	Q67046 9INFA	Q67046 influenza a
995	30	57.7	131	2	Q67047 9INFA	Q67047 influenza a
996	30	57.7	132	2	Q8CTU4 MOUSE	Q8CTU4 mus muscu
997	30	57.7	133	2	Q6S8W4 PLAF4	Q6S8W4 plasmodium
998	30	57.7	135	2	Q4N4C7 THEPA	Q4N4C7 theileria p
999	30	57.7	136	2	Q592U2 CANAL	Q592U2 candida alb
1000	30	57.7	139	2	Q6FR24 CANGA	Q6FR24 candida gla

ALIGNMENTS

RESULT 1

Q4HU43_GIBZE PRELIMINARY; PRT; 171 AA.

AC Q4HU43;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Predicted protein.
GN ORFNames=FG11515.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nussbaum C., Aboueleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barina N., Baetjen V., Bloom T., Boguslavsky L.,
RA Boughalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Engelano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gaele S., Graham L., Grand-Pierre N., Hatz N.,
RA Hagopian D., Hages B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Mathews C., Maudslayi E., McCarthy M., Meldrum J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachenk J., Ramaamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tefaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACM0100473; FGA78383.1; -; Genomic DNA.
SQ SEQUENCE 171 AA; 19534 MW; 51F97F968F1366B6 CRC64;

Query Match 78.8%; Score 41; DB 2; Length 171;
Best Local Similarity 77.8%; Pred. No. 5.2;

Matches	7;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	1	QOHNRYPLT 9							
Db	21	QOHNRYPLT 29							

RESULT 2

Q6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.

AC Q6GMX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant J.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -; mRNA.
DR SMR; O6GMX9; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-set; I.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25924 MW; FDE2033DC560CFF7 CRC64;

Query Match 76.9%; Score 40; DB 2; Length 236;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNRYPLT 9
Db 111 QOHNRYPLT 119

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
 RA Wood D.W., Secubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.B., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendinning J., Deatherage G., Gillet M., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Sempitmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan M., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Neester E.W.,
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinke J.G., Gattung S., Miller N., Blanchard M.,
 RA Quetio B., Goldman B.S., Cao Y., Askenzi M., Hailing C., Mullin L.,
 RA Houmlet K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.,
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328 (2001).
 DR EMBL; AE008998; ALA1286.1; -; Genomic_DNA.
 DR PIR; AH2608; AAK6080.1; -; Genomic_DNA.
 DR PIR; G97390; G97390.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR012287; Homeodomain-rel.
 DR InterPro; IPR000005; HTHARAC.
 DR InterPro; IPR002818; TH1J/PfPI.
 DR Pfam; PF01965; D1-1_PfPI; 1.
 DR Pfam; PF00165; HTH_ARAC; 2.
 DR PRINTS; PR00032; HTHARAC.
 DR SMART; SM00342; HTH_ARAC; 1.
 DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
 KM Activator; Complete proteome; DNA-binding; Transcription;
 KM Transcription regulation.
 SQ SEQUENCE 327 AA; 36504 MW; 0F77DAD56081CE2D CRC64;

Query Match 73.1%; Score 38; DB 2; Length 327;
 Best Local Similarity 85.7%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 OQHNEYP 7
 |||||
 DB 312 OQHNEYP 318

RESULT 6
 O54EP8 DICI PRELIMINARY; PRT; 1695 AA.
 AC O54EP8;
 DT 13-SEP-2005 (TRMBLrel. 31, Created)
 DT 13-SEP-2005 (TRMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=DD80183957;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN-AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugarc R., Berriman M., Song J., Olsen R., Szafianski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera P., Konfortov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pichner K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kethorou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desay B., Just E., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardeper A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Louised H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward G., Winkler T., Tanaka Y.,
 RA Shalshy G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer B., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
 RT "The genome of the social amoeba Dictyostelium discoideum.";
 RL Nature 0:0-0(2005).
 CC -! CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBD whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAF1000257; EAL61752.1; -; Genomic_DNA.
 DR Hypothetical protein.
 KM Hypothetical protein.
 SQ SEQUENCE 1695 AA; 192812 MW; 4FPD2E9E98F1F97 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 1695;
 Best Local Similarity 87.5%; Pred. No. 3,2e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 OQHNEYP 8
 |||||
 DB 1130 OQHNEYP 1137

RESULT 7
 O8ZSF7 ANASP PRELIMINARY; PRT; 248 AA.
 AC O8ZSF7;
 DT 01-MAR-2002 (TRMBLrel. 20, Created)
 DT 01-MAR-2002 (TRMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)
 DE A1r7553 protein.
 GN OrderedLocNames=alr7553;
 OS Anabaena sp. (strain PCC 7120).
 OC Cyanobacteria; Cyanobacteriales; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iritsugu M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.,
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003602; BAB77196.1; -; Genomic_DNA.
 DR PIR; AF2533; AF2533.
 KM Complete proteome; Plasmid.
 SQ SEQUENCE 248 AA; 28803 MW; 0561269338DC17C0 CRC64;

Query Match 71.2%; Score 37; DB 2; Length 248;
 Best Local Similarity 75.0%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 OQHNEYP 8
 |||||
 DB 64 OQHNEYP 71

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RESULT 8
060127 MYCHY PRELIMINARY; PRT: 507 AA.
ID 060127;
AC 060127;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE ATP synthase alpha chain (EC 3.6.1.34).
GN Name=atpA; OrderedLocNames=mbp053;
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OC NCBI_TaxID=2099;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=232;
RX PubMed=15489423; DOI=10.1128/JB.186.21.7123-7133.2004;
RA Minlon F.C., Lefkowitz E.J., Madson M.L., Cleary B.J., Swartzell S.M.,
RA Mahairas G.G.;
RT "The genome sequence of Mycoplasma hyopneumoniae strain 232, the agent
RT of swine mycoplasmosis."
RL J. Bacteriol. 186:7123-7133(2004).
CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
CC core - and CF(0) - the membrane proton channel. CF(1) has five
CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
CC has three main subunits: a, b and c (By similarity).
CC EMBL; A0017332; AA027378.1; -, Genomic DNA.
DR GO; GO:0045261; C:proton-transporting ATP synthase complex, c. .; IEA.
DR GO; GO:0015469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. .; IEA.
DR GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota. .; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0016820; F:hydrolyase activity, acting on acid anhydrid. .; IEA.
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro: IPR005294; ATP synthet. alph.
DR InterPro: IPR00793; ATPase_a/b/c.
DR InterPro: IPR004100; ATPase_a/b/N.
DR InterPro: IPR000194; ATPase_a/bcentre.
DR Pfam: PF00006; ATP-synt. ab; 1.
DR Pfam: PF00306; ATP-synt. ab C; 1.
DR Pfam: PF02874; ATP-synt. ab N; 1.
DR TIGRPFAM: TIGR00962; atpA; 1.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; 1.
KW ATP synthesis; ATP-binding; CF(1); Complete proteome; Hydrolyase;
KW ion transport; Nucleotide-binding; Transport.
SQ SEQUENCE 507 AA; 55733 MW; 0670100821A8EBB4 CRC64;

Query Match 71.2%; Score 37; DB 2; Length 507;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP 9
DB 420 KOENGYPLT 428

RESULT 9
07UXL8 RHOB A PRELIMINARY; PRT: 990 AA.
ID 07UXL8;
AC 07UXL8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Probable permease of ABC transporter.
GN OrderedLocNames=RB1250;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
ON NCBI_TaxID=117;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Hellmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294135; CAD71988.1; -, Genomic DNA.
KW Complete proteome.
SQ SEQUENCE 990 AA; 109306 MW; 5D2BF59561DD5F82 CRC64;

Query Match 71.2%; Score 37; DB 2; Length 990;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP 7
DB 651 QOHNEYP 657

RESULT 10
08YWC4 ANASP PRELIMINARY; PRT: 1302 AA.
ID 08YWC4;
AC 08YWC4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cobalam biosynthetic protein.
GN Name=CobN; OrderedLocNames=alr1689;
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
ON NCBI_TaxID=103690;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriuguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; BA000019; BAB78055.1; -, Genomic DNA.
DR PIR; AC2017; AC2017.
DR GO; GO:0009058; F:biosynthesis; IEA.
DR InterPro: IPR011953; Cobalto_cobN.
DR InterPro: IPR003672; CobN/Mg chltase.
DR Pfam: PF02514; CobN-Mg chel; 1.
DR TIGRPFAM: TIGR02257; cobalto_cobN; 1.
KW Complete proteome.
SQ SEQUENCE 1302 AA; 144493 MW; DC9240D58CDD6453 CRC64;

Query Match 71.2%; Score 37; DB 2; Length 1302;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOHNEYP 9
DB 924 QOHNEYP 924

RESULT 11
081622 PLAF7 PRELIMINARY; PRT: 5729 AA.
ID 081622;
AC 081622;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PFL0115w;

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OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
[1]
NP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Bertram M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow N., Suh B., Peterson J., Angiuoli S.,
RA Perera M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings I.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.G.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511 (2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RA Hyman R.W., Fung E., Conway A., Kurdi O., Mao J., Miranda M.,
RA Nakao B., Rowley D., Yamaki T., Wang F., Davis R.W.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB014844; AN36112.1; -; Genomic DNA.
DR GO; GO:0030286; C:dynactin complex; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PF03028; Dynein_heavy; 1.
KW Hypothetical protein.
SQ SEQUENCE 5729 AA; 691521 MW; 2377972B17CE0A99 CRC64;

Query Match 71.2%; Score 37; DB 2; Length 5729;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOHNEYPL 8
Db 1332 QOHNEYPL 1339

RESULT 12
KV1V HUMAN STANDARD; PRT; 108 AA.
ID KV1V HUMAN
AC P04430;
DT 13-AUG-1987 (rel. 05, Created)
DT 13-AUG-1987 (rel. 05, Last sequence update)
DT 10-MAY-2005 (rel. 47, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwaletz F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
[2]
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
[3]
DR PIR; A01878; KIHUBN.
DR HSSP; P80362; 1WTU.
DR SMR; P04430; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Framework-4.
FT REGION 98 107 Complementarity-determining-3.
FT DISULFID 23 88 Framework-4.
FT NON TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 69.2%; Score 36; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QOHNEYPL 9
Db 89 QOHNEYPL 97

RESULT 13
OBVIUO MOUSE PRELIMINARY; PRT; 108 AA.
ID OBVIUO
AC OBVIU0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN Name-Igk-v19-14; Synonyms=VK19;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CH/Heu-1pr/1pr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetcky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from CH-1pr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
[2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyclonal autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
[3]
NP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RA Tillman D.M., You N.T., Hill R.J., Marion T.N.;
RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT selective B cell stimulation in (NZB x NZW) F1 mice.";
RL J. Exp. Med. 176:761-779(1992).
[4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91115823; PubMed=1703577;
RA Goshorn S.C., Retzel B., Demmerson R.;
RT "Common structural features among monoclonal antibodies binding the
RT same antigenic region of cytochrome c.";
RL J. Biol. Chem. 266:2134-2142(1991).
DR EMBL; U59155; AA802917.1; -; mRNA.
DR PIR; A33933; A33933.
DR PIR; A37262; A37262.
DR PIR; PH1072; PH1072.

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DR HSPB, P01634, 11GC.
DR SMR, Q8V1U0, 1-108.
DR Ensembl; ENSMUSG00000053690; Mus musculus.
DR MGI; MGI:1330830; ICG-VI-9-14.
DR InterPro; IPR007110; Iq_1-like.
DR InterPro; IPR003596; Iq_v.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; Iq_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA, 11859 MW, 68506075613DBFBE CRC64;

Query Match 69.2%; Score 36; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOHNEVPL 9
DB 89 QOQNSYPY 97

RESULT 14
Q8CBK2 MOUSE PRELIMINARY; PRT; 147 AA.
AC Q8CBK2;
ID Q8CBK2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
DE enriched library, clone:963001IN22 product:phosphodiesterase 4D, cAMP
DE specific, full insert sequence.
GN Name=Pde4d; Synonyms=963001IN22Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saio T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Caaveira T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;

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RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitaura T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto K., Sakaguchi S., Ikegami T., Kaishogi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hirose K., Hirooka T., Hirozane T.,
RA Hori F., Iwamoto K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sato H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK035860; BAC29216.1; -; mRNA.
DR MGI; MGI:2444663; 963001IN22Rik.
DR MGI; MGI:2444663; Pde4d.
DR GO; GO:0006198; P:cAMP catabolism; IMP.
DR GO; GO:0006939; P:smooth muscle contraction; IMP.
SQ SEQUENCE 147 AA, 16396 MW, CF651F18828751C8 CRC64;

Query Match 69.2%; Score 36; DB 2; Length 147;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEVPL 8
DB 36 QOHNEVPL 43

RESULT 15
Q8GUP0 LACTC PRELIMINARY; PRT; 212 AA.
ID Q8GUP0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Deoxynucleoside kinase.
GN Name=dKb;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_Taxid=1359;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=MGI363;
RX MEDLINE=22670505; PubMed=12788700;

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RX DOI=10.1128/AEM.69.6.3069-3076.2003;
RA Sysbema W., Starrenburg M., Kleerebezem M., Mierau I., de Vos W.M.,
RA Hugenholtz J.;
RT "Increased production of folate by metabolic engineering of
RT Lactococcus lactis";
RL Appl. Environ. Microbiol. 69:3069-3076(2003).
DR EMBL; AY156932; AAN64310.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
DR GO; GO:0006133; F:nucleobase, nucleoside, nucleotide and nucl. . .; IEA.
DR InterPro; IPR002624; dmk.
DR Pfam; PF01712; dmk; 1.
KW Kinase.
SQ SEQUENCE 212 AA; 24738 MW; 3FD32A2A475CF708 CRC64;

Query Match 69.2%; Score 36; DB 2; Length 212;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEXP 7
DB 161 QVHNEXP 167

RESULT 16
Q7N3P6.PHOIL PRELIMINARY; PRT; 212 AA.
ID Q7N3P6.PHOIL PRELIMINARY; PRT; 212 AA.
AC Q7N3P6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphoribosylglycinamide formyltransferase 1 (GARF) (GAR
DE transformylase) (5'-phosphoribosylglycinamide transformylase).
GN Name=pun; OrderedLocNames=plu2761;
OS Photorhabdus luminescens (Subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OC NCBI_TaxID=141679;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=TT01;
RC MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA Duchaud E., Ruenloek C., Frangeul L., Buchrieser C., Glyaudan A.,
RA Taouit S., Bocs S., Boursaux-Bude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Deruelle S., Freyssinet G., Gaudault S.,
RA Medigue C., Lanois A., Powell K., Sigler P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RT Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571868; CAE15135.1; -; Genomic_DNA.
DR HSSP; P08179; IGAR.
DR Phocolat; plu2761; -.
DR GO; GO:0004644; F:phosphoribosylglycinamide formyltransferase. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006189; P:de novo IMP biosynthesis; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:000164; P:purine nucleotide biosynthesis; IEA.
DR InterPro; IPR002376; Formyl_transf_N.
DR InterPro; IPR001555; GARF AS.
DR InterPro; IPR004607; PurN trans.
DR Pfam; PR00551; Formyl_trans_N; 1.
DR PIRSF; PIRSF000413; GAR_Tfase; 1.
DR TIGRPFAM; TIGR00639; PurN; 1.
DR PROSITE; PS00373; GARF; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 212 AA; 23506 MW; 2791C85C6A6725B0 CRC64;

Query Match 69.2%; Score 36; DB 2; Length 212;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 QOHNEXP 8
DB 173 QVHNEXP 180

RESULT 17
Q58EU4.MOUSE PRELIMINARY; PRT; 238 AA.
ID Q58EU4.MOUSE PRELIMINARY; PRT; 238 AA.
AC Q58EU4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igr-C protease.
GN Name=Igr-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Colon;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.J.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Miliaty S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Colon;
RC NIH MGC Project;
RC Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091754; AAB91754.1; -; mRNA.
DR SMR; Q58EU4; 25-238.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00405; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN; 1.
SQ SEQUENCE 238 AA; 26440 MW; AE2B2BA90B9F7D5D CRC64;

Query Match 69.2%; Score 36; DB 2; Length 238;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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RESULT 18
 ID 065ZC9 HUMAN PRELIMINARY; PRT; 240 AA.
 AC 065ZC9;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Single-chain Fv (Fragment).
 GN Name=scFv;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C1q/7;
 RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
 RA Kontermann R.E., Wing M.G., Winter G.;
 RT "Complement recruitment using bispecific diabodies.";
 RL Nat. Biotechnol. 15:629-631(1997).
 DR EMBL: Y13056; CA73499.1; -, mRNA.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00406; IG; 2.
 DR PROSITE: PSS0835; IG_LIKE; 2.
 FT NON_TER 1
 FT TER 240
 SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 69.2%; Score 36; DB 2; Length 240;
 Best Local Similarity 66.7%; Pred. NO. 80;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNRYPLT 9
 ||:||||
 Db 221 QOYSNRYPLT 229

RESULT 19
 ID 065ZC8 HUMAN PRELIMINARY; PRT; 244 AA.
 AC 065ZC8;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Single-chain Fv (Fragment).
 GN Name=scFv;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
 RA Kontermann R.E., Wing M.G., Winter G.;
 RT "Complement recruitment using bispecific diabodies.";
 RL Nat. Biotechnol. 15:629-631(1997).
 DR EMBL: Y13057; CA73500.1; -, mRNA.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00406; IG; 2.
 DR PROSITE: PSS0835; IG_LIKE; 2.
 FT NON_TER 1
 FT TER 244
 SQ SEQUENCE 244 AA; 26127 MW; 4B1F17668338F2BF CRC64;

Query Match 69.2%; Score 36; DB 2; Length 244;

Best Local Similarity 66.7%; Pred. NO. 82;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNRYPLT 9
 ||:||||
 Db 225 QOYSNRYPLT 233

RESULT 20
 ID 096ZJ3 SULFO PRELIMINARY; PRT; 355 AA.
 AC 096ZJ3;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Hypothetical protein STR1842.
 GN OrderedLocusNames=STR1842;
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OC NCBI_TaxID=11955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takehashi M.,
 RA Sekine M., Baba S.-I., Anai A., Kosugi H., Hosooyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamaya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yamagishi M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL: BA000023; BAB6932.1; -, Genomic_DNA.
 DR InterPro: IPR005614; NRD.
 DR Pfam: PF03916; NRD; 1.
 DR Complete proteome; Hypothetical protein.
 SQ SEQUENCE 355 AA; 38407 MW; D748F63CB6139DB8 CRC64;

Query Match 69.2%; Score 36; DB 2; Length 355;
 Best Local Similarity 87.5%; Pred. NO. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNRYPL 8
 ||:||||
 Db 19 QOINRYPL 26

RESULT 21
 ID 07PYD2 ANOGA PRELIMINARY; PRT; 395 AA.
 AC 07PYD2;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE ENSANGP0000020799.
 GN ORNames=ENSANG00000018310;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OC NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (Apr-2003) to the EMBL/Genbank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAB01008987; EAA01664.1; -, Genomic_DNA.
 DR GO: GO:0005634; C:nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR011700; bZIP_2.
DR InterPro; IPR004827; TF_bZIP.
DR Pfam; PF07716; bZIP_2; 1.
DR PROSITE; PS50217; bZIP; 1.
DR PROSITE; PS00036; bZIP_BASIC; 1.
KW DNA-binding; Nuclear protein.
SQ SEQUENCE 395 AA; 43154 MW; 8A9870E4982A274F CRC64;

Query Match
Best Local Similarity 69.2%; Score 36; DB 2; Length 395;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEVPL 8
DB 187 QOHQOYPM 194

RESULT 22
Q5IGN5_ENTHI PRELIMINARY; PRT; 477 AA.
ID Q5IGN5_ENTHI
AC Q5IGN5;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE RING finger protein, putative.
GN ORFNames=2.t00075;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RC PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amodeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagers K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabbittowisch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N.G., Glitcher C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RT Nature 433:865-868 (2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SIMILARITY: contains 1 RING-type zinc finger.
CC EMBL; AAFB0100010; EAL5200.1; -; Genomic_DNA.
DR InterPro; IPR001841; Znf_RING.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Ubl conjugation pathway; Zinc; Zinc-finger.
SQ SEQUENCE 477 AA; 55112 MW; C409E8430AEDA9F9 CRC64;

Query Match
Best Local Similarity 69.2%; Score 36; DB 2; Length 477;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEVPLT 9
DB 19 EGHIEPPLT 27

RESULT 23
Q9FH77_ARATH PRELIMINARY; PRT; 571 AA.
ID Q9FH77_ARATH
AC Q9FH77;

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DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9E15
DE (Hypothetical protein) (At5g45330).
GN ORFNames=At5g45330;
OS Arabidopsis thaliana (Mouse ears cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RT DNA Res. 7:31-63 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Underwood B.A., Xiao Y., Moskal W., Monaghan E., Wang W., Redman J.,
RA Wu H.C., Unterback T., Town C.D.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Xiao Y., Underwood B., Moskal W., Wang W., Redman J., Wu H.C.,
RA Unterback T., Town C.D.;
RT "Reconstruction of cDNA sequences for hypothetical genes in
RT Arabidopsis thaliana from 5' and 3' RACE products.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Ecker J.R.;
RT "Arabidopsis cDNA clones." EMBL/GenBank/DBJ databases.
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020744; BAB10254.1; -; Genomic_DNA.
DR EMBL; AY954874; AAX5200.1; -; mRNA.
DR EMBL; AY735697; AAU44567.1; -; mRNA.
DR EMBL; BT022113; AAY34174.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 571 AA; 61798 MW; EACBFB2BC8706D43 CRC64;

Query Match
Best Local Similarity 69.2%; Score 36; DB 2; Length 571;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYP 7
DB 498 QOHNOFP 504

RESULT 24
Q17740_CAEEL PRELIMINARY; PRT; 641 AA.
ID Q17740_CAEEL
AC Q17740;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein C06G1.4.
GN ORFNames=C06G1.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Bristol N2;
RX MEDLINE=9906613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";

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RL Science 282:2012-2018(1998).
 DR EMBL; U41014; AAK32947.3; -; Genomic_DNA.
 DR PIR; T30077; T30077.
 DR Ensembl; C06G1.4; Caenorhabditis elegans.
 DR Wormbase; WBGene00015547; C06G1.4.
 DR Wormpep; C06G1.4; CE03967.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 641 AA; 70466 MW; 2BE1655143A10010 CRC64;

 Query Match 69.2%; Score 36; DB 2; Length 641;
 Best Local Similarity 62.5%; Pred. No. 2.6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 OOHNEHYPL 8
 |||:
 Db 156 QOHQOYPM 163

 RESULT 25
 PDB4D RAT STANDARD; PRT; 803 AA.
 ID P14270; Q35470; Q6TR10; Q8CG04; Q8CG06;
 AC 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-2005 (Rel. 46, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DN CAMP-specific 3', 5'-cyclic phosphodiesterase 4D (EC 3.1.4.17) (PDDE3).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RC NUCLEOTIDE SEQUENCE (ISOFORM 2), AND INDUCTION.
 RP TISSUE=Testis;
 RX MEDLINE=90046763; PubMed=2554303;
 RA Swinnen J.V., Joseph D.R., Conti M.;
 RT "The mRNA encoding a high-affinity CAMP phosphodiesterase is regulated
 by hormones and cAMP";
 RL J. Biol. Chem. 269:18271-18274(1994).
 RN [3]
 RP SEQUENCE REVISION TO 6.
 RA Conti M.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RC NUCLEOTIDE SEQUENCE (ISOFORM 1), AND NUCLEOTIDE
 RP SEQUENCE [MENA] OF 253-803 (ISOFORM 2).
 RX MEDLINE=95047482; PubMed=7958996; DOI=10.1016/0378-1119(94)90155-4;
 RA Bolger G.B., Rodgers L., Riggs M.;
 RT "Differential CNS expression of alternative mRNA isoforms of the
 mammalian genes encoding CAMP-specific phosphodiesterases";
 RL Gene 149:237-244(1994).
 RN [5]
 RC NUCLEOTIDE SEQUENCE (ISOFORMS 2 AND 3).
 RP STRAIN=Wistar;
 RX MEDLINE=94103234; PubMed=8276818;
 RA Monaco L., Vicini E., Conti M.;
 RT "Structure of two rat genes coding for closely related rolipram-
 sensitive CAMP phosphodiesterases. Multiple mRNA variants originate
 from alternative splicing and multiple start sites";
 RL J. Biol. Chem. 269:347-357(1994).
 RN [6]
 RP ERRATUM.
 RA Monaco L., Vicini E., Conti M.;
 RL J. Biol. Chem. 269:20806-20806(1994).
 RN [7]

RP NUCLEOTIDE SEQUENCE (ISOFORM 5).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA Jin S.-L.C., Kuo W.-P., Conti M.;
 RT "Characterization of a CAMP-specific phosphodiesterase variant
 (PDB4D4) expressed in the rat brain";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RC NUCLEOTIDE SEQUENCE (ISOFORMS 4 AND 7).
 RP STRAIN=Sprague-Dawley;
 RX MEDLINE=22718903; PubMed=12834813; DOI=10.1016/S0898-6568(03)00042-1;
 RA Wang D., Deng C., Bugaj-Gaweda B., Kwan M., Gunwaldsen C., Leonard C.,
 RA Xin X., Hu Y., Unterbeck A., De Vivo M.;
 RT "Cloning and characterization of novel PDB4D isoforms PDB4D6 and
 PDB4D7";
 RL Cell. Signal. 15:883-891(2003).
 RN [9]
 RC NUCLEOTIDE SEQUENCE (ISOFORM 6).
 RA Gaweda B., De Vivo M., Wang D.;
 RT "Novel PDB4D isoform, PDB4D9";
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RC NUCLEOTIDE SEQUENCE OF 224-672.
 RP TISSUE=Testis;
 RX MEDLINE=89315790; PubMed=2546153;
 RA Swinnen J.V., Joseph D.R., Conti M.;
 RT "Molecular cloning of rat homologues of the Drosophila melanogaster
 dunce CAMP phosphodiesterase: evidence for a family of genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
 RN [11]
 RP PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=9214625; PubMed=10187850; DOI=10.1074/jbc.274.15.10557;
 RA Liu H., Maurice D.H.;
 RT "Phosphorylation-mediated activation and translocation of the cyclic
 AMP-specific phosphodiesterase PDB4D3 by cyclic AMP-dependent protein
 kinase and mitogen-activated protein kinases. A potential mechanism
 allowing for the coordinated regulation of PDB4D activity and
 targeting";
 RL J. Biol. Chem. 274:10557-10565(1999).
 RN [12]
 RP SUBCELLULAR LOCATION, AND INTERACTION WITH THE CENTROSOME (ISOFORM 1).
 RX MEDLINE=21035570; PubMed=11285255; DOI=10.1074/jbc.C000911200;
 RA Tasken K.A., Collas P., Kemmer W.A., Witczak O., Conti M., Tasken K.;
 RT "Phosphodiesterase 4D and protein kinase a type II constitute a
 signaling unit in the centrosomal area";
 RL J. Biol. Chem. 276:21999-22002(2001).
 CC -1- FUNCTION: Regulates the levels of cAMP in the cell.
 CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 adenosine 5'-phosphate.
 CC -1- COFACTOR: Binds 2 divalent metal cations per subunit. Site 1 may
 preferentially bind zinc ions, while site 2 has a preference for
 magnesium and/or manganese ions (By similarity).
 CC -1- ENZYME REGULATION: Inhibited by rolipram. Activated by
 phosphatidic acid (by similarity).
 CC -1- PATHWAY: Cyclic nucleotide metabolism.
 CC -1- SUBUNIT: Homodimer for the long isoforms. Isoforms with truncated
 N-termini are monomeric. Binds ARRB2, PRKAR2B and AKAP9 (By
 ternary complex containing PRKAR2B, PRKAR2B and AKAP9 (By
 similarity)).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Found in the soluble fraction,
 associated with membranes, and associated with the cytoskeleton
 and the centrosome.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=7;
 CC Name=5; Synonyms=PDB4D4;
 CC IsoId=P14270-5; Sequence=Displayed;
 CC Name=1; Synonyms=PDB4D3, PDE3.3;
 CC IsoId=P14270-1; Sequence=VSP_012399, VSP_012399;
 CC Name=2; Synonyms=PDE3.1;
 CC IsoId=P14270-2; Sequence=VSP_004581;
 CC Name=3; Synonyms=PDE3.2;
 CC IsoId=P14270-3; Sequence=VSP_004582;
 CC Name=4; Synonyms=PDE4D7;
 CC IsoId=P14270-4; Sequence=VSP_012400, VSP_012401;

RX MEDLINE=22718903; PubMed=12834813; DOI=10.1016/S0898-6568(03)00042-1;
 RA Wang D., Deng C., Bugaj-Gawda B., Kwan M., Gunnwaldsen C., Leonard C.,
 RA Xin X., Hu Y., Unterbeck A., De Vivo M.;
 RT "Cloning and characterization of novel PDE4D isoforms PDE4D6 and
 RT PDE4D7.";
 RL Cell. Signal. 15:883-891(2003).
 [7]
 RX NUCLEOTIDE SEQUENCE (ISOPRIMS 10 AND 11).
 RA MEDLINE=22879938; PubMed=14517540; DOI=10.1038/ng1245;
 RA Greer-Schmidt S., Thorleifsson G., Reynisdottir S.T., Manolescu A.,
 RA Jonsdottir S., Jonsdottir T., Gudmundsdottir T., Bjarnadottir S.M.,
 RA Binarsson O.B., Gudmundsdottir H.M., Hawkins M., Gudmundsson G.,
 RA Gudmundsdottir H., Andarson H., Gudmundsdottir A.S.,
 RA Steindardottir M., Chou T.T., Namias J., Goss S.,
 RA Sveinbjornsdottir S., Valdimarsson E.M., Jakobsson F., Agnarsson U.,
 RA Gudnason V., Thorleifsson G., Fingler J., Gurney M., Gudjartsson D.,
 RA Frigge M.L., Kong A., Stefansson K., Gulcher J.R.;
 RT "The gene encoding phosphodiesterase 4D confers risk of ischemic
 RT stroke.";
 RL Nat. Genet. 35:131-138(2003).
 [8]
 RX NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOPRIM 8).
 RA TISSUE=Testis;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marisana K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Umed T.B., Tohyuki S., Carninci P., Prange C.,
 RA Raha S.A., Loughellano N.A., Peters G.J., Abramson R.D., Mlady S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [9]
 RX INTERACTION WITH GNB2L1.
 RA PubMed=12193273;
 RA Bolger G.B., McCallill A., Yarwood S.J., Steele M.S., Warwicker J.,
 RA Houslay M.D.;
 RT "Delineation of RA1D1, the RACK1 interaction domain located within the
 RT unique N-terminal region of the cAMP-specific phosphodiesterase,
 RT PDE4D5.";
 RL BMC Biochem. 3:24-24(2002).
 [10]
 RX INTERACTION WITH ARRB2, AND SUBCELLULAR LOCATION.
 RA PubMed=14500724; DOI=10.1074/jbc.M303772200;
 RA Bolger G.B., McCallill A., Huston E., Cheung Y.F., McSorley T.,
 RA Baillye G.S., Houslay M.D.;
 RT "The unique amino-terminal region of the PDE4D5 cAMP phosphodiesterase
 RT isoform confers preferential interaction with beta-arrestins.";
 RL J. Biol. Chem. 278:49230-49238(2003).
 [11]
 RX HOMODIMERIZATION OF LONG ISOPRIMS, ENZYME REGULATION BY ROLIPRAM AND
 RP PHOSPHATIDIC ACID, AND PHOSPHORYLATION SITE SER-53 (ISOPRIM 2).
 RA PubMed=15131123; DOI=10.1074/jbc.M312687200;
 RA Richter W., Conti M.;
 RT "The oligomerization state determines regulatory properties and
 RT inhibitor sensitivity of type 4 cAMP-specific phosphodiesterases.";
 RL J. Biol. Chem. 279:30338-30348(2004).
 [12]
 RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 388-715 IN COMPLEX WITH THE
 RP INHIBITOR ZARDANERINE AND DIVALENT METAL IONS, AND MUTAGENESIS OF
 RP ASP-527 AND ARG-563.

RX PubMed=12387865; DOI=10.1016/S0014-5793(02)03363-3;
 RA Lee M.E., Markowitz J., Lee J.-O., Lee H.;
 RT "Crystal structure of phosphodiesterase 4D and inhibitor complex.";
 RL FEBS Lett. 530:53-58(2002).
 [13]
 RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 381-739 IN COMPLEX WITH CAMP
 RP AND DIVALENT METAL IONS.
 RA PubMed=14609333; DOI=10.1021/bi034653e;
 RA Hual O., Colicelli J., Ke H.;
 RT "The crystal structure of AMP-bound PDE4 suggests a mechanism for
 RT phosphodiesterase catalysis.";
 RL Biochemistry 42:13220-13226(2003).
 [14]
 RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 381-739 IN COMPLEX WITH
 RP INHIBITOR.
 RA PubMed=12842049; DOI=10.1016/S0969-2126(03)00123-0;
 RA Hual O., Wang H., Sun Y., Kim H.Y., Liu Y., Ke H.;
 RT "Three-dimensional structures of PDE4D in complex with rolipram and
 RT implication on inhibitor selectivity.";
 RL Structure 11:865-873(2003).
 [15]
 RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 381-714 IN COMPLEX WITH METAL
 RP IONS AND INHIBITOR.
 RA PubMed=14683322; DOI=10.1074/jbc.M311556200;
 RA Hual O., Liu Y., Francis S.H., Corbin J.D., Ke H.;
 RT "Crystal structures of phosphodiesterases 4 and 5 in complex with
 RT inhibitor 3-isobutyl-1-methylxanthine suggest a conformation
 RT determinant of inhibitor selectivity.";
 RL J. Biol. Chem. 279:13095-13101(2004).
 [16]
 RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 380-756 IN COMPLEX WITH AMP;
 RP METAL IONS AND THE INHIBITOR ROLIPRAM.
 RA PubMed=15003452; DOI=10.1016/j.jmb.2004.01.040;
 RA Xu R.X., Rocque W.J., Lambert M.H., Vanderwall D.E., Luther M.A.,
 RA Nolte R.T.;
 RT "Crystal structures of the catalytic domain of phosphodiesterase 4B
 RT complexed with AMP, 8-Br-AMP, and rolipram.";
 RL J. Mol. Biol. 337:355-365(2004).
 CC -1- FUNCTION: Regulates the levels of cAMP in the cell.
 CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 CC adenosine 5'-phosphate.
 CC -1- COFACTOR: Binds 2 divalent metal cations per subunit. Site 1 may
 CC preferentially bind zinc ions, while site 2 has a preference for
 CC magnesium and/or manganese ions.
 CC -1- ENZYME REGULATION: Inhibited by rolipram. Activated by
 CC phosphatidic acid.
 CC -1- PATHWAY: Cyclic nucleotide metabolism.
 CC -1- SUBUNIT: Homodimer for the long isoforms. Isoforms with truncated
 CC N-termini are monomeric. Isoform 2 is part of a ternary complex
 CC containing PKAR2A, PKAR2B and AKAP9 (by similarity). Isoform 5
 CC binds GNB2L1 via its unique N-terminus. Binds ARRB2.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Found in the soluble fraction,
 CC associated with membranes, and associated with the cytoskeleton
 CC and the centrosome (by similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=11;
 CC Name=1; Synonyms=hPDE4D4;
 CC Name=2; Synonyms=hPDE4D3;
 CC Name=3; Synonyms=hPDE4D2;
 CC Name=4; Synonyms=hPDE4D1;
 CC Name=5; Synonyms=hPDE4D0;
 CC Name=6; Synonyms=hPDE4D5;
 CC Name=7; Synonyms=hPDE4D6;
 CC Name=8; Synonyms=hPDE4D7;
 CC Name=9; Synonyms=hPDE4D8;
 CC Name=10; Synonyms=hPDE4D9;
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Db :|||||
36 EQHNGYPL 43

RESULT 27
CHS1_PHYBL STANDARD; PRT; 841 AA.
ID CHS1_PHYBL
AC P87073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Chitin synthase 1 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl transferase 1) (Class-II chitin synthase 1).
GN Name=chsl;
OS Phycomyces blakesleeanus.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae; Phycomyces.
OX NCBI_TaxID=4837;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NRRL 1555;
RA Miyazaki A., Ootaki T.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE OF 172-370.
RC STRAIN=NRRL 1555;
RA MEDLINE=94063507; PubMed=8244024; DOI=10.1016/0378-1119(93)90186-7; Miyazaki A., Komany M., Szanislo P.J., Jayaram M., Ootaki T.;
RT "Chitin synthase-encoding gene(s) of the Zygomycete fungus Phycomyces blakesleeanus.";
RL Gene 134:129-134 (1993).
CC -!- FUNCTION: Plays a major role in cell wall biogenesis.
CC -!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + (1,4-(N-acetyl-beta-D-glucosaminyl)) (n) = UDP + (1,4-(N-acetyl-beta-D-glucosaminyl)) (n+1).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -!- SIMILARITY: Belongs to the chitin synthase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR EMBL; AB003043; BA19857.1; -; Genomic_DNA.
DR PIR; J07067; J07067.
DR InterPro; IPR004834; Chitin_synth.
DR InterPro; IPR001173; Glyco_trans_2.
DR Pfam; PF01644; Chitin_synth_1; 1.
DR ProDom; PD002998; Chitin_synth; 1.
KW Cell wall; Glycosyltransferase; Multigene family; Transferase; Transmembrane.
KM
FT TRANSMEM 302 322 Potential.
FT TRANSMEM 385 405 Potential.
FT TRANSMEM 526 546 Potential.
FT TRANSMEM 564 584 Potential.
FT TRANSMEM 602 622 Potential.
FT TRANSMEM 644 664 Potential.
FT TRANSMEM 673 693 Potential.
FT TRANSMEM 778 798 Potential.
FT TRANSMEM 816 836 Potential.
FT TRANSMEM 179 179 E -> EDE (in Ref. 2).
FT TRANSMEM 199 200 RV -> HI (in Ref. 2).
FT TRANSMEM 352 352 A -> G (in Ref. 2).
FT TRANSMEM 841 AA; 95227 MM; 71CD6C09ACB658B CRC64;
SQ SEQUENCE

Query Match 69.2%; Score 36; DB 1; Length 841;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYPL 8
Db 7 QEHNGYPL 14

RESULT 28
Q750F1_ASHGO PRELIMINARY; PRT; 851 AA.
ID Q750F1_ASHGO
AC Q750F1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE AGR004WD
GN Name=AGR004W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S., Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavler A., Rafferty T.D., Phillipsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient Saccharomycetes cerevisiae genome.";
RT Science 304:304-307 (2004).
DR EMBL; AE016820; AAS54493.1; -; Genomic_DNA.
DR AGD; AGR004W; -.
DR GO; GO:0005643; C:nuclear pore; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007231; NTC.
DR PANTHER; PTHR11225; NTC; 1.
DR Pfam; PF04097; NTC; 1.
KW Complete proteome.
SQ SEQUENCE 851 AA; 97531 MM; F72647958B71292C CRC64;

Query Match 69.2%; Score 36; DB 2; Length 851;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOHNEYPL 9
Db 232 QHNNFPL 240

RESULT 29
Q86M49_DICDI PRELIMINARY; PRT; 986 AA.
ID Q86M49_DICDI
AC Q86M49;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tyrosine phosphatase CDC25.
GN Name=cdc25;
OS Dictyostellium discoideum (slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ax-2;
RA Mayanagi T., Maeda Y., Hirose S., Arakane T., Araki T., Amagai A.;
RT "Cloning, sequencing, and expression of the genomic DNA encoding the protein phosphatase cdc25 in Dictyostellium discoideum.";
RL Dev. Genes Evol. 214:510-514 (2004).
DR EMBL; AB039883; BAC6469.2; -; Genomic_DNA.
DR DictyBase; DDB0191424; cdc25.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0007049; P:cell cycle; IEA.
DR GO; GO:0009010; P:cytokinesis; IEA.
DR GO; GO:0007067; P:mitosis; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000751; MPl_phosphatase.

DR InterPro: IPR001763; Rhodanese-like.
DR Pfam: PF00581; Rhodanese; 1.
DR PRINTS: PRO0716; MRIPHPHASE.
DR SMART: SM00450; RHOD; 1.
DR PROSITE: PSS0206; RHODANASE_3; 1.
DR SEQUENCE 986 AA; 10953 MW; 2900DE66C98C080 CRC64;

Query Match
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYP 7
: : : : :
Db 909 REHNEYP 915

RESULT 30
Q4MWV7_ASPFU PRELIMINARY; PRT; 1042 AA.
ID Q4MWV7_ASPFU PRELIMINARY;
AC Q4MWV7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Nontubosomal peptidyl synthase (NRPS), putative.
OS ORFNames=Afu6g08560;
OC Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NC NCB1_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nieman W., Pain A., Anderson M.J., Mortman J., Kim H. Stanley.,
RA Artroya J., Berriam M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horthuch H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Latton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Kumasos W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penava M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajadream M.-A., Reichard U.,
RA Renald H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Roming C.M., Ruter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferreiro J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrett B., Denning D.W.,
RT "Genomic sequence of the pathogenic and allegermic filamentous fungus
Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL:AAHFP0100006; EML88707.1; -, Genomic DNA.
SQ SEQUENCE 1042 AA; 115167 MW; F4D80F6F4FF52495 CRC64;

Query Match
Best Local Similarity 69.2%; Score 36; DB 2; Length 1042;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP 9
: : : : :
Db 172 QOHNEYP 180

RESULT 31
Q54QM6_DICDI
ID Q54QM6_DICDI PRELIMINARY; PRT; 1053 AA.
AC Q54QM6;

DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Tyrosine phosphatase.
CN Name=cdc25; ORFNames=DOB0191424;
OS Dictyostelium discoideum (slime mold).
OC Eukaryota; Metazoa; Dictyostelida; Dictyostelium.
NC NCB1_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajadream M.-A.,
RA Sugang R., Berriam M., Song J., Olsen R., Szatranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Fardouther P., Desany B., Just E., Morio T., Rost R., Chircher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchleser C.,
RA Wardrop A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegged H., Mungall K., Oliver K., Price C., Quail M.A., Sanders M.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Rivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shalinsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrett B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum.";
RL Nature 0:0-0(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL:AAHFP0100003; EAL5575.1; -, Genomic DNA.
SQ SEQUENCE 1053 AA; 117118 MW; F528DD893056A22B CRC64;

Query Match
Best Local Similarity 71.4%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYP 7
: : : : :
Db 976 REHNEYP 982

RESULT 32
Q8C5X1_MOUSE PRELIMINARY; PRT; 1059 AA.
ID Q8C5X1_MOUSE PRELIMINARY;
AC Q8C5X1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-UN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4931406P16 product:hypothetical protein, full insert
DE sequence.
GN Name=4931406P16R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NC NCB1_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=92779253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT Carninci P., Hayashizaki Y.;
RL "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi Y., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaubawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RA Nature 409:685-690 (2001).
RL [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RL [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RL [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=1076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RL [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi T., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hangaki T., Hara A., Hayatsu N., Hizamoto K., Hirooka T., Hori F.,
RA Imocani K., Ishii Y., Itoh M., Izawa M., Kaubawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito K., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamanka I., Yasunishi A.,
RA Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK076994; BAC3655.1; -; mRNA.
DR MGI; MGI:1924311; 4931406P16Rik.
KM Hypothetical protein.
SQ SEQUENCE 1059 AA; 115622 MW; 7ACB833CC6A0A21 CRC64;

Query Match 69.2%; Score 36; DB 2; Length 1059;
Best local Similarity 62.5%; Pred. No. 4.7e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 OOHNEVPL 8
Db 27 OOHQOYPM 34
RESULT 33
O6PAL5 MOUSE PRELIMINARY; PRT; 1059 AA.
ID O6PAL5_MOUSE
AC O6PAL5_MOUSE
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE RIKEN cDNA 4931406P16.
GN Name=4931406P16Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RL [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.O., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield J.S.N., Krzywinski M.T., Sklajala U., Smalins D.E.,
RA Schnerch A., Schin U.E., Jones S.J.W., Merra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC060233; AAH60233.1; -; mRNA.
DR MGI; MGI:1924311; 4931406P16Rik.
SQ SEQUENCE 1059 AA; 115621 MW; 742B833C26600A2B CRC64;
Query Match 69.2%; Score 36; DB 2; Length 1059;
Best local Similarity 62.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 OOHNEVPL 8
Db 27 OOHQOYPM 34
RESULT 34
Y0355_HUMAN STANDARD; PRT; 1070 AA.
ID Y0355_HUMAN
AC O15063;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein KIAA0355.
GN Name=KIAA0355;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=9749984; PubMed=9205841;
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
 Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. VII.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 4:141-150(1997).

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR EMBL: AB002353; BAA20812.2; ALT INT; mRNA.
 DR Ensembl: ENSG00000166398; Homo sapiens.
 DR HGNC: HGNC:29016; KIA0355.
 KW Hypothetical protein.
 FT COMPBIAS 551 555 Poly-Ser.
 FT COMPBIAS 695 700 Poly-Pro.
 FT COMPBIAS 1037 1044 Poly-Pro.
 SQ SEQUENCE 1070 AA; 116048 MW; 2D35C127C5EBA2F7 CRC64;

Query Match 69.2%; Score 36; DB 1; Length 1070;
 Best Local Similarity 62.5%; Pred. No. 4.8e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 OOHNEYPYL 8
 |||:|:
 DB 27 OOHQOYPM 34

RESULT 35
 Q5REB5_PONPY PRELIMINARY; PRT; 1070 AA.
 ID Q5REB5_PONPY PRELIMINARY;
 AC Q5REB5;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein DKF2p469A1915.
 GN Name=DKF2p469A1915;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney.
 RG The German cDNA Consortium;
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR857584; CAH89862.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 1070 AA; 116099 MW; 0D2212DDP50005D CRC64;

Query Match 69.2%; Score 36; DB 2; Length 1070;
 Best Local Similarity 62.5%; Pred. No. 4.8e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 OOHNEYPYL 8
 |||:|:
 DB 27 OOHQOYPM 34

RESULT 36
 Q4R3A1_MACPA PRELIMINARY; PRT; 1070 AA.
 ID Q4R3A1_MACPA PRELIMINARY;
 AC Q4R3A1;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Testis cDNA clone: QbsA-18369, similar to human KIA0355
 DE (KIA0355).
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA International consortium for macaque cDNA sequencing, analysis;
 RT "DNA sequences of macaque genes expressed in brain or testis and its
 RT evolutionary implications.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.
 RA Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
 RA Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
 RT "Substitution rate and structural divergence of 5'UTR evolution:
 RT Comparative analysis between human and cynomolgus monkey cDNAs.";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB179365; BAB02416.1; -; mRNA.
 SQ SEQUENCE 1070 AA; 116139 MW; 365B121F2748D05D CRC64;

Query Match 69.2%; Score 36; DB 2; Length 1070;
 Best Local Similarity 62.5%; Pred. No. 4.8e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 OOHNEYPYL 8
 |||:|:
 DB 27 OOHQOYPM 34

RESULT 37
 Q54MU4_DICDI PRELIMINARY; PRT; 1133 AA.
 ID Q54MU4_DICDI PRELIMINARY;
 AC Q54MU4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=DDB0186641;
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AX4;
 RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugeng R., Bertrian M., Song J., Olsen R., Szatranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
 RA Banker A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fay P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhrouc A., Nie X., Hall N., Anjard C., Hemphill L., Bacon N.,
 RA Farbrother P., Desany B., Just E., Morio T., Roit R., Churcher C.,
 RA Cooper J., Haydock T., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Moutier S., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Oules W., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardrop A., Felder M., Tangavelu M., Johnson D., Knights A.,
 RA Loulsegue H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Splegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Minckler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
 RA Chisnoim R.L., Gibbs R., Loomis W.F., Plutzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
 RT "The genome of the social amoeba Dictyostelium discoideum.";


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RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Ceiniker S., Carlson J., Wan K., Pfeiffer B., Fries E., George R.,
RA Hoskins R., Stapleton M., Paclad J., Park S., Switkas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- INTERACTION:
CC Q9W3J9:CG2116; NBExp=1; IntAct=EBI-109238, EBI-98170;
CC EMBL: AE003487; AAF48114.1; -; Genomic_DNA.
DR IntAct; Q9W3J9;
DR Ensembl; CG15737; Drosophila melanogaster.
DR FlyBase; FBgn030353; CG15737.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001201; PAP_25A core.
DR InterPro; IPR02058; PAP_aasec.
DR Pfam; PF03828; PAP_aasec.1
SQ SEQUENCE 1373 AA; 151311 MW; 348BC66BF5239BAE CRC64;

Query Match
Best Local Similarity 69.2%; Score 36; DB 2; Length 1373;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNHYPL 7
DB 398 QOHNHYPL 404

RESULT 40
ID KV3K_MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-II1 region PC 4050.
OS Mus musculus (Mouse).
OC Buckyota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Ioh E., Schilling J., Hood L.B.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity."
RL Nature 276:785-790(1978).
CC -----
CC CC This Swiss-Pro entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P01665; 1QNZ.
DR SMR; P01663; 1-111.
DR Ensembl; ENSMUSG0000006064; Mus musculus.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 38 Complementarity-determining-1.
FT REGION 39 53 Framework-2.
FT REGION 54 60 Complementarity-determining-2.

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FT REGION 61 92 Framework-3.
FT REGION 93 101 Complementarity-determining-3.
FT REGION 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match
Best Local Similarity 67.3%; Score 35; DB 1; Length 111;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNHYPL 9
DB 93 QOHNHYPL 101

RESULT 41
ID Q926L4_LISIN PRELIMINARY; PRT; 123 AA.
AC Q926L4;
DT 01-DEC-2001 (TRENDELREL. 19, Created)
DT 01-DEC-2001 (TRENDELREL. 19, Last sequence update)
DT 01-JUN-2003 (TRENDELREL. 24, Last annotation update)
DE P110046 protein.
GN OrderedLocustNames=pli0046;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangoul L., Buchrieser C., Rusnok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouni F., Couve E., de Darvar A., Deboux P.,
RA Domain E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunat F., Kuzepkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.;
RT "Comparative genomics of Listeria species."
RL Science 294:849-852(2001).
DR EMBL; AL592102; CAC42044.1; -; Genomic_DNA.
KW Complete proteome; Plasmid.
SQ SEQUENCE 123 AA; 14593 MW; 7A4656B06164EB14 CRC64;

Query Match
Best Local Similarity 67.3%; Score 35; DB 2; Length 123;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNHYPL 8
DB 115 KKHNYPL 122

RESULT 42
ID Q5HBT4_ERROR PRELIMINARY; PRT; 210 AA.
AC Q5HBT4;
DT 10-MAY-2005 (TRENDELREL. 30, Created)
DT 10-MAY-2005 (TRENDELREL. 30, Last sequence update)
DT 10-MAY-2005 (TRENDELREL. 30, Last annotation update)
DE Endonuclease III (EC 4.2.99.18).
GN Name=nh; OrderedLocustNames=Brum2430;
OS Ehrlichia ruminantium (strain Welgevonden).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Ehrlichia.
OC NCBI_TaxID=254945;
RN [1]

```

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed15637156; DOI=10.1073/pnas.0406631102;
 RA Collins N.E., Libenberg U., de Villiers E.P., Brayton K.A., Louw E.,
 RA Pretorius A., Raber F.E., van Heerden H., Josemans A., van Kleef M.,
 RA Steyn H.C., van Strijp M.F., Zweygarch E., Jongejan F., Mailhard J.C.,
 RA Berthier D., Botha M., Joubert F., Corton C.H., Thomson N.R.,
 RA Allsopp M.T., Allsopp B.A.;
 RT "The genome of the heartwater agent Ehrlichia ruminantium contains
 multiple tandem repeats of actively variable copy number.";
 RL Proc. Natl. Acad. Sci. U.S.A. 102:838-843 (2005).
 DR EMBL: CR767821; CAH57960.1; -; Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003906; F:DNA-(apurinic or apyrimidinic site) lyase a. . .; IEA.
 DR GO: GO:0004519; F:endonuclease activity; IEA.
 DR GO: GO:0005506; F:iron ion binding; IEA.
 DR GO: GO:0016829; F:lyase activity; IEA.
 DR GO: GO:0006284; F:base-excision repair; IEA.
 DR InterPro: IPR004035; EndoIII_FCL.
 DR InterPro: IPR003265; Endo_3c.
 DR InterPro: IPR003651; Fes_Bind.
 DR InterPro: IPR00445; Hnh.
 DR InterPro: IPR005759; Nth.
 DR Pfam: PF00633; HHH; 1.
 DR Pfam: PF00730; HNH-GPD; 1.
 DR SMART: SM00478; ENDO3C; 1.
 DR SMART: SM00525; FES; 1.
 DR TIGRFAMs: TIGR01083; nth; 1.
 DR PROSITE: PS00764; ENDONUCLEASE_III_1; 1.
 DR Complete proteome; Endonuclease; Lyase.
 KW SEQUENCE 210 AA; 23856 MW; B3442PD1PD25838B CRC64;

Query Match 67.3%; Score 35; DB 2; Length 210;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNEXP 7
 Db 14 QEHNHYP 20

RESULT 43
 OSFHC6_EHRRG PRELIMINARY; PRT; 211 AA.
 ID OSFHC6_EHRRG PRELIMINARY;
 AC OSFHC6;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Endonuclease III.
 GN Name=nth; OrderedLocustNames=ERGA_CDS_02430;
 OS Ehrlichia ruminantium (strain Gardel).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 OC NCBI_TaxID=302409;
 OX NCBI_TaxID=302409;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Gardel;
 RA Frutos R., Ferraz C., Bensaid A., Eychenie S., Kandassami Y.,
 RA Chantal I., Morgat A., Coissac E., Vachery N., Demaille J., Viari A.,
 RA Martinez D.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR925677; CA127695.1; -; Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003906; F:DNA-(apurinic or apyrimidinic site) lyase a. . .; IEA.
 DR GO: GO:0004519; F:endonuclease activity; IEA.
 DR GO: GO:0005506; F:iron ion binding; IEA.
 DR GO: GO:0006284; F:base-excision repair; IEA.
 DR InterPro: IPR004035; EndoIII_FCL.
 DR InterPro: IPR003265; Endo_3c.
 DR InterPro: IPR003651; Fes_Bind.
 DR InterPro: IPR005759; Nth.
 DR Pfam: PF00730; Hnh-GPD; 1.
 DR SMART: SM00478; ENDO3C; 1.
 DR SMART: SM00525; FES; 1.
 DR SMART: SM00525; FES; 1.

DR TIGRFAMs: TIGR01083; nth; 1.
 DR PROSITE: PS00764; ENDONUCLEASE_III_1; 1.
 KW Complete proteome; Endonuclease.
 SQ SEQUENCE 211 AA; 24009 MW; 1F7DAD9E7B3E58B CRC64;

Query Match 67.3%; Score 35; DB 2; Length 211;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNEXP 7
 Db 15 QEHNHYP 21

RESULT 44
 OSF34_EHRRW PRELIMINARY; PRT; 211 AA.
 ID OSF34_EHRRW PRELIMINARY;
 AC OSF34;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Endonuclease III.
 GN Name=nth; OrderedLocustNames=ERWE_CDS_02470;
 OS Ehrlichia ruminantium (strain Weigevonden).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Anaplasmataceae; Ehrlichia.
 OC NCBI_TaxID=254945;
 OX NCBI_TaxID=254945;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Weigevonden;
 RA Frutos R., Ferraz C., Bensaid A., Eychenie S., Kandassami Y.,
 RA Chantal I., Morgat A., Coissac E., Vachery N., Demaille J., Viari A.,
 RA Martinez D.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR925678; CA126741.1; -; Genomic_DNA.
 DR GO: GO:0005622; C:intracellular; IEA.
 DR GO: GO:0003906; F:DNA-(apurinic or apyrimidinic site) lyase a. . .; IEA.
 DR GO: GO:0004519; F:endonuclease activity; IEA.
 DR GO: GO:0005506; F:iron ion binding; IEA.
 DR GO: GO:0006284; F:base-excision repair; IEA.
 DR InterPro: IPR004035; EndoIII_FCL.
 DR InterPro: IPR003265; Endo_3c.
 DR InterPro: IPR003651; Fes_Bind.
 DR InterPro: IPR00445; Hnh.
 DR InterPro: IPR005759; Nth.
 DR Pfam: PF00633; HHH; 1.
 DR Pfam: PF00730; HNH-GPD; 1.
 DR SMART: SM00478; ENDO3C; 1.
 DR SMART: SM00525; FES; 1.
 DR TIGRFAMs: TIGR01083; nth; 1.
 DR PROSITE: PS00764; ENDONUCLEASE_III_1; 1.
 DR Complete proteome; Endonuclease; Lyase.
 KW SEQUENCE 211 AA; 23987 MW; A360CC57D639CD08 CRC64;

Query Match 67.3%; Score 35; DB 2; Length 211;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNEXP 7
 Db 15 QEHNHYP 21

RESULT 45
 O4KM66_RAT PRELIMINARY; PRT; 234 AA.
 ID O4KM66_RAT PRELIMINARY;
 AC O4KM66;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=thymus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh P.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC098746; AAH98746.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25692 MW; DPA12A3F8801666D CRC64;

Query Match 67.3%; Score 35; DB 2; Length 234;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 OOHNEPPLT 9
 DB 109 OQNNYPTWT 117

RESULT 46
 OS 0569Y8_MOUSE PRELIMINARY; PRT; 237 AA.
 ID 0569Y8_MOUSE PRELIMINARY; PRT; 237 AA.
 AC 0569Y8;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Iqg-C protein.
 GN Name=Iqg-C;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh P.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092251; AAH92251.1; -; mRNA.
 DR SMR; 0569Y8; 23-237.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003606; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_MHC; UNKNOWN 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 237 AA; 25978 MW; A88596AA47FFB932 CRC64;

Query Match 67.3%; Score 35; DB 2; Length 237;
 Best Local Similarity 77.8%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 OOHNEPPLT 9
 DB 112 OQNNYPTWT 120

RESULT 47
 OS 017228_CABEL PRELIMINARY; PRT; 270 AA.
 ID 017228_CABEL PRELIMINARY; PRT; 270 AA.
 AC 017228;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein M01D1.7.
 GN ORFNames=M01D1.7;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99063613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; AF025461; AAB70993.1; -; Genomic_DNA.
 DR PIR; F88035; F88035.
 DR Ensemble; M01D1.7; Caenorhabditis elegans.
 DR WormBase; WBGene00019702; M01D1.7.
 DR WormPep; M01D1.7; CE12254.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR PROSITE; PS50181; FBOX; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 270 AA; 30986 MW; 04D754EA7D62B5F8 CRC64;

Query Match 67.3%; Score 35; DB 2; Length 270;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 OHNEYP 7
:|||||
DB 85 EHNEYP 90

RESULT 48

Q5FWX9_ARATH PRELIMINARY; PRT; 290 AA.

AC Q5FWX9; 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE T14P4.13 protein.

GN Name=T14P4.13;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI_TaxId=3702;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., S.,

RA Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,

RA Buehler E., Chao Q., Chin C., Chion J., Choi E., Gonzalez A.,

RA Hong B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,

RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,

RA Toriumi M., Vaynsberg M., Yu G., Ecker J., Theologis A., Davis R.W.,

RA Submitted (SEP-2000) to the EMBL/GenBank/DBS databases.

RL EMBL; AC022521; MAG10629.1; -; Genomic DNA.

DR PIR; G86155; G86155.

SQ SEQUENCE 290 AA; 33803 MW; 2884419A5866A740 CRC64;

Query Match 67.3%; Score 35; DB 2; Length 290;

Best Local Similarity 75.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OHNEYP 8
:|||||
DB 87 QOHNEYP 94

RESULT 49

Q8R6G2_FUSNN PRELIMINARY; PRT; 290 AA.

AC Q8R6G2; 01-JUN-2002 (TRENBLrel. 21, Created)

DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Oxidoreductase (EC 1.1.1.-).

GN OrderedCusNames=FN1688;

OS Fusobacterium nucleatum (subsp. nucleatum).

OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;

OC Fusobacterium.

OX NCBI_TaxId=76856;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA STRAIN=ATCC 25586;

RA MEDLINE=2186394; PubMed=11889109;

RA DOI=10.1128/JB.184.7.2005-2018.2002;

RA Kapural V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,

RA Larsen N., D'Souza M., Malunas T., Puech G., Haasekorn R.,

RA Fongstein M., Kyriades N.C., Overbeek R.;

RA "Genome sequence and analysis of the oral bacterium Fusobacterium

RT nucleatum strain ATCC 25586."

RL J. Bacteriol. 184:2005-2018(2002).

DR EMBL; AEO09951; AAL93803.1; -; Genomic DNA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR InterPro; IPR001395; AldoKet_red.

DR Pfam; PF00248; AldoKet_red; I.

DR PRINTS; PR00069; ALDKETRDYASE.

DR ProDom; PD000288; AldoKet_red; 1.
SQ Complete proteome; Oxidoreductase.
SEQUENCE 290 AA; 33506 MW; EA7068413108B713 CRC64;

Query Match 67.3%; Score 35; DB 2; Length 290;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OHNEYP 7
:|||||
DB 193 KOHNKYP 199

RESULT 50

Q5AXE7_EMENI PRELIMINARY; PRT; 294 AA.

AC Q5AXE7; 10-MAY-2005 (TRENBLrel. 30, Created)

DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)

DE Hypothetical protein.

GN ORFNames=AN7033.2;

OS Aspergillus nidulans FGSC A4.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiiales; Trichocomaceae; Emicella.

OX NCBI_TaxId=227321;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA STRAIN=FGSC A4;

RA Birren B., Nudbaum C., Abouelleil A., Allen N., Anderson S.,

RA Archachl H.M., Barina N., Bastien V., Bloom T., Boguslavsky J.,

RA Bouchgaltier B., Butler J., Calvo S.E., Camarata J., Chang Y.,

RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArliano K.,

RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,

RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,

RA Garipya S., Gierre S., Graham L., Grand-Pierre N., Hafez N.,

RA Hagopian D., Hages B., Hall J., Horton L., Hulme W., Iliev I.,

RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,

RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,

RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,

RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Menus L.,

RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,

RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,

RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,

RA Rachupka A., Ramsamy U., Raymond C., Retta R., Rise C., Rogov P.,

RA Roman J., Schauer S., Schupack R., Seaman S., Severy P., Smirnov S.,

RA Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M.,

RA Talamas J., Testaye S., Theodore J., Totham K., Travers M.,

RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,

RA Wu X., Wyman D., Young G., Zainoun J., Zemek L., Zimmer A., Zody M.,

RA Lander E.;

RT "Genome Sequence of Aspergillus nidulans."

RL Submitted (JAN-2004) to the EMBL/GenBank/DBS databases.

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBS whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AACD01000117; EAA61679.1; -; Genomic DNA.

KW Hypothetical protein.

SQ SEQUENCE 294 AA; 33212 MW; 6CD2209842E5CB38 CRC64;

Query Match 67.3%; Score 35; DB 2; Length 294;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 OHNEYP 9
:|||||
DB 11 ESHGYP 19

Search completed: January 17, 2006, 12:07:02
Job time : 74.7273 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:50:24 ; Search time 15.5455 Seconds
(without alignments)
47.865 Million cell updates/sec

Title: US-10-665-658-15
Perfect score: 52
Sequence: 1 OOHNEYPLR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCOMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52	100.0	9	2	US-08-974-899-15	Sequence 15, Appl
2	52	100.0	9	2	US-09-795-798-15	Sequence 15, Appl
3	52	100.0	108	2	US-08-974-899-1	Sequence 1, Appl
4	52	100.0	108	2	US-08-974-899-2	Sequence 2, Appl
5	52	100.0	108	2	US-09-795-798-1	Sequence 1, Appl
6	52	100.0	108	2	US-09-795-798-2	Sequence 2, Appl
7	52	100.0	109	2	US-09-027-449-47	Sequence 47, Appl
8	52	100.0	109	2	US-08-804-444A-47	Sequence 47, Appl
9	52	100.0	109	2	US-09-026-985-47	Sequence 47, Appl
10	52	100.0	109	2	US-09-121-952A-47	Sequence 47, Appl
11	52	100.0	109	2	US-09-234-340A-47	Sequence 47, Appl
12	52	100.0	109	2	US-09-355-014-47	Sequence 47, Appl
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15	41	78.8	102	2	US-09-905-243-80	Sequence 80, Appl
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120	34	65.4	109	4	US-09-232-290-7	Sequence 7, Appl	193	34	65.4	652	2	US-08-996-441B-50	Sequence 50, Appl
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122	34	65.4	110	2	US-09-726-219A-237	Sequence 237, App	195	34	65.4	652	2	US-08-996-441B-58	Sequence 58, Appl
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137	34	65.4	133	2	US-08-603-024-4	Sequence 28, Appl	210	34	65.4	652	2	US-08-993-722A-2	Sequence 2, Appl
138	34	65.4	133	2	US-08-450-809-23	Sequence 27, Appl	211	34	65.4	652	2	US-08-993-722A-4	Sequence 4, Appl
139	34	65.4	143	1	US-08-438-123-7	Sequence 23, Appl	212	34	65.4	652	2	US-08-993-722A-6	Sequence 6, Appl
140	34	65.4	158	2	US-09-198-452A-383	Sequence 383, App	213	34	65.4	652	2	US-08-993-722A-8	Sequence 8, Appl
141	34	65.4	193	3	US-09-270-767-43200	Sequence 43200, A	214	34	65.4	652	2	US-08-993-722A-12	Sequence 12, Appl
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143	34	65.4	224	2	US-09-456-090A-84	Sequence 84, Appl	216	34	65.4	652	2	US-08-993-722A-20	Sequence 20, Appl
144	34	65.4	224	2	US-09-453-234-84	Sequence 84, Appl	217	34	65.4	652	2	US-08-993-722A-24	Sequence 24, Appl
145	34	65.4	225	6	5455030-5	Patent No. 5455030	218	34	65.4	652	2	US-08-993-722A-28	Sequence 28, Appl
146	34	65.4	226	6	5455030-7	Patent No. 5455030	219	34	65.4	652	2	US-08-993-722A-32	Sequence 32, Appl
147	34	65.4	242	6	5455030-15	Patent No. 5455030	220	34	65.4	652	2	US-08-993-722A-36	Sequence 36, Appl
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151	34	65.4	275	2	US-09-252-991A-29227	Sequence 29227, A	224	34	65.4	652	2	US-08-993-722A-52	Sequence 52, Appl
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167	34	65.4	651	2	US-08-993-722A-58	Sequence 58, Appl	240	34	65.4	652	2	US-08-993-722A-116	Sequence 116, Appl
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170	34	65.4	651	2	US-08-993-170A-58	Sequence 58, Appl	243	34	65.4	652	2	US-08-993-722A-128	Sequence 128, Appl
171	34	65.4	651	2	US-08-993-775B-52	Sequence 52, Appl	244	34	65.4	652	2	US-08-993-722A-132	Sequence 132, Appl
172	34	65.4	651	2	US-08-993-775B-56	Sequence 56, Appl	245	34	65.4	652	2	US-08-993-722A-136	Sequence 136, Appl
173	34	65.4	651	2	US-08-993-775B-58	Sequence 58, Appl	246	34	65.4	652	2	US-08-993-722A-140	Sequence 140, Appl

393	34	65.4	652	2	US-09-427-769-111	Sequence 111, App	466	33	63.5	108	2	US-09-920-262A-8	Sequence 8, Appl
394	34	65.4	652	2	US-10-232-665-2	Sequence 2, Appl	467	33	63.5	108	2	US-09-910-059-9	Sequence 9, Appl
395	34	65.4	652	2	US-10-232-665-4	Sequence 4, Appl	468	33	63.5	112	2	US-09-810-502-36	Sequence 36, Appl
396	34	65.4	652	2	US-10-232-665-6	Sequence 6, Appl	469	33	63.5	112	2	US-09-810-502-37	Sequence 37, Appl
397	34	65.4	652	4	PCR-US92-00040-2	Sequence 2, Appl	470	33	63.5	112	2	US-10-194-975-115	Sequence 115, App
398	34	65.4	652	6	5187091-2	Patent No. 5187091	471	33	63.5	112	2	US-10-194-975-116	Sequence 116, App
399	34	65.4	653	2	US-08-996-441B-100	Sequence 100, App	472	33	63.5	113	1	US-08-263-911-2	Sequence 2, Appl
400	34	65.4	653	2	US-08-993-722A-100	Sequence 100, App	473	33	63.5	113	1	US-08-819-033-1	Sequence 1, Appl
401	34	65.4	653	2	US-08-993-170A-100	Sequence 100, App	474	33	63.5	113	2	US-09-025-203-9	Sequence 9, Appl
402	34	65.4	653	2	US-08-993-775B-100	Sequence 100, App	475	33	63.5	113	2	US-09-025-203-7	Sequence 7, Appl
403	34	65.4	653	2	US-09-377-466B-8	Sequence 8, Appl	476	33	63.5	113	2	US-09-025-203-13	Sequence 13, Appl
404	34	65.4	653	2	US-09-377-466B-10	Sequence 10, Appl	477	33	63.5	113	2	US-09-025-203-14	Sequence 14, Appl
405	34	65.4	653	2	US-09-377-466B-12	Sequence 12, Appl	478	33	63.5	113	2	US-08-961-309-11	Sequence 11, Appl
406	34	65.4	653	2	US-09-377-466B-16	Sequence 16, Appl	479	33	63.5	113	2	US-08-961-309-13	Sequence 13, Appl
407	34	65.4	653	2	US-09-377-466B-18	Sequence 18, Appl	480	33	63.5	113	2	US-09-999-021-7	Sequence 7, Appl
408	34	65.4	653	2	US-09-377-466B-20	Sequence 20, Appl	481	33	63.5	113	2	US-09-999-021-13	Sequence 13, Appl
409	34	65.4	653	2	US-09-377-466B-22	Sequence 22, Appl	482	33	63.5	113	2	US-09-999-021-14	Sequence 14, Appl
410	34	65.4	653	2	US-09-377-466B-24	Sequence 24, Appl	483	33	63.5	113	2	US-09-999-025-7	Sequence 7, Appl
411	34	65.4	653	2	US-09-377-466B-37	Sequence 37, Appl	484	33	63.5	113	2	US-09-999-025-9	Sequence 9, Appl
412	34	65.4	653	2	US-09-377-466B-39	Sequence 39, Appl	485	33	63.5	113	2	US-09-999-025-13	Sequence 13, Appl
413	34	65.4	653	2	US-09-427-770-100	Sequence 100, App	486	33	63.5	113	2	US-09-999-025-14	Sequence 14, Appl
414	34	65.4	653	2	US-09-427-770-100	Sequence 100, App	487	33	63.5	113	2	US-10-040-997-7	Sequence 7, Appl
415	34	65.4	653	2	US-10-232-665-8	Sequence 8, Appl	488	33	63.5	113	2	US-10-040-997-9	Sequence 9, Appl
416	34	65.4	653	2	US-10-232-665-10	Sequence 10, Appl	489	33	63.5	113	2	US-10-040-997-13	Sequence 13, Appl
417	34	65.4	653	2	US-10-232-665-12	Sequence 12, Appl	490	33	63.5	113	2	US-10-040-997-14	Sequence 14, Appl
418	34	65.4	653	2	US-10-232-665-14	Sequence 14, Appl	491	33	63.5	113	2	US-09-999-040-7	Sequence 7, Appl
419	34	65.4	653	2	US-10-232-665-16	Sequence 16, Appl	492	33	63.5	113	2	US-09-999-040-9	Sequence 9, Appl
420	34	65.4	653	2	US-10-232-665-18	Sequence 18, Appl	493	33	63.5	113	2	US-09-999-040-13	Sequence 13, Appl
421	34	65.4	653	2	US-10-232-665-20	Sequence 20, Appl	494	33	63.5	113	2	US-09-999-817-7	Sequence 7, Appl
422	34	65.4	653	2	US-10-232-665-22	Sequence 22, Appl	495	33	63.5	113	2	US-09-998-817-9	Sequence 9, Appl
423	34	65.4	653	2	US-10-232-665-24	Sequence 24, Appl	496	33	63.5	113	2	US-09-998-817-13	Sequence 13, Appl
424	34	65.4	653	2	US-10-232-665-24	Sequence 24, Appl	497	33	63.5	113	2	US-09-998-817-14	Sequence 14, Appl
425	34	65.4	653	2	US-10-232-665-37	Sequence 37, Appl	498	33	63.5	113	2	US-09-998-817-14	Sequence 14, Appl
426	34	65.4	653	2	US-10-232-665-39	Sequence 39, Appl	499	33	63.5	113	2	US-09-830-748B-13	Sequence 13, Appl
427	34	65.4	653	2	US-08-996-441B-112	Sequence 112, App	500	33	63.5	113	2	US-09-698-705-5	Sequence 5, Appl
428	34	65.4	653	2	US-08-993-722A-112	Sequence 112, App	501	33	63.5	113	2	US-08-917-456-4	Sequence 4, Appl
429	34	65.4	653	2	US-08-993-170A-112	Sequence 112, App	502	33	63.5	120	1	US-08-917-456-4	Sequence 4, Appl
430	34	65.4	653	2	US-08-993-775B-112	Sequence 112, App	503	33	63.5	120	1	US-09-229-804-4	Sequence 4, Appl
431	34	65.4	653	2	US-09-427-770-112	Sequence 112, App	504	33	63.5	127	1	US-08-436-463-18	Sequence 18, Appl
432	34	65.4	653	2	US-09-427-769-112	Sequence 112, App	505	33	63.5	133	1	US-08-822-028-12	Sequence 12, Appl
433	34	65.4	653	2	US-09-427-769-112	Sequence 112, App	506	33	63.5	133	2	US-08-463-903-4	Sequence 4, Appl
434	34	65.4	653	2	US-09-427-769-112	Sequence 112, App	507	33	63.5	133	2	US-08-479-285-12	Sequence 12, Appl
435	34	65.4	653	2	US-09-487-558B-40	Sequence 40, Appl	508	33	63.5	133	2	US-07-935-695-4	Sequence 4, Appl
436	34	65.4	653	2	US-09-487-558B-394	Sequence 394, App	509	33	63.5	133	2	US-09-503-653A-12	Sequence 12, Appl
437	34	65.4	653	2	US-09-438-185A-959	Sequence 959, App	510	33	63.5	134	2	US-08-961-309-58	Sequence 58, Appl
438	33	63.5	9	2	US-09-171-945-28	Sequence 28, Appl	511	33	63.5	158	1	US-08-917-456-2	Sequence 2, Appl
439	33	63.5	9	2	US-09-406-535-10	Sequence 10, Appl	512	33	63.5	158	2	US-09-229-804-2	Sequence 2, Appl
440	33	63.5	9	2	US-09-830-748B-3	Sequence 3, Appl	513	33	63.5	171	2	US-08-463-903-20	Sequence 20, Appl
441	33	63.5	9	2	US-09-920-262A-6	Sequence 6, Appl	514	33	63.5	171	2	US-07-935-695-20	Sequence 20, Appl
442	33	63.5	72	2	US-09-910-059-28	Sequence 28, Appl	515	33	63.5	235	2	US-09-171-945-17	Sequence 17, Appl
443	33	63.5	95	2	US-09-248-796A-26147	Sequence 26147, A	516	33	63.5	235	2	US-09-171-945-52	Sequence 52, Appl
444	33	63.5	95	2	US-10-194-975-59	Sequence 59, Appl	517	33	63.5	235	2	US-09-171-945-97	Sequence 97, Appl
445	33	63.5	95	2	US-10-194-975-60	Sequence 60, Appl	518	33	63.5	235	2	US-09-171-945-99	Sequence 99, Appl
446	33	63.5	95	2	US-10-330-613A-47	Sequence 47, Appl	519	33	63.5	235	2	US-09-910-058-17	Sequence 17, Appl
447	33	63.5	95	2	US-10-330-613A-48	Sequence 48, Appl	520	33	63.5	235	2	US-09-910-059-52	Sequence 52, Appl
448	33	63.5	95	2	US-10-330-613A-51	Sequence 51, Appl	521	33	63.5	235	2	US-09-910-059-97	Sequence 97, Appl
449	33	63.5	95	2	US-10-330-613A-52	Sequence 52, Appl	522	33	63.5	235	2	US-09-910-059-99	Sequence 99, Appl
450	33	63.5	103	1	US-08-436-463-21	Sequence 21, Appl	523	33	63.5	236	1	US-08-157-101A-5	Sequence 5, Appl
451	33	63.5	104	1	US-09-489-039A-13556	Sequence 13556, A	524	33	63.5	238	2	US-09-698-705-10	Sequence 10, Appl
452	33	63.5	107	1	US-08-276-852-107	Sequence 107, App	525	33	63.5	241	2	US-09-791-540-6	Sequence 6, Appl
453	33	63.5	107	1	US-08-899-575-107	Sequence 107, App	526	33	63.5	241	2	US-09-791-578-6	Sequence 6, Appl
454	33	63.5	107	2	US-08-899-575-107	Sequence 107, App	527	33	63.5	242	1	US-08-224-591-14	Sequence 14, Appl
455	33	63.5	107	2	US-09-171-945-50	Sequence 50, Appl	528	33	63.5	242	1	US-08-392-338A-23	Sequence 23, Appl
456	33	63.5	107	2	US-09-171-945-61	Sequence 61, Appl	529	33	63.5	242	1	US-08-392-338A-23	Sequence 23, Appl
457	33	63.5	107	2	US-09-171-945-65	Sequence 65, Appl	530	33	63.5	242	2	US-08-926-789-14	Sequence 14, Appl
458	33	63.5	107	2	US-09-171-945-71	Sequence 71, Appl	531	33	63.5	242	2	US-09-166-750-23	Sequence 23, Appl
459	33	63.5	107	2	US-09-171-945-71	Sequence 71, Appl	532	33	63.5	242	2	US-09-166-093-23	Sequence 23, Appl
460	33	63.5	107	2	US-09-171-945-71	Sequence 71, Appl	533	33	63.5	242	2	US-09-166-093-23	Sequence 23, Appl
461	33	63.5	107	2	US-09-171-945-71	Sequence 71, Appl	534	33	63.5	242	2	US-09-166-093-23	Sequence 23, Appl
462	33	63.5	107	2	US-09-171-945-71	Sequence 71, Appl	535	33	63.5	244	1	US-09-443-213-23	Sequence 23, Appl
463	33	63.5	107	4	PCT-US95-08743-107	Sequence 107, App	536	33	63.5	244	1	US-08-392-338A-13	Sequence 13, Appl
464	33	63.5	108	2	US-09-157-370-4	Sequence 4, Appl	537	33	63.5	244	2	US-09-166-750-13	Sequence 13, Appl
465	33	63.5	108	2	US-09-171-945-9	Sequence 9, Appl	538	33	63.5	244	2	US-09-172-019-13	Sequence 13, Appl

539	33	63.5	244	2	US-09-166-094-13	Sequence 13, Appl	612	32	61.5	107	1	US-08-480-434-73	Sequence 73, Appl
540	33	63.5	244	2	US-09-443-213-13	Sequence 13, Appl	613	32	61.5	107	1	US-08-053-451B-73	Sequence 73, Appl
541	33	63.5	244	4	PCT-US93-11138-14	Sequence 14, Appl	614	32	61.5	107	1	US-08-053-451B-174	Sequence 174, Appl
542	33	63.5	246	2	US-09-791-540-2	Sequence 2, Appl	615	32	61.5	107	2	US-08-646-265A-130	Sequence 130, Appl
543	33	63.5	246	2	US-09-791-540-2	Sequence 2, Appl	616	32	61.5	107	2	US-08-646-265A-131	Sequence 131, Appl
544	33	63.5	248	1	US-08-323-445A-6	Sequence 6, Appl	617	32	61.5	107	2	US-09-240-274-29	Sequence 29, Appl
545	33	63.5	248	1	US-08-515-903A-6	Sequence 6, Appl	618	32	61.5	107	2	US-09-848-798-29	Sequence 29, Appl
546	33	63.5	248	4	PCT-US95-12840-6	Sequence 6, Appl	619	32	61.5	108	1	US-08-378-939-18	Sequence 18, Appl
547	33	63.5	249	2	US-09-069-821-2	Sequence 2, Appl	620	32	61.5	108	2	US-08-752-693A-1	Sequence 1, Appl
548	33	63.5	249	2	US-09-956-086-2	Sequence 2, Appl	621	32	61.5	108	2	US-09-155-106-22	Sequence 22, Appl
549	33	63.5	249	2	US-09-956-087-2	Sequence 2, Appl	622	32	61.5	108	2	US-09-155-106-23	Sequence 23, Appl
550	33	63.5	251	1	US-08-401-068-12	Sequence 12, Appl	623	32	61.5	108	2	US-09-155-106-24	Sequence 24, Appl
551	33	63.5	251	1	US-08-846-338-12	Sequence 12, Appl	624	32	61.5	108	2	US-09-155-106-28	Sequence 28, Appl
552	33	63.5	251	2	US-08-411-768B-3	Sequence 3, Appl	625	32	61.5	108	2	US-09-155-106-30	Sequence 30, Appl
553	33	63.5	257	2	US-09-420-592A-2	Sequence 2, Appl	626	32	61.5	109	2	US-09-726-219A-268	Sequence 268, Appl
554	33	63.5	257	2	US-09-985-442-2	Sequence 2, Appl	627	32	61.5	109	2	US-09-196-522-468	Sequence 268, Appl
555	33	63.5	257	2	US-09-983-580-2	Sequence 2, Appl	628	32	61.5	112	2	US-09-627-2188-1	Sequence 1, Appl
556	33	63.5	257	2	US-09-791-540-4	Sequence 4, Appl	629	32	61.5	113	2	US-09-301-593-2	Sequence 2, Appl
557	33	63.5	257	2	US-09-791-540-4	Sequence 4, Appl	630	32	61.5	113	2	US-09-301-593-4	Sequence 4, Appl
558	33	63.5	260	2	US-08-463-903-2	Sequence 2, Appl	631	32	61.5	113	2	US-09-301-593-6	Sequence 6, Appl
559	33	63.5	260	2	US-07-935-695-2	Sequence 2, Appl	632	32	61.5	113	2	US-09-301-593-33	Sequence 33, Appl
560	33	63.5	260	2	US-08-961-309-64	Sequence 2, Appl	633	32	61.5	113	2	US-09-301-593-34	Sequence 34, Appl
561	33	63.5	262	1	US-08-323-445A-4	Sequence 4, Appl	634	32	61.5	117	2	US-09-042-353-48	Sequence 48, Appl
562	33	63.5	262	1	US-08-515-903A-4	Sequence 4, Appl	635	32	61.5	117	2	US-08-758-417A-313	Sequence 313, Appl
563	33	63.5	262	1	PCT-US95-12840-4	Sequence 4, Appl	636	32	61.5	117	2	US-08-646-265A-43	Sequence 43, Appl
564	33	63.5	264	1	US-08-323-445A-8	Sequence 8, Appl	637	32	61.5	126	2	US-08-646-265A-47	Sequence 47, Appl
565	33	63.5	264	1	US-08-515-903A-8	Sequence 8, Appl	638	32	61.5	126	2	US-08-646-265A-51	Sequence 51, Appl
566	33	63.5	264	4	PCT-US95-12840-8	Sequence 8, Appl	639	32	61.5	126	2	US-08-646-265A-53	Sequence 53, Appl
567	33	63.5	269	2	US-09-420-592A-4	Sequence 4, Appl	640	32	61.5	126	2	US-08-646-265A-57	Sequence 57, Appl
568	33	63.5	269	2	US-09-985-442-4	Sequence 4, Appl	641	32	61.5	126	2	US-08-646-265A-59	Sequence 59, Appl
569	33	63.5	269	2	US-09-983-580-4	Sequence 4, Appl	642	32	61.5	126	2	US-08-646-265A-63	Sequence 63, Appl
570	33	63.5	274	2	US-08-961-309-66	Sequence 6, Appl	643	32	61.5	126	2	US-08-646-265A-65	Sequence 65, Appl
571	33	63.5	275	2	US-08-463-903-6	Sequence 6, Appl	644	32	61.5	126	2	US-08-646-265A-69	Sequence 69, Appl
572	33	63.5	275	2	US-08-463-903-8	Sequence 8, Appl	645	32	61.5	126	2	US-08-646-265A-73	Sequence 73, Appl
573	33	63.5	275	2	US-08-463-903-17	Sequence 17, Appl	646	32	61.5	126	2	US-08-646-265A-75	Sequence 75, Appl
574	33	63.5	275	2	US-07-935-695-6	Sequence 6, Appl	647	32	61.5	126	2	US-08-646-265A-77	Sequence 77, Appl
575	33	63.5	275	2	US-07-935-695-8	Sequence 8, Appl	648	32	61.5	126	2	US-08-646-265A-81	Sequence 81, Appl
576	33	63.5	275	2	US-07-935-695-17	Sequence 17, Appl	649	32	61.5	126	2	US-08-646-265A-85	Sequence 85, Appl
577	33	63.5	280	2	US-08-463-903-10	Sequence 10, Appl	650	32	61.5	126	2	US-08-646-265A-87	Sequence 87, Appl
578	33	63.5	280	2	US-07-935-695-10	Sequence 10, Appl	651	32	61.5	126	2	US-08-646-265A-91	Sequence 91, Appl
579	33	63.5	281	2	US-09-423-439-44	Sequence 44, Appl	652	32	61.5	126	2	US-08-646-265A-97	Sequence 97, Appl
580	33	63.5	282	2	US-08-463-903-12	Sequence 12, Appl	653	32	61.5	127	2	US-08-646-265A-27	Sequence 27, Appl
581	33	63.5	282	2	US-08-463-903-15	Sequence 15, Appl	654	32	61.5	130	2	US-09-339-596A-24	Sequence 24, Appl
582	33	63.5	282	2	US-07-935-695-12	Sequence 12, Appl	655	32	61.5	130	2	US-09-339-596A-28	Sequence 28, Appl
583	33	63.5	282	2	US-07-935-695-15	Sequence 15, Appl	656	32	61.5	132	1	US-08-253-877C-55	Sequence 55, Appl
584	33	63.5	284	2	US-08-961-309-70	Sequence 20, Appl	657	32	61.5	132	1	US-08-452-164A-55	Sequence 55, Appl
585	33	63.5	285	2	US-08-463-903-22	Sequence 22, Appl	658	32	61.5	132	2	US-08-976-183A-36	Sequence 36, Appl
586	33	63.5	285	2	US-07-935-695-45	Sequence 45, Appl	659	32	61.5	132	2	US-09-716-183A-37	Sequence 37, Appl
587	33	63.5	422	2	US-09-724-864-45	Sequence 45, Appl	660	32	61.5	133	2	US-09-301-593-34	Sequence 34, Appl
588	33	63.5	483	1	US-08-392-338A-19	Sequence 19, Appl	661	32	61.5	138	1	US-08-480-434-63	Sequence 63, Appl
589	33	63.5	483	2	US-09-166-750-19	Sequence 19, Appl	662	32	61.5	138	1	US-08-053-451B-63	Sequence 63, Appl
590	33	63.5	483	2	US-09-166-093-19	Sequence 19, Appl	663	32	61.5	147	2	US-08-976-183A-46	Sequence 46, Appl
591	33	63.5	483	2	US-09-172-019-19	Sequence 19, Appl	664	32	61.5	147	1	US-08-653-402B-4	Sequence 4, Appl
592	33	63.5	483	2	US-09-166-094-19	Sequence 19, Appl	665	32	61.5	184	2	US-09-949-016-7507	Sequence 7507, Appl
593	33	63.5	483	2	US-09-443-213-19	Sequence 19, Appl	666	32	61.5	220	2	US-09-301-593-17	Sequence 17, Appl
594	33	63.5	553	1	US-08-263-911-7	Sequence 7, Appl	667	32	61.5	237	1	US-08-224-591-167	Sequence 167, Appl
595	33	63.5	553	1	US-08-263-911-9	Sequence 9, Appl	668	32	61.5	237	1	US-08-926-789-16	Sequence 16, Appl
596	33	63.5	666	2	US-09-423-439-51	Sequence 51, Appl	669	32	61.5	240	2	US-09-301-593-36	Sequence 36, Appl
597	33	63.5	1050	2	US-09-538-092-131	Sequence 131, Appl	670	32	61.5	240	2	US-08-224-591-18	Sequence 18, Appl
598	32	61.5	9	1	US-08-480-434-72	Sequence 72, Appl	671	32	61.5	241	1	US-08-926-789-19	Sequence 19, Appl
599	32	61.5	9	1	US-08-480-434-79	Sequence 79, Appl	672	32	61.5	242	1	US-08-553-497A-26	Sequence 26, Appl
600	32	61.5	9	1	US-08-053-451B-72	Sequence 72, Appl	673	32	61.5	242	1	US-08-553-497A-28	Sequence 28, Appl
601	32	61.5	9	1	US-08-053-451B-79	Sequence 79, Appl	674	32	61.5	245	2	US-09-069-821-5	Sequence 5, Appl
602	32	61.5	9	2	US-08-646-265A-120	Sequence 120, Appl	675	32	61.5	245	2	US-09-956-086-5	Sequence 5, Appl
603	32	61.5	9	2	US-09-155-106-6	Sequence 6, Appl	676	32	61.5	245	2	US-09-956-087-5	Sequence 5, Appl
604	32	61.5	9	2	US-09-339-596A-40	Sequence 40, Appl	677	32	61.5	245	2	US-09-702-705-1677	Sequence 1677, Appl
605	32	61.5	21	2	US-09-747-802-88	Sequence 88, Appl	678	32	61.5	250	2	US-09-736-457-1677	Sequence 1677, Appl
606	32	61.5	95	2	US-10-194-975-61	Sequence 61, Appl	679	32	61.5	250	2	US-09-671-335-1677	Sequence 1677, Appl
607	32	61.5	95	2	US-10-194-975-62	Sequence 62, Appl	680	32	61.5	250	2	US-09-658-824-1677	Sequence 1677, Appl
608	32	61.5	104	2	US-09-270-767-39446	Sequence 39446, A	681	32	61.5	250	2	US-10-017-754-1874	Sequence 1874, Appl
609	32	61.5	104	2	US-09-270-767-35463	Sequence 35463, A	682	32	61.5	250	2	US-10-017-754-1874	Sequence 1874, Appl
610	32	61.5	107	1	US-08-491-845-4	Sequence 4, Appl	683	32	61.5	250	2	US-10-017-754-1874	Sequence 1874, Appl
611	32	61.5	107	1	US-08-491-845-12	Sequence 12, Appl	684	32	61.5	250	2	US-10-017-754-2004	Sequence 2004, Appl

685	32	61.5	250	2	US-09-651-563-1677	Sequence 1677, Ap	758	31	59.6	128	1	US-08-474-040-31	Sequence 31, Appl
686	32	61.5	265	2	US-09-420-592A-5	Sequence 5, Appli	759	31	59.6	128	1	US-08-487-200-31	Sequence 31, Appl
687	32	61.5	265	2	US-09-985-442-5	Sequence 5, Appli	760	31	59.6	128	2	US-08-484-537-31	Sequence 31, Appl
688	32	61.5	265	2	US-09-983-580-5	Sequence 5, Appli	761	31	59.6	129	2	US-09-513-999C-7947	Sequence 7947, Ap
689	32	61.5	268	2	US-09-747-802-1	Sequence 1, Appli	762	31	59.6	129	2	US-10-104-047-2560	Sequence 2560, Ap
690	32	61.5	269	2	US-08-646-265A-109	Sequence 109, App	763	31	59.6	128	2	US-09-270-767-57185	Sequence 57185, A
691	32	61.5	279	2	US-09-900-575-23	Sequence 23, Appl	764	31	59.6	195	2	US-09-248-796A-2608	Sequence 2608, A
692	32	61.5	279	2	US-09-900-575-24	Sequence 24, Appl	765	31	59.6	209	2	US-09-270-767-40354	Sequence 40354, A
693	32	61.5	279	2	US-09-900-575-25	Sequence 25, Appl	766	31	59.6	209	2	US-09-270-767-41935	Sequence 41935, A
694	32	61.5	279	2	US-09-900-575-26	Sequence 26, Appl	767	31	59.6	209	2	US-09-270-767-55570	Sequence 55570, A
695	32	61.5	279	2	US-09-900-575-27	Sequence 27, Appl	768	31	59.6	210	2	US-09-270-767-57495	Sequence 57495, A
696	32	61.5	279	2	US-09-900-575-28	Sequence 28, Appl	769	31	59.6	219	2	US-09-583-110-3045	Sequence 3045, Ap
697	32	61.5	279	2	US-09-900-575-29	Sequence 29, Appl	770	31	59.6	221	2	US-09-107-433-4852	Sequence 4852, Ap
698	32	61.5	279	2	US-09-900-575-31	Sequence 31, Appl	771	31	59.6	264	2	US-10-114-116A-46	Sequence 46, Appl
699	32	61.5	279	2	US-09-900-575-32	Sequence 32, Appl	772	31	59.6	288	2	US-09-248-796A-19340	Sequence 19340, A
700	32	61.5	279	2	US-09-900-575-33	Sequence 33, Appl	773	31	59.6	339	2	US-09-328-352-1447	Sequence 1447, Ap
701	32	61.5	279	2	US-09-900-575-34	Sequence 34, Appl	774	31	59.6	340	2	US-09-902-540-11600	Sequence 11600, A
702	32	61.5	279	2	US-09-900-575-35	Sequence 35, Appl	775	31	59.6	371	2	US-09-252-991A-29890	Sequence 29890, A
703	32	61.5	279	2	US-09-900-575-36	Sequence 36, Appl	776	31	59.6	403	2	US-09-248-796A-14339	Sequence 14339, A
704	32	61.5	279	2	US-09-900-575-37	Sequence 37, Appl	777	31	59.6	443	2	US-09-902-540-16336	Sequence 16336, A
705	32	61.5	279	2	US-09-900-575-38	Sequence 38, Appl	778	31	59.6	480	2	US-09-902-540-10711	Sequence 10711, A
706	32	61.5	279	2	US-09-900-575-39	Sequence 39, Appl	779	31	59.6	481	2	US-09-248-796A-20797	Sequence 20797, A
707	32	61.5	279	2	US-09-900-575-40	Sequence 40, Appl	780	31	59.6	520	1	US-08-261-822A-10	Sequence 10, Appl
708	32	61.5	279	2	US-09-900-575-41	Sequence 41, Appl	781	31	59.6	520	4	PCT-US95-0744A-10	Sequence 42, Appl
709	32	61.5	279	2	US-09-900-575-42	Sequence 42, Appl	782	31	59.6	681	2	US-09-270-767-42219	Sequence 42219, A
710	32	61.5	279	2	US-09-900-575-43	Sequence 43, Appl	783	31	59.6	734	2	US-09-252-991A-30703	Sequence 30703, A
711	32	61.5	279	2	US-09-900-575-44	Sequence 44, Appl	784	31	59.6	744	2	US-08-265-967C-3	Sequence 3, Appli
712	32	61.5	279	2	US-09-900-575-45	Sequence 45, Appl	785	31	59.6	2474	2	US-08-305-790B-4	Sequence 4, Appli
713	32	61.5	279	2	US-09-900-575-55	Sequence 55, Appl	786	30	57.7	179	2	US-09-248-796A-18193	Sequence 18193, A
714	32	61.5	280	2	US-09-900-575-30	Sequence 30, Appl	787	30	57.7	9	1	US-08-672-345C-27	Sequence 27, Appl
715	32	61.5	286	2	US-10-017-754-1878	Sequence 1878, Ap	788	30	57.7	9	2	US-09-214-095D-27	Sequence 27, Appl
716	32	61.5	300	2	US-09-298-494-2	Sequence 2, Appli	789	30	57.7	9	2	US-09-798-689-6	Sequence 6, Appli
717	32	61.5	300	2	US-09-489-039A-367	Sequence 367, App	790	30	57.7	9	2	US-09-940-727B-27	Sequence 36, Appl
718	32	61.5	314	2	US-08-118-270-44	Sequence 11890, A	791	30	57.7	62	2	US-09-270-767-42717	Sequence 42717, A
719	32	61.5	316	4	PCT-US93-08528-44	Sequence 44, Appl	792	30	57.7	84	2	US-09-513-999C-5435	Sequence 5435, Ap
720	32	61.5	316	4	US-09-146-980-2	Sequence 2, Appli	793	30	57.7	100	2	US-09-899-886-8	Sequence 8, Appli
721	32	61.5	362	2	US-10-017-754-1876	Sequence 1876, Ap	794	30	57.7	106	2	US-09-798-689-8	Sequence 8, Appli
722	32	61.5	384	2	US-09-328-352-4504	Sequence 4504, Ap	795	30	57.7	107	2	US-10-330-613A-6	Sequence 6, Appli
723	32	61.5	614	2	US-09-248-796A-18728	Sequence 18728, A	796	30	57.7	107	2	US-10-330-613A-34	Sequence 34, Appl
724	31.5	60.6	745	2	US-08-350-260A-523	Sequence 523, App	797	30	57.7	107	2	US-10-330-613A-67	Sequence 67, Appl
725	31	59.6	9	1	US-09-042-353-358	Sequence 368, App	798	30	57.7	112	2	US-09-232-280-10	Sequence 10, Appl
726	31	59.6	9	2	US-08-758-417A-216	Sequence 216, App	799	30	57.7	112	2	US-08-672-345C-98	Sequence 98, Appl
727	31	59.6	9	2	US-09-104-337A-523	Sequence 523, App	800	30	57.7	113	1	US-08-672-345C-98	Sequence 98, Appl
728	31	59.6	67	2	US-09-270-767-48238	Sequence 33021, A	801	30	57.7	113	2	US-09-214-095D-8	Sequence 8, Appli
729	31	59.6	67	2	US-09-328-352-6645	Sequence 6645, Ap	802	30	57.7	113	2	US-09-214-095D-108	Sequence 108, App
730	31	59.6	82	2	US-07-634-278-35	Sequence 35, Appl	803	30	57.7	113	2	US-09-940-727B-8	Sequence 8, Appli
731	31	59.6	100	2	US-07-634-278-58	Sequence 58, Appl	804	30	57.7	113	2	US-10-104-047-3567	Sequence 108, App
732	31	59.6	106	1	US-07-634-278-59	Sequence 59, Appl	805	30	57.7	118	2	US-08-111-080-18	Sequence 18, Appl
733	31	59.6	106	1	US-07-634-278-59	Sequence 59, Appl	806	30	57.7	121	1	US-08-211-980-18	Sequence 18, Appl
734	31	59.6	106	1	US-08-487-728-35	Sequence 35, Appl	807	30	57.7	121	1	PCT-US92-07111-17	Sequence 17, Appl
735	31	59.6	106	1	US-08-477-728-35	Sequence 35, Appl	808	30	57.7	121	4	PCT-US93-07967-18	Sequence 18, Appl
736	31	59.6	106	1	US-08-477-728-58	Sequence 58, Appl	809	30	57.7	121	4	US-08-822-028-28	Sequence 28, Appl
737	31	59.6	106	1	US-08-477-728-59	Sequence 59, Appl	810	30	57.7	126	1	US-08-478-285-28	Sequence 28, Appl
738	31	59.6	106	1	US-08-474-040-35	Sequence 35, Appl	811	30	57.7	126	2	US-09-503-653A-28	Sequence 28, Appl
739	31	59.6	106	1	US-08-474-040-58	Sequence 58, Appl	812	30	57.7	126	2	US-08-478-285-28	Sequence 28, Appl
740	31	59.6	106	1	US-08-474-040-59	Sequence 59, Appl	813	30	57.7	126	2	US-09-405-653A-28	Sequence 28, Appl
741	31	59.6	106	1	US-08-487-200-35	Sequence 35, Appl	814	30	57.7	129	2	US-08-943-136-2	Sequence 2, Appli
742	31	59.6	106	1	US-08-487-200-58	Sequence 58, Appl	815	30	57.7	129	2	US-08-973-518-2	Sequence 2, Appli
743	31	59.6	106	1	US-08-487-200-58	Sequence 58, Appl	816	30	57.7	134	2	US-09-465-558-48	Sequence 48, Appl
744	31	59.6	106	2	US-08-487-200-59	Sequence 59, Appl	817	30	57.7	140	1	US-08-691-071-4	Sequence 4, Appli
745	31	59.6	106	2	US-08-484-537-35	Sequence 35, Appl	818	30	57.7	140	1	US-09-270-767-31856	Sequence 31856, A
746	31	59.6	106	2	US-08-484-537-59	Sequence 58, Appl	819	30	57.7	141	2	US-09-248-796A-21898	Sequence 21898, A
747	31	59.6	106	2	US-08-484-537-59	Sequence 59, Appl	820	30	57.7	155	2	US-09-543-681A-7783	Sequence 7783, Ap
748	31	59.6	107	2	US-09-240-274-40	Sequence 40, Appl	821	30	57.7	172	2	US-09-270-767-34789	Sequence 34789, A
749	31	59.6	107	2	US-09-848-798-40	Sequence 40, Appl	822	30	57.7	205	2	US-09-270-767-50006	Sequence 50006, A
750	31	59.6	108	2	US-09-065-059-3	Sequence 3, Appli	823	30	57.7	206	2	US-09-270-767-31856	Sequence 31856, A
751	31	59.6	108	2	US-09-621-976-6606	Sequence 6606, Ap	824	30	57.7	206	2	US-09-270-767-47073	Sequence 47073, A
752	31	59.6	108	2	US-08-913-555-3	Sequence 3, Appli	825	30	57.7	216	2	US-09-540-236-2216	Sequence 2316, Ap
753	31	59.6	108	2	US-08-913-555-21	Sequence 21, Appl	826	30	57.7	234	2	US-09-049-672A-17	Sequence 2, Appli
754	31	59.6	114	2	US-09-902-540-12268	Sequence 12268, A	827	30	57.7	239	2	US-09-798-669-21	Sequence 21, Appli
755	31	59.6	120	2	US-09-621-976-6605	Sequence 6605, Ap	828	30	57.7	241	2	US-09-581-345-5	Sequence 5, Appli
756	31	59.6	128	1	US-07-634-278-31	Sequence 31, Appl	829	30	57.7	249	1	US-08-797-669-18	Sequence 18, Appli
757	31	59.6	128	1	US-08-477-728-31	Sequence 31, Appl	830	30	57.7				

831	30	57.7	249	2	US-09-984-186-18	Sequence 18, Appl	904	29	55.8	107	1	US-07-634-278-50	Sequence 50, Appl
832	30	57.7	252	2	US-09-583-110-3515	Sequence 3515, Ap	905	29	55.8	107	1	US-07-634-278-51	Sequence 51, Appl
833	30	57.7	256	2	US-09-107-433-4151	Sequence 4151, Ap	906	29	55.8	107	1	US-08-477-728-54	Sequence 54, Appl
834	30	57.7	263	2	US-09-248-796A-19569	Sequence 19569, A	907	29	55.8	107	1	US-08-477-728-50	Sequence 50, Appl
835	30	57.7	294	2	US-09-949-016-1136	Sequence 1136, A	908	29	55.8	107	1	US-08-477-728-51	Sequence 51, Appl
836	30	57.7	329	2	US-08-887-534A-24	Sequence 24, Appl	909	29	55.8	107	1	US-08-474-040-14	Sequence 34, Appl
837	30	57.7	329	2	US-09-527-431-24	Sequence 24, Appl	910	29	55.8	107	1	US-08-474-040-51	Sequence 51, Appl
838	30	57.7	329	2	US-09-446-861-24	Sequence 24, Appl	911	29	55.8	107	1	US-08-487-200-50	Sequence 50, Appl
839	30	57.7	348	1	US-08-229-781-50	Sequence 50, Appl	912	29	55.8	107	1	US-08-487-200-50	Sequence 50, Appl
840	30	57.7	348	1	US-08-630-918-50	Sequence 50, Appl	913	29	55.8	107	1	US-08-487-200-51	Sequence 51, Appl
841	30	57.7	348	2	US-09-004-422-50	Sequence 50, Appl	915	29	55.8	107	2	US-08-484-537-14	Sequence 34, Appl
842	30	57.7	348	2	US-09-918-568-50	Sequence 50, Appl	916	29	55.8	107	2	US-08-484-537-50	Sequence 50, Appl
843	30	57.7	357	2	US-09-444-336-9	Sequence 9, Appl1	917	29	55.8	107	2	US-08-484-537-51	Sequence 51, Appl
844	30	57.7	357	2	US-10-093-045-9	Sequence 9, Appl1	918	29	55.8	107	2	US-09-434-870-2	Sequence 2, Appl1
845	30	57.7	357	2	US-10-093-046-9	Sequence 9, Appl1	919	29	55.8	109	2	US-09-270-767-59728	Sequence 59728, A
846	30	57.7	359	2	US-09-444-336-1	Sequence 1, Appl1	920	29	55.8	112	2	US-09-065-059-13	Sequence 13, Appl
847	30	57.7	359	2	US-10-093-045-1	Sequence 1, Appl1	921	29	55.8	112	2	US-08-913-555-13	Sequence 13, Appl
848	30	57.7	359	2	US-10-093-246-1	Sequence 1, Appl1	922	29	55.8	113	1	US-08-553-487A-6	Sequence 6, Appl1
849	30	57.7	362	2	US-09-444-336-2	Sequence 2, Appl1	923	29	55.8	113	1	US-08-553-487A-10	Sequence 10, Appl1
850	30	57.7	362	2	US-10-093-045-2	Sequence 2, Appl1	924	29	55.8	113	2	US-08-483-749A-16	Sequence 16, Appl1
851	30	57.7	362	2	US-10-093-246-2	Sequence 2, Appl1	925	29	55.8	113	4	PCT-US93-11611-5	Sequence 5, Appl1
852	30	57.7	365	2	US-09-270-767-44042	Sequence 44042, A	926	29	55.8	120	1	US-08-111-080-26	Sequence 26, Appl1
853	30	57.7	383	2	US-09-492-709A-265	Sequence 265, App	927	29	55.8	120	1	US-08-211-980-26	Sequence 26, Appl1
854	30	57.7	386	1	US-08-758-213-1	Sequence 1, Appl1	928	29	55.8	120	4	PCT-US93-07967-26	Sequence 26, Appl1
855	30	57.7	386	1	US-08-692-787-48	Sequence 48, Appl1	929	29	55.8	121	2	US-09-471-276-1394	Sequence 12, Appl1
856	30	57.7	386	2	US-09-097-199-48	Sequence 48, Appl1	930	29	55.8	125	1	US-08-039-198B-12	Sequence 12, Appl1
857	30	57.7	386	2	US-09-949-016-6022	Sequence 6022, Ap	931	29	55.8	125	1	US-08-182-067-2	Sequence 2, Appl1
858	30	57.7	387	2	US-09-328-352-5082	Sequence 5082, Ap	932	29	55.8	125	1	US-08-465-313-2	Sequence 2, Appl1
859	30	57.7	395	2	US-09-489-039A-12314	Sequence 12314, A	933	29	55.8	125	1	US-09-809-729-1	Sequence 1, Appl1
860	30	57.7	474	2	US-09-252-991A-32449	Sequence 32449, A	934	29	55.8	125	2	US-09-378-967-2	Sequence 2, Appl1
861	30	57.7	497	2	US-09-270-767-46538	Sequence 46538, A	935	29	55.8	125	2	US-09-809-729-10	Sequence 10, Appl1
862	30	57.7	503	2	US-09-252-991A-30892	Sequence 30892, A	936	29	55.8	129	1	US-08-217-918-2	Sequence 2, Appl1
863	30	57.7	515	1	US-09-146-283-2	Sequence 2, Appl1	937	29	55.8	129	1	US-08-116-778B-2	Sequence 2, Appl1
864	30	57.7	515	2	US-08-579-823A-2	Sequence 2, Appl1	938	29	55.8	129	1	US-08-438-562-2	Sequence 2, Appl1
865	30	57.7	515	2	US-09-344-195-2	Sequence 2, Appl1	939	29	55.8	129	1	US-08-483-528B-92	Sequence 92, Appl1
866	30	57.7	521	2	US-09-252-991A-27321	Sequence 27321, A	940	29	55.8	130	2	US-09-393-385B-111	Sequence 111, App
867	30	57.7	528	2	US-09-270-767-44826	Sequence 44826, A	941	29	55.8	130	2	US-09-393-385B-113	Sequence 113, App
868	30	57.7	540	2	US-09-489-039A-13022	Sequence 13022, A	942	29	55.8	130	2	US-10-195-752-111	Sequence 111, App
869	30	57.7	572	2	US-09-248-796A-15230	Sequence 15230, A	943	29	55.8	130	2	US-10-195-752-113	Sequence 113, App
870	30	57.7	591	2	US-09-248-796A-14394	Sequence 14394, A	944	29	55.8	131	2	US-09-248-796A-25786	Sequence 25786, A
871	30	57.7	840	2	US-09-489-039A-11722	Sequence 11722, A	945	29	55.8	133	1	US-08-116-778B-37	Sequence 37, Appl
872	30	57.7	1033	2	US-09-489-039A-13524	Sequence 13524, A	946	29	55.8	133	1	US-08-438-562-37	Sequence 37, Appl
873	30	57.7	1103	2	US-09-162-373-1	Sequence 1, Appl1	947	29	55.8	133	1	US-08-483-528B-101	Sequence 101, App
874	30	57.7	1103	2	US-09-467-946-1	Sequence 9, Appl1	948	29	55.8	133	4	PCT-US93-11611-2	Sequence 2, Appl1
875	30	57.7	1123	2	US-09-949-016-9935	Sequence 9935, Ap	949	29	55.8	133	4	US-09-024-020B-12	Sequence 12, Appl1
876	29	55.8	9	1	US-08-318-970B-22	Sequence 22, Appl	950	29	55.8	138	2	US-09-425-043-127	Sequence 12, Appl1
877	29	55.8	9	1	US-08-116-778B-11	Sequence 11, Appl1	951	29	55.8	138	2	US-09-248-796A-20873	Sequence 20873, A
878	29	55.8	9	1	US-08-438-562-11	Sequence 11, Appl1	952	29	55.8	139	2	US-09-270-767-48278	Sequence 48278, A
879	29	55.8	9	1	US-08-483-528B-99	Sequence 99, Appl1	953	29	55.8	144	2	US-09-270-767-32802	Sequence 32802, A
880	29	55.8	9	1	US-08-182-067-8	Sequence 8, Appl1	954	29	55.8	146	2	US-09-270-767-3767	Sequence 3767, A
881	29	55.8	9	1	US-08-465-313-8	Sequence 8, Appl1	955	29	55.8	148	2	US-09-270-767-59584	Sequence 59584, A
882	29	55.8	9	2	US-09-393-385B-110	Sequence 110, App	956	29	55.8	148	2	US-09-270-767-44317	Sequence 44317, A
883	29	55.8	9	2	US-09-809-739-4	Sequence 4, Appl1	957	29	55.8	149	1	US-08-894-922A-6	Sequence 6, Appl1
884	29	55.8	9	2	US-09-378-967-8	Sequence 8, Appl1	958	29	55.8	151	2	US-09-270-767-44306	Sequence 44306, A
885	29	55.8	9	2	US-10-195-752-110	Sequence 110, App	959	29	55.8	151	2	US-09-489-039A-7759	Sequence 7759, App
886	29	55.8	9	4	PCT-US94-14106-43	Sequence 43, Appl	960	29	55.8	163	2	US-09-270-767-59741	Sequence 59741, A
887	29	55.8	31	2	US-09-270-767-57033	Sequence 57033, A	961	29	55.8	163	2	US-09-270-767-34382	Sequence 34382, A
888	29	55.8	64	1	US-08-765-179B-14	Sequence 14, Appl	962	29	55.8	164	2	US-09-270-767-49599	Sequence 49599, A
889	29	55.8	76	2	US-09-107-532A-4783	Sequence 4783, Ap	963	29	55.8	193	2	US-09-949-016-7639	Sequence 7639, Ap
890	29	55.8	81	2	US-09-270-767-37904	Sequence 37904, A	964	29	55.8	194	2	US-09-252-991A-19340	Sequence 19340, A
891	29	55.8	81	2	US-09-270-767-53121	Sequence 53121, A	965	29	55.8	196	2	US-09-270-767-46722	Sequence 46722, A
892	29	55.8	86	2	US-09-640-211A-695	Sequence 695, App	966	29	55.8	206	2	US-09-134-000C-4084	Sequence 4084, Ap
893	29	55.8	87	2	US-09-270-767-41296	Sequence 41296, A	967	29	55.8	209	2	US-09-270-767-56668	Sequence 56668, A
894	29	55.8	87	2	US-09-270-767-56512	Sequence 56512, A	968	29	55.8	213	2	US-09-270-767-44317	Sequence 44317, A
895	29	55.8	95	2	US-10-194-975-63	Sequence 63, Appl	969	29	55.8	234	2	US-09-710-279-1034	Sequence 1034, Ap
896	29	55.8	95	2	US-10-194-975-64	Sequence 64, Appl	970	29	55.8	252	2	US-08-894-922A-14	Sequence 14, Appl1
897	29	55.8	102	2	US-09-538-092-79	Sequence 79, Appl1	971	29	55.8	256	2	US-09-526-738A-2	Sequence 2, Appl1
898	29	55.8	106	2	US-08-466-151-6	Sequence 6, Appl1	972	29	55.8	258	2	US-09-526-738A-4	Sequence 4, Appl1
899	29	55.8	106	2	US-08-466-163B-6	Sequence 6, Appl1	973	29	55.8	259	2	US-09-248-796A-20254	Sequence 20254, A
900	29	55.8	106	2	US-09-802-096-6	Sequence 6, Appl1	974	29	55.8	262	1	US-08-015-986A-11	Sequence 11, Appl1
901	29	55.8	106	2	US-09-802-077-6	Sequence 6, Appl1	975	29	55.8	262	1	US-08-446-363-11	Sequence 11, Appl1
902	29	55.8	106	2	US-09-925-179-6	Sequence 34, Appl1	976	29	55.8	268	2	US-10-104-047-2981	Sequence 2981, Ap
903	29	55.8	107	1	US-07-634-278-34								

ALIGNMENTS

Sequence 10, Appl
Sequence 390, Appl
Sequence 49, Appl
Sequence 21735, A
Sequence 12, Appl
Sequence 41750, A
Sequence 20893, A
Sequence 4, Appl
Sequence 4, Appl
Sequence 17777, A
Sequence 5229, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 59131, A
Sequence 16702, A
Sequence 14542, A
Sequence 28650, A
Sequence 16374, A
Sequence 16748, A
Sequence 32, Appl
Sequence 4759, Appl
Sequence 251, Appl

Matches	9;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	QOHNREPLT 9							
Db	1	QOHNREPLT 9							
RESULT 2									
	US-09-795-798-15								
	/ Sequence 15, Application US/09795798								
	/ Patent No. 6703018								
	GENERAL INFORMATION:								
	APPLICANT: Presta, Leonard G.								
	Jardieu, Paula M.								
	TITLE OF INVENTION: Humanized Anti-CD11a Antibodies								
	NUMBER OF SEQUENCES: 24								
	CORRESPONDENCE ADDRESS:								
	ADDRESSEE: Genentech, Inc.								
	STREET: 1 DNA Way								
	CITY: South San Francisco								
	STATE: California								
	COUNTRY: USA								
	ZIP: 94080								
	COMPUTER READABLE FORM:								
	MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk								
	COMPUTER: IBM PC compatible								
	OPERATING SYSTEM: PC-DOS/MS-DOS								
	SOFTWARE: WinPatIn (Genentech)								
	CURRENT APPLICATION DATA:								
	APPLICATION NUMBER: US/09/795,798								
	FILING DATE: 28-Feb-2001								
	CLASSIFICATION: <Unknown>								
	PRIOR APPLICATION DATA:								
	APPLICATION NUMBER: 08/974,899								
	FILING DATE: <Unknown>								
	ATTORNEY/AGENT INFORMATION:								
	NAME: Lee, Wendy M.								
	REGISTRATION NUMBER: 40,378								
	REFERENCE/DOCKET NUMBER: P1014P1								
	TELECOMMUNICATION INFORMATION:								
	TELEPHONE: 650/225-1994								
	TELEFAX: 650/952-9881								
	INFORMATION FOR SEQ ID NO: 15:								
	SEQUENCE CHARACTERISTICS:								
	LENGTH: 9 amino acids								
	TYPE: Amino Acid								
	TOPOLOGY: Linear								
	SEQUENCE DESCRIPTION: SEQ ID NO: 15:								
	US-09-795-798-15								
	Query Match 100.0%; Score 52; DB 2; Length 9;								
	Best Local Similarity 100.0%; Pred. No. 4.6e+05;								
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
QY	1	QOHNREPLT 9							
Db	1	QOHNREPLT 9							
RESULT 3									
	US-08-974-899-1								
	/ Sequence 1, Application US/08974899								
	/ Patent No. 6037454								
	GENERAL INFORMATION:								
	APPLICANT: Presta, Leonard G.								
	Jardieu, Paula M.								
	TITLE OF INVENTION: Humanized Anti-CD11a Antibodies								
	NUMBER OF SEQUENCES: 24								
	CORRESPONDENCE ADDRESS:								
	ADDRESSEE: Genentech, Inc.								
	STREET: 1 DNA Way								
	CITY: South San Francisco								
	STATE: California								

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-974-899-1

Query Match 100.0%; Score 52; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 00HNEYPLT 9
DB 89 00HNEYPLT 97

RESULT 4
US-08-974-899-2
Sequence 2, Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-974-899-1

SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-974-899-2

Query Match 100.0%; Score 52; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 00HNEYPLT 9
DB 89 00HNEYPLT 97

RESULT 5
US-09-795-798-1
Sequence 1, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-795-798-1

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-795-798-1

Query Match 100.0%; Score 52; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 00HNEYPLT 9
DB 89 00HNEYPLT 97

RESULT 6
US-09-795-798-2
Sequence 2, Application US/09795798
Patent No. 6703018
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.

Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-795-798-2
Query Match 100.0%; Score 52; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QQHNEYPLT 9
Db 89 QQHNEYPLT 97
RESULT 7
US-09-027-449-47
Sequence 47, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESSES:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-47
Query Match 100.0%; Score 52; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QQHNEYPLT 9
Db 90 QQHNEYPLT 98
RESULT 8
US-08-804-444A-47
Sequence 47, Application US/0880444A
Patent No. 6117980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESSES:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-804-444A-47
Query Match 100.0%; Score 52; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QQHNEYPLT	9
Db	90	QQHNEYPLT	98

RESULT 9
US-09-026-985-47

```

1
2
3 GENERAL INFORMATION:
4 APPLICANT: Gonzalez, Tania R.
5 APPLICANT: Leong, Steven R.
6 APPLICANT: Presta, Leonard G.
7 TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
8 TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
9 NUMBER OF SEQUENCES: 72

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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
3 OPERATING SYSTEM: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Winpatin (genentech)
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/09/026,985
8 FILING DATE: 20-Feb-1998

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Query Match	100.0%;	Score 52;	DB 2;	Length 109;
Best local Similarity	100.0%;	Pred. NO. 0.031;		
Matches 9; Conservative	0;	Mismatches	0;	Gaps 0;

RESULT 10
 US-09-121-952A--47
 ; Sequence 47, Application US/09121952A
 ; Patent No. 6458355
 ;
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc., Hsej, Vanessa
 ; APPLICANT: Koumentis, Iphigenia
 ; APPLICANT: Leong, Steven R.
 ; APPLICANT: Presta, Leonard G.
 ; APPLICANT: Shatrokh, Zahra
 ; APPLICANT: Zapata, Gerardo A.
 ; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
 ; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
 ; NUMBER OF SEQUENCES: 72
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco

```
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
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Query Match	100.0%;	Score 52;	DB 2;	Length 109;
Best Local Similarity	100.0%;	Pred. No. 0.031;		
Matches	9;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

RESULT 11
 US-09-234-340A-47
 Sequence 47, Application us/09234340A
 Patent No. 6468532
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc., Haei, Vanessa
 APPLICANT: Koumentsis, Iphigenia
 APPLICANT: Leong, Steven R.
 APPLICANT: Presta, Leonard G.
 APPLICANT: Shahrokh, Zahra
 APPLICANT: Zapata, Gerardo A.
 TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
 TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPalin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/234,340A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA: US/09/121,952
 APPLICATION NUMBER:

FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-47

Query Match 100.0%; Score 52; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
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Db 90 QOHNEYP1T 98

RESULT 12
US-09-355-014-47
Sequence 47, Application US/09355014
Patent No. 6870033
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsui, Vanessa
Koumenis, Iphigenia
Leon, Steven R.
Presta, Leonard G.
Shahrokhi, Zahra
Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
FILING DATE: 21-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-355-014-47

Query Match 100.0%; Score 52; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
|||
Db 90 QOHNEYP1T 98

RESULT 13
US-10-330-613A-14
Sequence 14, Application US/10330613A
Patent No. 6924360
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
FILE REFERENCE: ABGENIX.022A
CURRENT APPLICATION NUMBER: US/10/330,613A
CURRENT FILING DATE: 2002-12-26
PRIOR APPLICATION NUMBER: 60/346299
PRIOR FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 107
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-330-613A-14

Query Match 80.8%; Score 42; DB 2; Length 107;
Best Local Similarity 87.5%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNSYPLT 9
|||
Db 90 QHNSYPLT 97

RESULT 14
US-09-508-413A-12
Sequence 12, Application US/09508413A
Patent No. 6667035
GENERAL INFORMATION:
APPLICANT: von Bichel-Streibler, Christoph
TITLE OF INVENTION: AMINO ACID SEQUENCES FOR THERAPEUTIC AND PROPHYLACTIC USE AGAINST DISEASES DUE TO CLOSTRIDIUM DIFFICILE TOXINS
FILE REFERENCE: 415142000200
CURRENT APPLICATION NUMBER: US/09/508,413A
CURRENT FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: PCT/EP98/05759
PRIOR FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 9
TYPE: PRT
ORGANISM: Mus musculus
US-09-508-413A-12

Query Match 78.8%; Score 41; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.6e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
|||
Db 90 QOHNEYP1T 9

RESULT 15
US-09-905-243-80


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; Sequence 80, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: murine/human sequence
US-09-905-243-80

Query Match          78.8%; Score 41; DB 2; Length 102;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
DB 89 QOYNSYPLT 97

RESULT 16
US-09-508-413A-16
; Sequence 16, Application US/09508413A
; Patent No. 6667035
; GENERAL INFORMATION:
; APPLICANT: von Eichel-Streiber, Christoph
; APPLICANT: Moos, Michael
; TITLE OF INVENTION: AMINO ACID SEQUENCES FOR THERAPEUTIC AND
; TITLE OF INVENTION: PROPHYLACTIC USE AGAINST DISEASES DUE TO CLOSTRIDIUM
; TITLE OF INVENTION: DIFFICILE TOXINS
; FILE REFERENCE: 415142000200
; CURRENT APPLICATION NUMBER: US/09/508,413A
; CURRENT FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: PCT/EP98/05759
; PRIOR FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-508-413A-16

Query Match          78.8%; Score 41; DB 2; Length 104;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
DB 87 QOYNSYPLT 95

RESULT 17
US-08-838-682-19
; Sequence 19, Application US/08838682
; Patent No. 6107090
; GENERAL INFORMATION:
; APPLICANT: Bander M.D., Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
```

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; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,682
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1300
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-838-682-19

Query Match          78.8%; Score 41; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
DB 89 QOYNSYPLT 97

RESULT 18
US-08-895-914-19
; Sequence 19, Application US/08895914
; Patent No. 6136311
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603-1051
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,914
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/016,976
; FILING DATE: 06-MAY-1996
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 60/022,125
FILING DATE: 18-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,682
FILING DATE: 09-ARR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1173
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-895-914-19

Query Match 78.8%; Score 41; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
||:|||||
Db 89 QOYNSYPLT 97

RESULT 19
US-09-357-710A-19
Sequence 19, Application US/09357710A
Patent No. 6280956

GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/025
CURRENT APPLICATION NUMBER: US/09/357,710A
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 107
TYPE: PRT
ORGANISM: Mus sp.
US-09-357-710A-19

Query Match 78.8%; Score 41; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
||:|||||
Db 89 QOYNSYPLT 97

RESULT 20
US-09-357-707-19
Sequence 19, Application US/09357707
Patent No. 6649163
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/078
CURRENT APPLICATION NUMBER: US/09/357,707
CURRENT FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: US 08/895,914
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 107
TYPE: PRT
ORGANISM: Mus sp.
US-09-357-707-19

Query Match 78.8%; Score 41; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
||:|||||
Db 89 QOYNSYPLT 97

RESULT 21
US-09-357-708-19
Sequence 19, Application US/09357708
Patent No. 6770450
GENERAL INFORMATION:
APPLICANT: Bander, Neil H.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/028
CURRENT APPLICATION NUMBER: US/09/357,708
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: US 08/895,914
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: US 08/838,682
PRIOR FILING DATE: 1997-04-09
PRIOR APPLICATION NUMBER: US 60/016,976
PRIOR FILING DATE: 1996-05-06
PRIOR APPLICATION NUMBER: US 60/022,125
PRIOR FILING DATE: 1996-07-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 107
TYPE: PRT
ORGANISM: Mus sp.
US-09-357-708-19

Query Match 78.8%; Score 41; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
||:|||||
Db 89 QOYNSYPLT 97

RESULT 22
US-09-905-243-77
Sequence 77, Application US/09905243
Patent No. 6936698
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
Immunogenicity
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 77
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: murine/chimpanzee sequence
US-09-905-243-77

Query Match 78.8%; Score 41; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPILT 9
DB 89 QOYNITPILT 97

RESULT 23
US-09-270-767-42025
Sequence 42025, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42025
LENGTH: 373
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42025

Query Match 75.0%; Score 39; DB 2; Length 373;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QOHNEYPILT 9
DB 180 QOHNEYPILT 187

RESULT 24
US-08-767-128-32
Sequence 32, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-32

Query Match 73.1%; Score 38; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPILT 9
DB 89 QOYNITPILT 97

RESULT 25
US-08-398-613A-20
Sequence 20, Application US/08398613A
Patent No. 5677426
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,613A
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fiteb, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874P1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-398-613A-20

Query Match 73.1%; Score 38; DB 1; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNIEPLT 9
||:|||||
Db 89 QOYNITPLT 97

RESULT 26
US-08-398-612A-20
Sequence 20, Application US/08398612A
Patent No. 5686070
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
TITLE OF INVENTION: Treatment of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,612A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-398-612A-20

TOPOLOGY: linear
US-08-398-612A-20

Query Match 73.1%; Score 38; DB 1; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNIEPLT 9
||:|||||
Db 89 QOYNITPLT 97

RESULT 27
US-08-398-611A-20
Sequence 20, Application US/08398611A
Patent No. 5702946
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
TITLE OF INVENTION: of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,611A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-398-611A-20

Query Match 73.1%; Score 38; DB 1; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNIEPLT 9
||:|||||
Db 89 QOYNITPLT 97

RESULT 28
US-08-491-334A-20
Sequence 20, Application US/08491334A
Patent No. 5874080
GENERAL INFORMATION:

APPLICANT: Hebert, Caroline A.
APPLICANT: Kabakoff, Rhona C.
APPLICANT: Moore, Mark W.
TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
Disorders and Asthma
TITLE OF INVENTION: Disorders and Asthma
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,334A
FILING DATE: 27-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-491-334A-20

Query Match 73.1%; Score 38; DB 1; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNXYPLT 9
Db 89 QOYNYPLT 97

RESULT 29
US-09-027-449-17
Sequence 17, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
Humanized Anti-IL-8 Monoclonal Antibodies
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-17

Query Match 73.1%; Score 38; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNXYPLT 9
Db 89 QOYNYPLT 97

RESULT 30
US-08-804-444A-17
Sequence 17, Application US/0880444A
Patent No. 6117980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-804-444A-17

Query Match 73.1%; Score 38; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOHNHYPLT 9
||:|||||
DB 89 QOYNIYPLT 97

RESULT 31

US-09-026-985-17
; Sequence 17, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-17

Query Match 73.1%; Score 38; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOHNHYPLT 9
||:|||||
DB 89 QOYNIYPLT 97

RESULT 32

US-09-121-952A-17
; Sequence 17, Application US/09121952A
; Patent No. 6458355
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsai, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES

; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-121-952A-17

Query Match 73.1%; Score 38; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOHNHYPLT 9
||:|||||
DB 89 QOYNIYPLT 97

RESULT 33

US-09-234-340A-17
; Sequence 17, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsai, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-17

Query Match 73.1%; Score 38; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNHYPLT 9
Db 89 QOHNHYPLT 97

RESULT 34
US-09-355-014-17
Sequence 17, Application US/09355014
Patent No. 6870033
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
Koumenis, Iphigenia
Leong, Steven R.
Presta, Leonard G.
Shahrokh, Zahra
Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
FILING DATE: 21-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-355-014-17

Query Match 73.1%; Score 38; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNHYPLT 9
Db 89 QOHNHYPLT 97

RESULT 35
US-08-398-612A-28
Sequence 28, Application US/08398612A
Patent No. 5686070
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,612A
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-Mar-1995
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-612A-28

Query Match 73.1%; Score 38; DB 1; Length 237;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNHYPLT 9
Db 112 QOHNHYPLT 120

RESULT 36
US-08-398-611A-28
Sequence 28, Application US/08398611A
Patent No. 5702946
GENERAL INFORMATION:
APPLICANT: Doershuk, Claire M.
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
TITLE OF INVENTION: of Inflammatory Disorders
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,611A
FILING DATE: 01-Mar-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 08/205864
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-611A-28
Query Match 73.1%; Score 38; DB 1; Length 237;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQHNHYPLT 9
||:|||||
Db 112 QQYNYPLT 120
RESULT 37
US-08-491-334A-28
Sequence 28, Application US/08491334A
Patent No. 5874080
GENERAL INFORMATION:
APPLICANT: Hebert, Caroline A.
APPLICANT: Kadakoff, Rhona C.
APPLICANT: Moore, Mark W.
TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
TITLE OF INVENTION: Disorders and Asthma
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,334A
FILING DATE: 27-Jun-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-491-334A-28
Query Match 73.1%; Score 38; DB 1; Length 237;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQHNHYPLT 9
||:|||||
Db 112 QQYNYPLT 120
RESULT 38
US-09-027-449-25
Sequence 25, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664

FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-25

Query Match 73.1%; Score 38; DB 2; Length 237;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEVPLT 9
||:|||||
DB 112 QOYNIYPLT 120

RESULT 39
US-08-804-444A-25
Sequence 25, Application US/08804444A
Patent No. 6117980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-804-444A-25

Query Match 73.1%; Score 38; DB 2; Length 237;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEVPLT 9
||:|||||
DB 112 QOYNIYPLT 120

RESULT 40
US-09-026-985-25
Sequence 25, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-026-985-25

Query Match 73.1%; Score 38; DB 2; Length 237;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEVPLT 9
||:|||||
DB 112 QOYNIYPLT 120

RESULT 41
US-09-121-952A-25
Sequence 25, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., HseI, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shatrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-25

Query Match 73.1%; Score 38; DB 2; Length 237;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNEXPLT 9
||:|||||
Db 112 QOYNITPLT 120

RESULT 42
US-09-234-340A-25
Sequence 25, Application US/09234340A
Patent No. 646832
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsai, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shatrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467

FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-25

Query Match 73.1%; Score 38; DB 2; Length 237;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNEXPLT 9
||:|||||
Db 112 QOYNITPLT 120

RESULT 43
US-09-355-014-25
Sequence 25, Application US/09355014
Patent No. 6670033
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsai, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shatrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/355,014
FILING DATE: 21-Jul-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-355-014-25

Query Match 73.1%; Score 38; DB 2; Length 237;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEYPILT 9
 ||:||||
 Db 112 QOYNIPILT 120

RESULT 44
 US-08-398-613A-28

; Sequence 28, Application US/08398613A
 ; Patent No. 5677426

GENERAL INFORMATION:

APPLICANT: Fong, Sherman
 APPLICANT: Hebert, Caroline Alice
 APPLICANT: Kim, Kyung Jin
 APPLICANT: Leong, Steven R.
 TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/398,613A
 FILING DATE: 01-MAR-1994
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/205864
 FILING DATE: 03-MAR-1994
 ATTORNEY/AGENT INFORMATION:

NAME: Filts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 874P1-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1489

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 238 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-398-613A-28

Query Match 73.1%; Score 38; DB 1; Length 238;
 Best Local Similarity 77.8%; Pred. No. 22;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OOHNEYPILT 9
 ||:||||
 Db 112 QOYNIPILT 120

RESULT 45
 US-08-478-039-85

; Sequence 85, Application US/08478039

; Patent No. 5681722

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Hanna, Nabil

APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA
 COUNTRY: USA
 ZIP: 22313-1404
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/478,039

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/379,072

FILING DATE: 25-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/912,292

FILING DATE: 10-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/735,064

FILING DATE: 25-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Teskin Esq., Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-160

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Monkey

POSITION IN GENOME:

CHROMOSOME/SEGMENT: VKI clone KI-3

US-08-478-039-85

Query Match 71.2%; Score 37; DB 1; Length 108;
 Best Local Similarity 77.8%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 OOHNEYPILT 9
 ||:||||
 Db 90 QOQNSYPLT 98

RESULT 46
 US-08-476-349A-85

; Sequence 85, Application US/08476349A

; Patent No. 5750105

GENERAL INFORMATION:

APPLICANT: Newman, Roland A.

APPLICANT: Hanna, Nabil

APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince St.

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-6620
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VK1 clone KL-3
US-08-476-349A-85

Query Match          71.2%; Score 37; DB 1; Length 108;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOHNEYPPLT 9
DB 90 QOHNSYPLT 98

RESULT 47
US-08-752-693A-2
Sequence 2, Application US/08752693A
Patent No. 6190640
GENERAL INFORMATION:
APPLICANT: Sydney Welt
Gerd Ritter
Leonard Cohen
Clarence William Jr.
Elizabeth Carswell Richards
Mary John
TITLE OF INVENTION: METHOD FOR TREATING NEOPLASIA
USING HUMANIZED ANTIBODIES WHICH
BIND TO ANTIGEN A33
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PAULINE STASIAK, PH.D./2
OPERATING SYSTEM: PC-DOS
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SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,693A
FILING DATE: 19-No. 6190640-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07321
FILING DATE: May 21, 1996
APPLICATION NUMBER: 08/020,223
FILING DATE: February 16, 1993
APPLICATION NUMBER: 07/573,153
FILING DATE: March 18, 1991
APPLICATION NUMBER: 07/327,765
FILING DATE: March 23, 1989
APPLICATION NUMBER: 07/118,411
FILING DATE: No. 6190640ember 6, 1987
APPLICATION NUMBER: 06/724,991
FILING DATE: April 19, 1985
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5381.1 CIP - JEL/MAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
DESCRIPTION: SEQ ID NO: 2
ORIGINAL SOURCE:
ORGANISM: Human A33
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-752-693A-2

Query Match          71.2%; Score 37; DB 2; Length 108;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOHNEYPPLT 9
DB 89 QOHWSYPLT 97

RESULT 48
US-08-918-148-24
Sequence 24, Application US/08918148A
Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
W.
APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 24
LENGTH: 9
TYPE: PRT
ORGANISM: artificial
FEATURE:
NAME/KEY: SE5scfv, 10D10scfv, 12B5scfv VL CDR3
LOCATION: 1-9
OTHER INFORMATION: also 12D5scfv VL CDR3
US-08-918-148-24

Query Match          69.2%; Score 36; DB 2; Length 9;
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Job time : 18.5455 secs

Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPLT 9
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Db 1 QOYSNYPLT 9

RESULT 49
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; Sequence 24, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Rendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; CURRENT FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-138-091A-24

Query Match 69.2%; Score 36; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPLT 9
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Db 1 QOYSNYPLT 9

RESULT 50
US-10-226-795-20
; Sequence 20, Application US/10226795
; Patent No. 6875433
; GENERAL INFORMATION:
; APPLICANT: HART, MARY KATE
; APPLICANT: WILSON, JULIE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
; TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
; FILE REFERENCE: ARMY 166
; CURRENT APPLICATION NUMBER: US/10/226,795
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic light
; OTHER INFORMATION: chain of Mab EGP13C6-1-1 amino acid sequence
US-10-226-795-20

Query Match 69.2%; Score 36; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPLT 9
||:||||
Db 1 QOYSNYPLT 9

Search completed: January 17, 2006, 12:07:52

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 17, 2006, 11:50:44 ; Search time 43.7727 Seconds
(without alignments)
85.909 Million cell updates/sec

Title: US-10-665-658-15

Perfect score: 52

Sequence: 1 OOHNEYPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : Published Applications AA Main:*

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- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	52	100.0	9	4	US-10-727-737-60
3	52	100.0	107	6	US-11-003-819-10
4	52	100.0	108	3	US-09-795-798-1
5	52	100.0	108	3	US-09-795-798-2
6	52	100.0	108	4	US-10-727-737-1
7	52	100.0	108	4	US-10-727-737-2
8	52	100.0	108	5	US-10-877-532-5
9	52	100.0	109	3	US-09-726-258-47
10	52	100.0	214	4	US-10-423-299-3
11	47	90.4	101	4	US-10-010-729-23
12	47	90.4	108	4	US-10-010-729-43
13	46	88.5	9	4	US-10-727-737-64
14	44	84.6	9	4	US-10-727-737-63
15	43	82.7	9	4	US-10-727-737-65
16	42	80.8	9	4	US-10-727-737-62
17	42	80.8	9	5	US-10-726-332-151
18	42	80.8	9	5	US-10-893-576-88
19	42	80.8	107	4	US-10-330-613-14
20	42	80.8	107	4	US-10-330-530-14
21	42	80.8	107	4	US-10-041-860-14
22	42	80.8	107	4	US-10-041-860-18
23	42	80.8	107	4	US-10-041-860-229
24	42	80.8	107	4	US-10-041-860-233
25	42	80.8	107	4	US-10-041-860-263
26	42	80.8	107	4	US-10-041-860-267
27	42	80.8	107	4	US-10-041-860-285

28	42	80.8	107	4	US-10-309-762-51	Sequence 51, Appl
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30	42	80.8	107	4	US-10-038-591-14	Sequence 14, Appl
31	42	80.8	107	4	US-10-660-357-14	Sequence 14, Appl
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33	42	80.8	107	4	US-10-665-383-16	Sequence 16, Appl
34	42	80.8	107	4	US-10-775-444A-14	Sequence 14, Appl
35	42	80.8	107	5	US-10-727-155-4	Sequence 4, Appl
36	42	80.8	107	5	US-10-727-155-8	Sequence 8, Appl
37	42	80.8	107	5	US-10-727-155-12	Sequence 12, Appl
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43	42	80.8	107	5	US-10-727-155-180	Sequence 180, Appl
44	42	80.8	107	5	US-10-727-155-208	Sequence 208, Appl
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48	42	80.8	107	5	US-10-727-155-256	Sequence 256, Appl
49	42	80.8	107	5	US-10-727-155-273	Sequence 273, Appl
50	42	80.8	107	5	US-10-727-155-305	Sequence 305, Appl
51	42	80.8	107	5	US-10-877-773-24	Sequence 24, Appl
52	42	80.8	107	5	US-10-877-774-24	Sequence 24, Appl
53	42	80.8	107	5	US-10-893-576-176	Sequence 176, Appl
54	42	80.8	108	4	US-10-041-860-273	Sequence 273, Appl
55	42	80.8	108	5	US-10-805-177-4	Sequence 4, Appl
56	42	80.8	108	5	US-10-805-177-62	Sequence 62, Appl
57	42	80.8	129	5	US-10-893-576-40	Sequence 40, Appl
58	42	80.8	153	4	US-10-309-762-245	Sequence 245, Appl
59	42	80.8	168	5	US-10-805-177-115	Sequence 115, Appl
60	42	80.8	215	4	US-10-462-040A-2	Sequence 2, Appl
61	41	78.8	9	4	US-10-160-506-6	Sequence 6, Appl
62	41	78.8	9	4	US-10-160-506-104	Sequence 104, Appl
63	41	78.8	9	4	US-10-449-379-6	Sequence 6, Appl
64	41	78.8	9	4	US-10-449-379-104	Sequence 104, Appl
65	41	78.8	9	4	US-10-688-015-6	Sequence 6, Appl
66	41	78.8	9	4	US-10-688-015-104	Sequence 104, Appl
67	41	78.8	9	4	US-10-745-107-12	Sequence 12, Appl
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69	41	78.8	9	4	US-10-160-506-104	Sequence 104, Appl
70	41	78.8	9	5	US-10-783-311-130	Sequence 130, Appl
71	41	78.8	9	6	US-11-102-403-51	Sequence 51, Appl
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73	41	78.8	102	6	US-11-099-331-80	Sequence 80, Appl
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84	41	78.8	107	4	US-10-688-015-20	Sequence 20, Appl
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88	41	78.8	107	4	US-10-160-505-20	Sequence 20, Appl
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91	41	78.8	107	6	US-11-003-819-59	Sequence 59, Appl
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97	41	78.8	126	4	US-10-449-379-28	Sequence 28, Appl
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102	-41	78.8	492	4	US-10-682-845-59	Sequence 59, Appl	175	37	71.2	5	5	US-10-893-576-85	Sequence 85, Appl
103	-41	78.8	492	4	US-10-682-845-61	Sequence 61, Appl	176	37	71.2	9	4	US-10-425-115-356105	Sequence 356105,
104	-41	78.8	492	4	US-10-682-845-63	Sequence 63, Appl	177	37	71.2	71	4	US-10-916-840-72	Sequence 22, Appl
105	-41	78.8	492	4	US-10-682-845-65	Sequence 65, Appl	178	37	71.2	102	5	US-10-890-165-83	Sequence 93, Appl
106	-41	78.8	492	4	US-10-682-845-67	Sequence 67, Appl	179	37	71.2	107	3	US-10-300-215-143	Sequence 143, Appl
107	-41	78.8	492	4	US-10-682-845-69	Sequence 69, Appl	180	37	71.2	107	4	US-10-300-215-145	Sequence 145, Appl
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109	-41	78.8	492	4	US-10-682-845-73	Sequence 73, Appl	182	37	71.2	107	4	US-10-300-215-247	Sequence 247, Appl
110	-41	78.8	492	4	US-10-682-845-75	Sequence 75, Appl	183	37	71.2	107	4	US-10-309-764-43	Sequence 43, Appl
111	-41	78.8	492	4	US-10-682-845-77	Sequence 77, Appl	184	37	71.2	107	4	US-10-221-529-8	Sequence 4, Appl
112	-41	78.8	492	4	US-10-682-845-79	Sequence 79, Appl	185	37	71.2	107	4	US-10-383-447-16	Sequence 16, Appl
113	-41	78.8	492	4	US-10-682-845-81	Sequence 81, Appl	186	37	71.2	107	5	US-10-727-155-24	Sequence 24, Appl
114	-41	78.8	492	4	US-10-682-845-83	Sequence 83, Appl	187	37	71.2	107	5	US-10-877-773-25	Sequence 25, Appl
115	-41	78.8	492	4	US-10-682-845-85	Sequence 85, Appl	188	37	71.2	107	5	US-10-877-773-26	Sequence 26, Appl
116	-41	78.8	492	4	US-10-682-845-87	Sequence 87, Appl	189	37	71.2	107	5	US-10-877-774-25	Sequence 25, Appl
117	-41	78.8	507	4	US-10-074-536-11	Sequence 11, Appl	190	37	71.2	107	5	US-10-877-774-26	Sequence 26, Appl
118	-41	78.8	513	5	US-10-926-731A-12	Sequence 12, Appl	191	37	71.2	107	5	US-10-893-576-175	Sequence 175, Appl
119	-39	75.0	9	3	US-09-974-449-50	Sequence 50, Appl	192	37	71.2	107	5	US-10-510-523-2	Sequence 2, Appl
120	-39	75.0	9	5	US-10-726-333-154	Sequence 154, Appl	193	37	71.2	108	4	US-10-769-612-4	Sequence 4, Appl
121	-39	75.0	105	3	US-09-974-449-4	Sequence 4, Appl	194	37	71.2	127	4	US-10-395-894-25	Sequence 25, Appl
122	-39	75.0	107	5	US-10-815-449-6	Sequence 6, Appl	195	37	71.2	127	4	US-10-695-667-25	Sequence 25, Appl
123	-39	75.0	127	4	US-10-395-894-21	Sequence 21, Appl	196	37	71.2	127	5	US-10-976-352-25	Sequence 25, Appl
124	-39	75.0	127	4	US-10-695-667-21	Sequence 21, Appl	197	37	71.2	129	5	US-10-893-576-34	Sequence 34, Appl
125	-39	75.0	127	4	US-10-976-352-21	Sequence 21, Appl	198	37	71.2	134	4	US-10-309-764-133	Sequence 133, Appl
126	-39	75.0	128	5	US-10-389-221-12	Sequence 12, Appl	199	37	71.2	152	5	US-10-644-277-60	Sequence 60, Appl
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133	-38	73.1	9	3	US-09-875-221A-6	Sequence 6, Appl	206	36	69.2	9	3	US-09-977-797A-62	Sequence 62, Appl
134	-38	73.1	9	4	US-10-320-094-10	Sequence 10, Appl	207	36	69.2	9	3	US-09-977-797A-66	Sequence 66, Appl
135	-38	73.1	9	4	US-10-372-719-13	Sequence 13, Appl	208	36	69.2	9	4	US-10-703-714-30	Sequence 30, Appl
136	-38	73.1	9	5	US-10-728-420B-6	Sequence 6, Appl	209	36	69.2	9	4	US-10-703-714-36	Sequence 36, Appl
137	-38	73.1	9	5	US-10-914-015-6	Sequence 6, Appl	210	36	69.2	9	4	US-10-703-714-42	Sequence 42, Appl
138	-38	73.1	9	5	US-10-891-658-16	Sequence 16, Appl	211	36	69.2	9	4	US-10-703-714-48	Sequence 48, Appl
139	-38	73.1	9	5	US-10-505-747-13	Sequence 13, Appl	212	36	69.2	9	4	US-10-703-714-54	Sequence 54, Appl
140	-38	73.1	107	3	US-09-949-559-9	Sequence 9, Appl	213	36	69.2	9	4	US-10-632-706-133	Sequence 133, Appl
141	-38	73.1	107	3	US-09-949-559-11	Sequence 11, Appl	214	36	69.2	9	4	US-10-630-009-51	Sequence 51, Appl
142	-38	73.1	107	3	US-09-875-221A-9	Sequence 9, Appl	215	36	69.2	9	5	US-10-778-394-24	Sequence 24, Appl
143	-38	73.1	107	3	US-09-875-221A-11	Sequence 11, Appl	216	36	69.2	9	5	US-11-102-403-49	Sequence 49, Appl
144	-38	73.1	107	4	US-10-172-317-4	Sequence 4, Appl	217	36	69.2	9	6	US-10-473-287-42	Sequence 42, Appl
145	-38	73.1	107	4	US-10-041-860-20	Sequence 20, Appl	218	36	69.2	14	5	US-10-473-287-6	Sequence 6, Appl
146	-38	73.1	107	4	US-10-041-860-228	Sequence 228, Appl	219	36	69.2	97	5	US-10-473-287-6	Sequence 10, Appl
147	-38	73.1	107	4	US-10-041-860-291	Sequence 291, Appl	220	36	69.2	100	4	US-10-038-591-10	Sequence 10, Appl
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149	-38	73.1	107	4	US-10-251-085B-127	Sequence 127, Appl	222	36	69.2	104	3	US-09-828-708-2	Sequence 2, Appl
150	-38	73.1	107	4	US-10-665-383-20	Sequence 20, Appl	223	36	69.2	104	5	US-10-630-009-2	Sequence 2, Appl
151	-38	73.1	107	4	US-10-737-252-127	Sequence 127, Appl	224	36	69.2	107	3	US-09-863-693-25	Sequence 25, Appl
152	-38	73.1	107	5	US-10-891-658-12	Sequence 12, Appl	225	36	69.2	107	3	US-09-874-141-1	Sequence 1, Appl
153	-38	73.1	108	3	US-09-949-559-104	Sequence 104, Appl	226	36	69.2	107	3	US-09-874-141-2	Sequence 2, Appl
154	-38	73.1	108	3	US-09-875-221A-104	Sequence 104, Appl	227	36	69.2	107	3	US-09-874-141-3	Sequence 3, Appl
155	-38	73.1	108	3	US-10-067-800-66	Sequence 66, Appl	228	36	69.2	107	3	US-09-874-141-4	Sequence 4, Appl
156	-38	73.1	108	5	US-10-994-679-66	Sequence 66, Appl	229	36	69.2	107	3	US-09-874-141-9	Sequence 9, Appl
157	-38	73.1	123	3	US-09-726-258-17	Sequence 17, Appl	230	36	69.2	107	3	US-09-373-403-25	Sequence 25, Appl
158	-38	73.1	142	4	US-10-372-719-1	Sequence 1, Appl	231	36	69.2	107	4	US-10-143-437-25	Sequence 25, Appl
159	-38	73.1	142	4	US-10-505-747-1	Sequence 1, Appl	232	36	69.2	107	4	US-10-320-613-18	Sequence 18, Appl
160	-38	73.1	152	5	US-10-644-277-96	Sequence 96, Appl	233	36	69.2	107	4	US-10-330-530-18	Sequence 18, Appl
161	-38	73.1	208	4	US-10-634-581-1	Sequence 1, Appl	234	36	69.2	107	4	US-10-041-860-24	Sequence 24, Appl
162	-38	73.1	208	5	US-10-634-581-1	Sequence 1, Appl	235	36	69.2	107	4	US-10-041-860-26	Sequence 26, Appl
163	-38	73.1	214	3	US-09-949-559-128	Sequence 128, Appl	236	36	69.2	107	4	US-10-041-860-28	Sequence 28, Appl
164	-38	73.1	214	3	US-09-875-221A-128	Sequence 128, Appl	237	36	69.2	107	4	US-10-041-860-36	Sequence 36, Appl
165	-38	73.1	214	4	US-10-310-454-4	Sequence 4, Appl	238	36	69.2	107	4	US-10-041-860-20	Sequence 20, Appl
166	-38	73.1	214	4	US-10-728-420B-113	Sequence 113, Appl	239	36	69.2	107	4	US-10-041-860-231	Sequence 231, Appl
167	-38	73.1	214	5	US-10-914-015-113	Sequence 113, Appl	240	36	69.2	107	4	US-10-041-860-232	Sequence 233, Appl
168	-38	73.1	214	5	US-10-891-658-44	Sequence 44, Appl	241	36	69.2	107	4	US-10-041-860-234	Sequence 234, Appl
169	-38	73.1	227	3	US-09-726-258-25	Sequence 25, Appl	242	36	69.2	107	4	US-10-041-860-264	Sequence 265, Appl
170	-38	73.1	227	3	US-09-880-748-1943	Sequence 1943, Ap	243	36	69.2	107	4	US-10-041-860-265	Sequence 265, Appl
171	-38	73.1	243	3	US-09-880-748-2064	Sequence 2064, Ap	244	36	69.2	107	4	US-10-041-860-266	Sequence 266, Appl
172	-38	73.1	243	4	US-10-293-418-1943	Sequence 1943, Ap	245	36	69.2	107	4	US-10-041-860-268	Sequence 268, Appl
173	-38	73.1	243	4	US-10-293-418-2064	Sequence 2064, Ap	246	36	69.2	107	4	US-10-041-860-303	Sequence 303, Appl

247	36	69.2	107	4	US-10-041-860-309	Sequence 309, App	320	36	69.2	163	5	US-10-452-593-20	Sequence 20, Appl
248	36	69.2	107	4	US-10-041-860-316	Sequence 316, App	321	36	69.2	177	5	US-10-450-763-3214	Sequence 32184, A
249	36	69.2	107	4	US-10-041-860-340	Sequence 340, App	322	36	69.2	232	5	US-10-511-794-17	Sequence 17, Appl
250	36	69.2	107	4	US-10-171-681-1	Sequence 1, Appl	323	36	69.2	234	3	US-09-800-129-150	Sequence 150, App
251	36	69.2	107	4	US-10-171-681-2	Sequence 2, Appl	324	36	69.2	234	3	US-09-833-245-2210	Sequence 2210, App
252	36	69.2	107	4	US-10-171-681-3	Sequence 3, Appl	325	36	69.2	236	4	US-10-038-591-51	Sequence 51, Appl
253	36	69.2	107	4	US-10-171-681-4	Sequence 4, Appl	326	36	69.2	236	4	US-10-038-591-52	Sequence 52, Appl
254	36	69.2	107	4	US-10-171-680-1	Sequence 1, Appl	327	36	69.2	236	4	US-10-775-444A-51	Sequence 51, Appl
255	36	69.2	107	4	US-10-171-680-2	Sequence 2, Appl	328	36	69.2	236	4	US-10-775-444A-52	Sequence 52, Appl
256	36	69.2	107	4	US-10-171-680-3	Sequence 3, Appl	329	36	69.2	236	5	US-10-917-073A-5	Sequence 5, Appl
257	36	69.2	107	4	US-10-171-680-4	Sequence 4, Appl	330	36	69.2	236	5	US-10-917-073A-6	Sequence 6, Appl
258	36	69.2	107	4	US-10-010-729-47	Sequence 47, Appl	331	36	69.2	239	3	US-09-880-748-1882	Sequence 1882, App
259	36	69.2	107	4	US-10-447-331-3	Sequence 3, Appl	332	36	69.2	239	3	US-09-880-748-1922	Sequence 1922, App
260	36	69.2	107	4	US-10-309-764-42	Sequence 42, Appl	333	36	69.2	239	4	US-10-151-882-23	Sequence 23, Appl
261	36	69.2	107	4	US-10-309-764-44	Sequence 44, Appl	334	36	69.2	239	4	US-10-293-418-1882	Sequence 1882, App
262	36	69.2	107	4	US-10-309-764-48	Sequence 48, Appl	335	36	69.2	239	4	US-10-293-418-1922	Sequence 1922, App
263	36	69.2	107	4	US-10-309-762-52	Sequence 52, Appl	336	36	69.2	239	5	US-10-935-290-80	Sequence 80, Appl
264	36	69.2	107	4	US-10-309-762-166	Sequence 166, App	337	36	69.2	239	5	US-10-935-290-80	Sequence 80, Appl
265	36	69.2	107	4	US-10-257-864A-103	Sequence 103, App	338	36	69.2	240	5	US-10-151-882-22	Sequence 22, Appl
266	36	69.2	107	4	US-10-251-085B-117	Sequence 117, App	339	36	69.2	240	5	US-10-935-290-80	Sequence 80, Appl
267	36	69.2	107	4	US-10-399-518-132	Sequence 132, App	340	36	69.2	241	3	US-09-880-748-1889	Sequence 1889, App
268	36	69.2	107	4	US-10-660-357-18	Sequence 18, Appl	341	36	69.2	241	3	US-09-880-748-1901	Sequence 1901, App
269	36	69.2	107	4	US-10-665-383-28	Sequence 28, Appl	342	36	69.2	241	3	US-10-151-882-21	Sequence 21, Appl
270	36	69.2	107	4	US-10-665-383-32	Sequence 32, Appl	343	36	69.2	241	4	US-10-293-418-1889	Sequence 1889, App
271	36	69.2	107	4	US-10-665-383-36	Sequence 36, Appl	344	36	69.2	241	4	US-10-293-418-1889	Sequence 1889, App
272	36	69.2	107	4	US-10-665-383-52	Sequence 52, Appl	345	36	69.2	241	4	US-10-293-418-1901	Sequence 1901, App
273	36	69.2	107	4	US-10-703-714-4	Sequence 4, Appl	346	36	69.2	241	4	US-10-293-418-1948	Sequence 1948, App
274	36	69.2	107	4	US-10-703-714-8	Sequence 8, Appl	347	36	69.2	241	5	US-10-511-794-16	Sequence 16, Appl
275	36	69.2	107	4	US-10-703-714-12	Sequence 12, Appl	348	36	69.2	242	6	US-11-090-847-89	Sequence 89, Appl
276	36	69.2	107	4	US-10-703-714-16	Sequence 16, Appl	349	36	69.2	243	3	US-09-880-748-1883	Sequence 1883, App
277	36	69.2	107	4	US-10-703-714-20	Sequence 20, Appl	350	36	69.2	243	3	US-09-880-748-1935	Sequence 1935, App
278	36	69.2	107	4	US-10-737-252-117	Sequence 117, App	351	36	69.2	243	3	US-09-880-748-1945	Sequence 1945, App
279	36	69.2	107	4	US-10-481-212-3	Sequence 3, Appl	352	36	69.2	243	3	US-09-880-748-2063	Sequence 2063, App
280	36	69.2	107	5	US-10-399-585-131	Sequence 131, App	353	36	69.2	243	4	US-10-293-418-1883	Sequence 1883, App
281	36	69.2	107	5	US-10-645-085A-103	Sequence 103, App	354	36	69.2	243	4	US-10-293-418-1935	Sequence 1935, App
282	36	69.2	107	5	US-10-727-155-32	Sequence 32, Appl	355	36	69.2	243	4	US-10-293-418-1945	Sequence 1945, App
283	36	69.2	107	5	US-10-727-155-60	Sequence 60, Appl	356	36	69.2	243	4	US-10-778-394-75	Sequence 75, Appl
284	36	69.2	107	5	US-10-727-155-64	Sequence 64, Appl	357	36	69.2	244	5	US-11-090-847-59	Sequence 59, Appl
285	36	69.2	107	5	US-10-727-155-72	Sequence 72, Appl	358	36	69.2	244	6	US-11-090-847-66	Sequence 66, Appl
286	36	69.2	107	5	US-10-727-155-146	Sequence 146, App	359	36	69.2	244	6	US-11-090-847-89	Sequence 89, Appl
287	36	69.2	107	5	US-10-727-155-216	Sequence 216, App	360	36	69.2	245	3	US-09-880-748-1900	Sequence 1900, App
288	36	69.2	107	5	US-10-727-155-216	Sequence 216, App	361	36	69.2	245	3	US-09-880-748-1900	Sequence 1900, App
289	36	69.2	107	5	US-10-727-155-260	Sequence 260, App	362	36	69.2	245	4	US-10-293-418-1900	Sequence 1900, App
290	36	69.2	107	5	US-10-727-155-274	Sequence 274, App	363	36	69.2	245	4	US-10-293-418-1902	Sequence 1902, App
291	36	69.2	107	5	US-10-727-155-307	Sequence 307, App	364	36	69.2	245	5	US-10-778-394-73	Sequence 73, Appl
292	36	69.2	107	5	US-10-727-155-313	Sequence 313, App	365	36	69.2	245	5	US-10-778-394-74	Sequence 74, Appl
293	36	69.2	107	5	US-10-901-736-2	Sequence 2, Appl	366	36	69.2	245	5	US-10-778-394-76	Sequence 76, Appl
294	36	69.2	107	6	US-11-102-403-7	Sequence 7, Appl	367	36	69.2	246	3	US-09-880-748-1920	Sequence 1920, App
295	36	69.2	107	6	US-11-102-403-7	Sequence 7, Appl	368	36	69.2	246	4	US-09-880-748-2062	Sequence 2062, App
296	36	69.2	108	3	US-09-215-163-21	Sequence 21, Appl	369	36	69.2	246	4	US-10-293-418-1920	Sequence 1920, App
297	36	69.2	108	4	US-10-803-622-244	Sequence 244, App	370	36	69.2	246	4	US-10-293-418-2062	Sequence 2062, App
298	36	69.2	108	4	US-10-803-653-244	Sequence 244, App	371	36	69.2	247	3	US-09-880-748-1969	Sequence 1969, App
299	36	69.2	112	4	US-10-148-737-2	Sequence 2, Appl	372	36	69.2	247	3	US-09-880-748-1177	Sequence 1177, App
300	36	69.2	112	6	US-11-054-041-2	Sequence 2, Appl	373	36	69.2	247	3	US-09-880-748-1923	Sequence 1923, App
301	36	69.2	113	4	US-10-364-743-47	Sequence 47, Appl	374	36	69.2	247	4	US-10-293-418-1969	Sequence 1969, App
302	36	69.2	113	5	US-10-452-593-47	Sequence 47, Appl	375	36	69.2	247	4	US-10-293-418-1923	Sequence 1923, App
303	36	69.2	115	4	US-10-297-371A-8	Sequence 8, Appl	376	36	69.2	247	4	US-10-293-418-1923	Sequence 1923, App
304	36	69.2	116	4	US-10-010-729-27	Sequence 27, Appl	377	36	69.2	247	4	US-10-293-418-1922	Sequence 1922, App
305	36	69.2	119	4	US-10-665-383-78	Sequence 78, Appl	378	36	69.2	247	5	US-10-935-290-104	Sequence 104, App
306	36	69.2	127	4	US-10-309-764-129	Sequence 129, App	379	36	69.2	248	3	US-09-880-748-1008	Sequence 1008, App
307	36	69.2	127	4	US-10-309-764-137	Sequence 137, App	380	36	69.2	248	3	US-09-880-748-1421	Sequence 1421, App
308	36	69.2	129	4	US-10-257-864A-105	Sequence 105, App	381	36	69.2	248	3	US-09-880-748-1700	Sequence 1700, App
309	36	69.2	129	4	US-10-399-518-134	Sequence 134, App	382	36	69.2	248	3	US-09-880-748-1771	Sequence 1771, App
310	36	69.2	129	5	US-10-399-585-133	Sequence 133, App	383	36	69.2	248	3	US-09-880-748-1778	Sequence 1778, App
311	36	69.2	129	5	US-10-645-085A-105	Sequence 105, App	384	36	69.2	248	4	US-10-293-418-1008	Sequence 1008, App
312	36	69.2	133	3	US-09-874-141-45	Sequence 45, Appl	385	36	69.2	248	4	US-10-293-418-1421	Sequence 1421, App
313	36	69.2	133	3	US-09-874-141-47	Sequence 47, Appl	386	36	69.2	248	4	US-10-293-418-1700	Sequence 1700, App
314	36	69.2	133	3	US-09-874-141-51	Sequence 51, Appl	387	36	69.2	248	4	US-10-293-418-1771	Sequence 1771, App
315	36	69.2	136	4	US-10-038-591-2	Sequence 2, Appl	388	36	69.2	249	3	US-10-293-418-1778	Sequence 1778, App
316	36	69.2	136	4	US-10-775-444A-2	Sequence 2, Appl	389	36	69.2	249	3	US-09-880-748-919	Sequence 919, App
317	36	69.2	145	4	US-10-226-795-17	Sequence 17, Appl	390	36	69.2	249	3	US-09-880-748-919	Sequence 919, App
318	36	69.2	154	4	US-10-665-383-82	Sequence 82, Appl	391	36	69.2	249	3	US-09-880-748-926	Sequence 926, App
319	36	69.2	163	4	US-10-364-743-20	Sequence 20, Appl	392	36	69.2	249	3	US-09-880-748-1188	Sequence 1188, App

393	36	69.2	249	4	US-10-293-418-918	Sequence 918, App	466	35	67.3	216	4	US-10-425-115-193776	Sequence 193776,
394	36	69.2	249	4	US-10-293-418-919	Sequence 919, App	467	35	67.3	217	4	US-10-425-114-68831	Sequence 68831, A
395	36	69.2	249	4	US-10-293-418-926	Sequence 926, App	468	35	67.3	223	5	US-10-769-144-6	Sequence 6, Appli
396	36	69.2	249	4	US-10-293-418-1188	Sequence 1188, Ap	469	35	67.3	233	5	US-10-903-191-6	Sequence 6, Appli
397	36	69.2	250	3	US-09-880-748-932	Sequence 932, App	470	35	67.3	234	4	US-10-684-109-97	Sequence 97, Appl
398	36	69.2	250	3	US-10-293-418-932	Sequence 932, App	471	35	67.3	234	4	US-10-684-109-103	Sequence 103, App
399	36	69.2	250	6	US-11-090-847-87	Sequence 87, Appl	472	35	67.3	234	4	US-10-684-109-115	Sequence 115, App
400	36	69.2	251	3	US-09-880-748-922	Sequence 922, App	473	35	67.3	241	4	US-10-221-945-1	Sequence 1, Appli
401	36	69.2	251	3	US-09-880-748-1320	Sequence 1320, Ap	474	35	67.3	244	4	US-10-264-049-342	Sequence 442, Ap
402	36	69.2	251	3	US-10-293-418-922	Sequence 922, App	475	35	67.3	291	4	US-10-406-830-12	Sequence 10, Appl
403	36	69.2	251	4	US-10-293-418-1320	Sequence 1320, Ap	476	35	67.3	411	5	US-10-769-144-12	Sequence 12, Appl
404	36	69.2	255	3	US-09-880-748-1603	Sequence 1603, Ap	477	35	67.3	411	5	US-10-903-191-12	Sequence 12, Appl
405	36	69.2	255	4	US-10-293-418-1603	Sequence 1603, Ap	478	35	67.3	692	4	US-10-211-462-227	Sequence 227, App
406	36	69.2	255	5	US-10-511-794-21	Sequence 21, Appl	479	35	67.3	1092	4	US-10-369-493-2674	Sequence 2674, Ap
407	36	69.2	266	4	US-10-257-864A-108	Sequence 108, App	480	34	65.4	9	3	US-09-948-939-36	Sequence 36, Appl
408	36	69.2	266	4	US-10-399-518-137	Sequence 137, App	481	34	65.4	9	4	US-10-173-551-32	Sequence 32, Appl
409	36	69.2	266	4	US-10-399-585-135	Sequence 135, App	482	34	65.4	9	4	US-10-338-366-48	Sequence 48, Appl
410	36	69.2	266	5	US-10-399-585-135	Sequence 135, App	483	34	65.4	9	4	US-10-312-316-32	Sequence 32, Appl
411	36	69.2	295	5	US-10-645-085A-108	Sequence 108, App	484	34	65.4	9	4	US-10-312-316-34	Sequence 34, Appl
412	36	69.2	332	4	US-10-211-488-7	Sequence 54392, A	485	34	65.4	9	6	US-11-009-731-80	Sequence 80, Appl
413	36	69.2	337	4	US-10-094-886-36	Sequence 7, Appli	486	34	65.4	9	6	US-11-040-846-36	Sequence 36, Appl
414	36	69.2	356	5	US-10-450-765-48355	Sequence 36, Appl	487	34	65.4	9	6	US-11-040-846-36	Sequence 36, Appl
415	36	69.2	809	4	US-10-067-514-2	Sequence 48355, A	488	34	65.4	27	4	US-11-102-403-47	Sequence 47, Appl
416	36	69.2	809	4	US-10-419-723-2	Sequence 2, Appli	489	34	65.4	27	4	US-10-269-711-51	Sequence 51, Appl
417	36	69.2	809	4	US-10-255-120-2	Sequence 2, Appli	490	34	65.4	84	5	US-10-684-109-62	Sequence 62, Appl
418	36	69.2	809	5	US-10-735-973-7	Sequence 7, Appli	491	34	65.4	88	4	US-10-688-255-9	Sequence 9, Appli
419	36	69.2	809	5	US-10-868-397-2	Sequence 2, Appli	492	34	65.4	88	4	US-10-424-599-176655	Sequence 176655,
420	36	69.2	851	5	US-10-488-197-37	Sequence 37, Appl	493	34	65.4	4	4	US-10-425-115-127108	Sequence 37108,
421	36	69.2	1373	6	US-11-097-143-39900	Sequence 37, Appl	494	34	65.4	107	3	US-09-948-939-13	Sequence 13, Appl
422	35	67.3	9	5	US-10-769-144-18	Sequence 39900, A	495	34	65.4	107	3	US-09-144-886-76	Sequence 76, Appl
423	35	67.3	9	5	US-10-823-253-20	Sequence 18, Appl	496	34	65.4	107	4	US-10-073-644C-4	Sequence 4, Appli
424	35	67.3	9	5	US-10-823-253-20	Sequence 20, Appl	497	34	65.4	107	4	US-10-173-551-29	Sequence 29, Appl
425	35	67.3	9	5	US-10-726-333-193	Sequence 20, Appl	498	34	65.4	107	4	US-10-338-366-12	Sequence 12, Appl
426	35	67.3	9	5	US-10-891-658-121	Sequence 121, App	499	34	65.4	107	4	US-10-309-762-58	Sequence 58, Appl
427	35	67.3	9	5	US-10-891-658-127	Sequence 127, App	500	34	65.4	107	4	US-10-269-711-5	Sequence 5, Appli
428	35	67.3	9	5	US-10-823-810-20	Sequence 20, Appl	501	34	65.4	107	4	US-10-251-085B-108	Sequence 108, App
429	35	67.3	9	5	US-10-903-191-18	Sequence 18, Appl	502	34	65.4	107	4	US-10-251-085B-119	Sequence 119, App
430	35	67.3	83	4	US-10-424-599-253918	Sequence 253918,	503	34	65.4	107	4	US-10-251-085B-121	Sequence 121, App
431	35	67.3	105	5	US-10-823-253-30	Sequence 30, Appl	504	34	65.4	107	4	US-10-251-085B-125	Sequence 125, App
432	35	67.3	105	5	US-10-823-810-30	Sequence 30, Appl	505	34	65.4	107	4	US-10-251-085B-125	Sequence 125, App
433	35	67.3	107	3	US-09-851-614-2	Sequence 2, Appli	506	34	65.4	107	4	US-10-251-085B-128	Sequence 128, App
434	35	67.3	107	4	US-10-035-637-2	Sequence 2, Appli	507	34	65.4	107	4	US-10-632-706-73	Sequence 73, Appl
435	35	67.3	107	4	US-10-300-215-169	Sequence 169, App	508	34	65.4	107	4	US-10-737-252-108	Sequence 108, App
436	35	67.3	107	4	US-10-374-600-113	Sequence 113, App	509	34	65.4	107	4	US-10-737-252-109	Sequence 109, App
437	35	67.3	107	4	US-10-374-531-113	Sequence 113, App	510	34	65.4	107	4	US-10-737-252-112	Sequence 112, App
438	35	67.3	107	4	US-10-309-762-50	Sequence 50, Appl	511	34	65.4	107	4	US-10-737-252-119	Sequence 119, App
439	35	67.3	107	4	US-10-309-762-55	Sequence 55, Appl	512	34	65.4	107	4	US-10-737-252-119	Sequence 119, App
440	35	67.3	107	4	US-10-309-762-160	Sequence 160, App	513	34	65.4	107	4	US-10-737-252-121	Sequence 121, App
441	35	67.3	107	4	US-10-251-085B-118	Sequence 118, App	514	34	65.4	107	4	US-10-737-252-125	Sequence 125, App
442	35	67.3	107	4	US-10-684-109-49	Sequence 45, Appl	515	34	65.4	107	5	US-10-737-252-128	Sequence 128, App
443	35	67.3	107	4	US-10-684-109-57	Sequence 49, Appl	516	34	65.4	107	5	US-10-815-449-2	Sequence 2, Appli
444	35	67.3	107	4	US-10-737-252-118	Sequence 57, Appl	517	34	65.4	107	5	US-10-815-449-4	Sequence 4, Appli
445	35	67.3	107	5	US-10-769-144-8	Sequence 118, App	518	34	65.4	107	5	US-10-727-155-126	Sequence 126, App
446	35	67.3	107	5	US-10-823-253-25	Sequence 25, Appl	519	34	65.4	107	5	US-10-727-155-110	Sequence 310, App
447	35	67.3	107	5	US-10-823-253-28	Sequence 28, Appl	520	34	65.4	107	5	US-10-510-523-13	Sequence 13, Appl
448	35	67.3	107	5	US-10-823-253-32	Sequence 32, Appl	521	34	65.4	107	5	US-10-822-306A-17	Sequence 17, Appl
449	35	67.3	107	5	US-10-891-658-88	Sequence 88, Appl	522	34	65.4	107	6	US-11-009-771-91	Sequence 91, Appl
450	35	67.3	107	5	US-10-823-810-25	Sequence 28, Appl	523	34	65.4	107	6	US-11-040-846-13	Sequence 13, Appl
451	35	67.3	107	5	US-10-823-810-28	Sequence 28, Appl	524	34	65.4	107	6	US-11-102-403-1	Sequence 1, Appli
452	35	67.3	107	5	US-10-903-191-8	Sequence 32, Appl	525	34	65.4	108	4	US-10-408-901-12	Sequence 12, Appl
453	35	67.3	107	5	US-10-822-306A-16	Sequence 16, Appl	526	34	65.4	108	4	US-10-408-901-20	Sequence 20, Appl
454	35	67.3	108	5	US-10-726-332-10	Sequence 211, App	527	34	65.4	109	5	US-10-312-316-50	Sequence 50, Appl
455	35	67.3	108	5	US-10-726-332-211	Sequence 211, App	528	34	65.4	109	5	US-10-895-135-51	Sequence 51, Appl
456	35	67.3	108	5	US-10-891-658-90	Sequence 90, Appl	529	34	65.4	110	4	US-10-312-316-52	Sequence 52, Appl
457	35	67.3	108	5	US-10-891-658-90	Sequence 90, Appl	530	34	65.4	110	4	US-10-803-622-237	Sequence 237, App
458	35	67.3	113	4	US-10-364-743-44	Sequence 44, Appl	531	34	65.4	110	4	US-10-803-622-254	Sequence 254, App
459	35	67.3	113	4	US-10-364-743-46	Sequence 46, Appl	532	34	65.4	110	4	US-10-803-622-255	Sequence 255, App
460	35	67.3	113	5	US-10-452-593-44	Sequence 46, Appl	533	34	65.4	110	4	US-10-803-622-257	Sequence 257, App
461	35	67.3	113	5	US-10-452-593-46	Sequence 46, Appl	534	34	65.4	110	4	US-10-803-623-337	Sequence 237, App
462	35	67.3	114	4	US-10-275-046-83	Sequence 83, Appl	535	34	65.4	110	4	US-10-803-653-254	Sequence 254, App
463	35	67.3	129	4	US-10-365-123-47	Sequence 47, Appl	536	34	65.4	110	4	US-10-803-653-255	Sequence 255, App
464	35	67.3	161	3	US-09-187-693-56	Sequence 56, Appl	537	34	65.4	110	4	US-10-803-653-255	Sequence 255, App
465	35	67.3	161	6	US-11-021-795-56	Sequence 56, Appl	538	34	65.4	110	4	US-10-803-653-256	Sequence 256, App

539	34	65.4	110	4	US-10-803-653-257	Sequence 257, App	612	34	65.4	652	4	US-10-614-076-64	Sequence 64, Appl
540	34	65.4	110	5	US-10-688-255-4	Sequence 4, Appl1	613	34	65.4	652	4	US-10-614-076-66	Sequence 66, Appl
541	34	65.4	112	4	US-10-632-706-82	Sequence 82, Appl1	614	34	65.4	652	4	US-10-614-076-68	Sequence 68, Appl
542	34	65.4	116	4	US-10-408-765A-306	Sequence 306, App	615	34	65.4	652	4	US-10-614-076-98	Sequence 98, Appl
543	34	65.4	122	4	US-10-425-115-283217	Sequence 283217, App	616	34	65.4	652	4	US-10-614-076-108	Sequence 108, Appl
544	34	65.4	132	4	US-10-469-304-23	Sequence 23, Appl1	617	34	65.4	652	4	US-10-614-076-110	Sequence 110, App
545	34	65.4	139	4	US-10-424-599-241298	Sequence 241298, App	618	34	65.4	652	4	US-10-614-076-111	Sequence 111, App
546	34	65.4	145	3	US-09-867-550-604	Sequence 604, App	619	34	65.4	652	4	US-10-782-141-11	Sequence 11, Appl
547	34	65.4	158	4	US-10-289-762-383	Sequence 783, App	620	34	65.4	652	4	US-10-782-096-13	Sequence 13, Appl
548	34	65.4	184	4	US-10-684-109-78	Sequence 78, Appl	621	34	65.4	652	5	US-10-781-979-13	Sequence 13, Appl
549	34	65.4	194	4	US-10-437-963-145550	Sequence 145550, App	622	34	65.4	653	4	US-10-232-665-8	Sequence 8, Appl1
550	34	65.4	204	4	US-10-437-963-164312	Sequence 164312, App	623	34	65.4	653	4	US-10-232-665-10	Sequence 10, Appl
551	34	65.4	214	4	US-10-408-901-36	Sequence 36, Appl1	624	34	65.4	653	4	US-10-232-665-12	Sequence 12, Appl
552	34	65.4	214	4	US-10-408-901-44	Sequence 44, Appl1	625	34	65.4	653	4	US-10-232-665-14	Sequence 14, Appl
553	34	65.4	224	3	US-09-453-234-84	Sequence 84, Appl	626	34	65.4	653	4	US-10-232-665-16	Sequence 16, Appl
554	34	65.4	236	5	US-10-858-186-20	Sequence 20, Appl	627	34	65.4	653	4	US-10-232-665-18	Sequence 18, Appl
555	34	65.4	241	4	US-10-425-115-271760	Sequence 271760, App	628	34	65.4	653	4	US-10-232-665-20	Sequence 20, Appl
556	34	65.4	244	4	US-10-425-115-317082	Sequence 317082, App	629	34	65.4	653	4	US-10-232-665-22	Sequence 22, Appl
557	34	65.4	244	5	US-10-609-671-2	Sequence 2, Appl1	630	34	65.4	653	4	US-10-232-665-24	Sequence 24, Appl
558	34	65.4	250	4	US-10-333-235A-55	Sequence 55, Appl1	631	34	65.4	653	4	US-10-232-665-37	Sequence 37, Appl
559	34	65.4	271	4	US-10-467-433-20	Sequence 20, Appl1	632	34	65.4	653	4	US-10-232-665-39	Sequence 39, Appl
560	34	65.4	284	4	US-10-282-122A-51132	Sequence 51132, A	633	34	65.4	653	4	US-10-614-076-100	Sequence 100, App
561	34	65.4	284	5	US-10-504-582-153	Sequence 153, App	634	34	65.4	659	4	US-10-614-076-112	Sequence 112, App
562	34	65.4	284	5	US-10-504-582-155	Sequence 155, App	635	34	65.4	659	4	US-10-782-096-12	Sequence 12, Appl
563	34	65.4	285	5	US-10-609-671-4	Sequence 4, Appl1	636	34	65.4	659	4	US-10-782-570-9	Sequence 9, Appl1
564	34	65.4	285	5	US-10-609-671-6	Sequence 6, Appl1	637	34	65.4	659	5	US-10-783-417-7	Sequence 7, Appl1
565	34	65.4	290	4	US-10-437-963-145583	Sequence 145583, App	638	34	65.4	690	3	US-09-801-366-40	Sequence 40, Appl
566	34	65.4	301	4	US-10-369-493-19044	Sequence 19044, A	639	34	65.4	803	3	US-09-801-366-394	Sequence 394, App
567	34	65.4	309	4	US-10-467-433-14	Sequence 14, Appl	640	34	65.4	842	4	US-10-369-493-1940	Sequence 1940, Ap
568	34	65.4	339	4	US-10-312-273-369	Sequence 369, App	641	34	65.4	942	4	US-10-282-122A-54936	Sequence 54936, A
569	34	65.4	362	4	US-10-289-762-1029	Sequence 1029, Ap	642	34	65.4	998	6	US-11-097-143-10842	Sequence 10842, A
570	34	65.4	368	4	US-10-333-235A-58	Sequence 58, Appl	643	34	65.4	998	6	US-11-097-143-10953	Sequence 10953, A
571	34	65.4	407	4	US-10-437-963-187891	Sequence 187891, App	644	34	65.4	2285	6	US-11-097-143-15963	Sequence 15963, A
572	34	65.4	465	4	US-10-333-235A-59	Sequence 59, Appl	645	34	65.4	10421	4	US-10-282-122A-61631	Sequence 61631, A
573	34	65.4	504	4	US-10-437-963-164310	Sequence 164310, App	646	33	63.5	9	3	US-09-910-055-28	Sequence 28, Appl
574	34	65.4	511	6	US-11-097-143-21171	Sequence 21171, A	647	33	63.5	9	3	US-09-920-262A-6	Sequence 6, Appl1
575	34	65.4	524	4	US-10-425-115-323831	Sequence 323831, App	648	33	63.5	9	4	US-10-072-301-47	Sequence 47, Appl
576	34	65.4	556	3	US-09-819-266-28	Sequence 28, Appl	649	33	63.5	9	4	US-10-071-886-47	Sequence 47, Appl
577	34	65.4	624	4	US-10-437-963-110476	Sequence 110476, App	650	33	63.5	9	4	US-10-360-882-47	Sequence 47, Appl
578	34	65.4	651	4	US-10-614-076-52	Sequence 52, Appl	651	33	63.5	9	4	US-10-436-783-20	Sequence 20, Appl
579	34	65.4	651	4	US-10-614-076-56	Sequence 56, Appl	652	33	63.5	9	5	US-10-912-994-6	Sequence 6, Appl1
580	34	65.4	651	4	US-10-614-076-58	Sequence 58, Appl	653	33	63.5	9	5	US-10-783-311-138	Sequence 138, App
581	34	65.4	652	4	US-10-332-665-2	Sequence 2, Appl1	654	33	63.5	9	5	US-10-975-883-6	Sequence 6, Appl1
582	34	65.4	652	4	US-10-332-665-4	Sequence 4, Appl1	655	33	63.5	9	5	US-10-988-485-47	Sequence 47, Appl
583	34	65.4	652	4	US-10-332-665-6	Sequence 6, Appl1	656	33	63.5	9	5	US-10-927-433-3	Sequence 3, Appl1
584	34	65.4	652	4	US-10-614-076-2	Sequence 2, Appl1	657	33	63.5	9	5	US-10-975-740A-6	Sequence 6, Appl1
585	34	65.4	652	4	US-10-614-076-4	Sequence 4, Appl1	658	33	63.5	9	5	US-10-975-708-6	Sequence 6, Appl1
586	34	65.4	652	4	US-10-614-076-6	Sequence 6, Appl1	659	33	63.5	9	6	US-11-004-795A-20	Sequence 20, Appl
587	34	65.4	652	4	US-10-614-076-8	Sequence 8, Appl1	660	33	63.5	9	6	US-11-004-794A-20	Sequence 20, Appl
588	34	65.4	652	4	US-10-614-076-10	Sequence 10, Appl	661	33	63.5	14	5	US-10-473-287-43	Sequence 43, Appl
589	34	65.4	652	4	US-10-614-076-12	Sequence 12, Appl	662	33	63.5	36	3	US-09-864-761-34133	Sequence 34133, A
590	34	65.4	652	4	US-10-614-076-14	Sequence 14, Appl	663	33	63.5	71	4	US-10-424-599-210976	Sequence 210976, App
591	34	65.4	652	4	US-10-614-076-16	Sequence 16, Appl	664	33	63.5	74	4	US-10-424-599-252185	Sequence 252185, App
592	34	65.4	652	4	US-10-614-076-18	Sequence 18, Appl	665	33	63.5	74	4	US-10-425-115-258526	Sequence 258526, App
593	34	65.4	652	4	US-10-614-076-18	Sequence 20, Appl	666	33	63.5	77	4	US-10-424-599-226696	Sequence 226696, App
594	34	65.4	652	4	US-10-614-076-20	Sequence 22, Appl	667	33	63.5	87	5	US-10-473-287-11	Sequence 11, Appl
595	34	65.4	652	4	US-10-614-076-22	Sequence 22, Appl	668	33	63.5	87	4	US-10-424-599-194962	Sequence 194962, App
596	34	65.4	652	4	US-10-614-076-26	Sequence 26, Appl	669	33	63.5	91	4	US-10-308-817-135	Sequence 135, App
597	34	65.4	652	4	US-10-614-076-28	Sequence 28, Appl	670	33	63.5	91	4	US-10-453-698-125	Sequence 125, App
598	34	65.4	652	4	US-10-614-076-30	Sequence 30, Appl	671	33	63.5	94	4	US-10-309-762-47	Sequence 47, Appl
599	34	65.4	652	4	US-10-614-076-32	Sequence 32, Appl	672	33	63.5	95	4	US-10-194-975-59	Sequence 59, Appl
600	34	65.4	652	4	US-10-614-076-34	Sequence 34, Appl	673	33	63.5	95	4	US-10-194-975-60	Sequence 60, Appl
601	34	65.4	652	4	US-10-614-076-36	Sequence 36, Appl	674	33	63.5	95	4	US-10-041-860-11	Sequence 11, Appl
602	34	65.4	652	4	US-10-614-076-38	Sequence 38, Appl	675	33	63.5	95	4	US-10-041-860-11	Sequence 11, Appl
603	34	65.4	652	4	US-10-614-076-40	Sequence 40, Appl	676	33	63.5	95	4	US-10-041-860-286	Sequence 286, App
604	34	65.4	652	4	US-10-614-076-42	Sequence 42, Appl	677	33	63.5	95	4	US-10-041-860-287	Sequence 287, App
605	34	65.4	652	4	US-10-614-076-44	Sequence 44, Appl	678	33	63.5	95	4	US-10-041-860-282	Sequence 282, App
606	34	65.4	652	4	US-10-614-076-46	Sequence 46, Appl	679	33	63.5	95	4	US-10-041-860-293	Sequence 293, App
607	34	65.4	652	4	US-10-614-076-48	Sequence 48, Appl	680	33	63.5	95	4	US-10-041-860-304	Sequence 304, App
608	34	65.4	652	4	US-10-614-076-50	Sequence 50, Appl	681	33	63.5	95	4	US-10-041-860-305	Sequence 305, App
609	34	65.4	652	4	US-10-614-076-54	Sequence 54, Appl	682	33	63.5	95	4	US-10-041-860-310	Sequence 310, App
610	34	65.4	652	4	US-10-614-076-60	Sequence 60, Appl	683	33	63.5	95	4	US-10-041-860-311	Sequence 311, App
611	34	65.4	652	4	US-10-614-076-62	Sequence 62, Appl	684	33	63.5	95	4	US-10-041-860-315	Sequence 315, App

685	33	63.5	95	4	US-10-041-860-317	Sequence 317, App	758	33	63.5	113	3	US-09-999-025-9	Sequence 9, Appli
686	33	63.5	95	4	US-10-041-860-339	Sequence 339, App	759	33	63.5	113	3	US-09-999-025-13	Sequence 11, Appl
687	33	63.5	95	4	US-10-041-860-341	Sequence 341, App	760	33	63.5	113	3	US-09-999-025-14	Sequence 12, Appl
688	33	63.5	95	4	US-10-041-860-351	Sequence 351, App	761	33	63.5	113	3	US-09-999-040-7	Sequence 7, Appli
689	33	63.5	95	4	US-10-308-817-6	Sequence 6, Appli	762	33	63.5	113	3	US-09-999-040-9	Sequence 9, Appli
690	33	63.5	95	4	US-10-308-817-7	Sequence 7, Appli	763	33	63.5	113	3	US-09-999-040-13	Sequence 13, Appl
691	33	63.5	95	4	US-10-453-698-6	Sequence 6, Appli	764	33	63.5	113	3	US-09-999-040-14	Sequence 14, Appl
692	33	63.5	95	4	US-10-453-698-7	Sequence 7, Appli	765	33	63.5	113	3	US-09-998-817-7	Sequence 7, Appli
693	33	63.5	95	4	US-10-379-392-70	Sequence 70, Appl	766	33	63.5	113	3	US-09-998-817-9	Sequence 9, Appli
694	33	63.5	95	4	US-10-379-392-71	Sequence 71, Appl	767	33	63.5	113	3	US-09-998-817-13	Sequence 13, Appl
695	33	63.5	96	4	US-10-041-860-274	Sequence 274, App	768	33	63.5	113	3	US-09-998-817-14	Sequence 14, Appl
696	33	63.5	96	4	US-10-041-860-275	Sequence 275, App	769	33	63.5	113	3	US-09-999-021-9	Sequence 9, Appli
697	33	63.5	96	4	US-10-038-591-40	Sequence 40, Appl	770	33	63.5	113	3	US-09-999-021-9	Sequence 9, Appli
698	33	63.5	96	4	US-10-775-444A-40	Sequence 40, Appl	771	33	63.5	113	3	US-09-999-021-13	Sequence 13, Appl
699	33	63.5	96	4	US-10-425-115-287231	Sequence 287231,	772	33	63.5	113	3	US-09-999-021-13	Sequence 13, Appl
700	33	63.5	97	5	US-10-473-287-7	Sequence 7, Appli	773	33	63.5	113	3	US-09-215-163-42	Sequence 42, Appl
701	33	63.5	106	4	US-10-072-301-39	Sequence 39, Appl	774	33	63.5	113	4	US-10-040-997-9	Sequence 9, Appli
702	33	63.5	106	4	US-10-071-866-39	Sequence 39, Appl	775	33	63.5	113	4	US-10-040-997-9	Sequence 9, Appli
703	33	63.5	106	4	US-10-360-828-39	Sequence 39, Appl	776	33	63.5	113	4	US-10-040-997-13	Sequence 13, Appl
704	33	63.5	106	4	US-10-466-242-26	Sequence 26, Appl	777	33	63.5	113	4	US-10-040-997-14	Sequence 14, Appl
705	33	63.5	106	4	US-10-466-242-28	Sequence 28, Appl	778	33	63.5	113	4	US-10-255-478-71	Sequence 71, Appl
706	33	63.5	106	4	US-10-466-242-40	Sequence 40, Appl	779	33	63.5	113	4	US-10-255-478-73	Sequence 73, Appl
707	33	63.5	106	4	US-10-466-242-46	Sequence 46, Appl	780	33	63.5	113	5	US-10-937-046-5	Sequence 5, Appli
708	33	63.5	106	4	US-10-466-242-50	Sequence 50, Appl	781	33	63.5	113	5	US-10-880-028-28	Sequence 28, Appl
709	33	63.5	106	4	US-10-988-485-39	Sequence 39, Appl	782	33	63.5	113	5	US-10-880-028-30	Sequence 30, Appl
710	33	63.5	106	5	US-10-492-228-10	Sequence 10, Appl	783	33	63.5	113	5	US-10-880-028-31	Sequence 31, Appl
711	33	63.5	107	3	US-09-910-059-50	Sequence 50, Appl	784	33	63.5	113	5	US-10-880-320-10	Sequence 10, Appl
712	33	63.5	107	3	US-09-910-059-61	Sequence 61, Appl	785	33	63.5	113	5	US-10-880-320-11	Sequence 11, Appl
713	33	63.5	107	3	US-09-910-059-65	Sequence 65, Appl	786	33	63.5	113	5	US-10-880-320-11	Sequence 11, Appl
714	33	63.5	107	3	US-09-910-059-71	Sequence 71, Appl	787	33	63.5	113	5	US-10-927-433-13	Sequence 13, Appl
715	33	63.5	107	4	US-10-184-300A-4	Sequence 4, Appli	788	33	63.5	115	4	US-10-160-506-82	Sequence 82, Appl
716	33	63.5	107	4	US-10-184-300A-5	Sequence 5, Appli	789	33	63.5	115	4	US-10-449-379-92	Sequence 92, Appl
717	33	63.5	107	4	US-10-184-300A-6	Sequence 6, Appli	790	33	63.5	115	4	US-10-688-015-92	Sequence 92, Appl
718	33	63.5	107	4	US-10-016-986-107	Sequence 107, App	791	33	63.5	115	4	US-10-160-505-92	Sequence 92, Appl
719	33	63.5	107	4	US-10-292-088-105	Sequence 105, App	792	33	63.5	115	5	US-10-473-287-16	Sequence 16, App
720	33	63.5	107	4	US-10-309-762-62	Sequence 62, App	793	33	63.5	116	5	US-10-783-311-134	Sequence 134, App
721	33	63.5	107	4	US-10-436-782-17	Sequence 164, App	794	33	63.5	120	3	US-09-817-414-4	Sequence 4, Appli
722	33	63.5	107	4	US-10-038-591-6	Sequence 6, Appli	795	33	63.5	127	4	US-10-452-646-28	Sequence 28, Appl
723	33	63.5	107	4	US-10-684-109-41	Sequence 41, Appl	796	33	63.5	128	4	US-10-006-773-6	Sequence 6, Appli
724	33	63.5	107	4	US-10-684-109-53	Sequence 53, Appl	797	33	63.5	129	4	US-10-910-901-17	Sequence 17, Appl
725	33	63.5	107	4	US-10-684-109-56	Sequence 56, Appli	798	33	63.5	134	5	US-10-255-478-58	Sequence 58, Appl
726	33	63.5	107	4	US-10-775-444A-6	Sequence 6, Appli	799	33	63.5	156	5	US-10-805-177-133	Sequence 133, App
727	33	63.5	107	5	US-10-923-068-507	Sequence 507, App	800	33	63.5	158	4	US-09-817-414-2	Sequence 2, Appli
728	33	63.5	107	5	US-10-923-068-511	Sequence 511, App	801	33	63.5	178	4	US-10-424-599-262936	Sequence 262936,
729	33	63.5	107	5	US-10-923-068-513	Sequence 513, App	802	33	63.5	195	4	US-10-424-599-262247	Sequence 262247,
730	33	63.5	107	5	US-10-923-068-514	Sequence 514, App	803	33	63.5	200	4	US-10-425-115-315262	Sequence 315262,
731	33	63.5	107	5	US-10-923-068-515	Sequence 515, App	804	33	63.5	212	5	US-10-513-725-7	Sequence 7, Appli
732	33	63.5	107	5	US-10-920-899-1776	Sequence 1776, Ap	805	33	63.5	214	5	US-10-488-074-68	Sequence 68, Appl
733	33	63.5	107	5	US-10-920-899-1780	Sequence 1780, Ap	806	33	63.5	214	5	US-10-488-074-70	Sequence 70, Appl
734	33	63.5	107	5	US-10-920-899-1781	Sequence 1781, Ap	807	33	63.5	215	4	US-10-128-520-118	Sequence 118, App
735	33	63.5	107	5	US-10-994-091A-28	Sequence 28, Appl	808	33	63.5	220	5	US-10-880-028-19	Sequence 19, Appl
736	33	63.5	107	6	US-11-004-795A-17	Sequence 17, Appl	809	33	63.5	220	5	US-10-880-320-19	Sequence 19, Appl
737	33	63.5	107	6	US-11-004-794A-17	Sequence 17, Appl	810	33	63.5	220	5	US-10-880-320-27	Sequence 27, Appl
738	33	63.5	107	6	US-11-071-304A-1	Sequence 1, Appli	811	33	63.5	220	5	US-10-880-320-27	Sequence 27, Appl
739	33	63.5	107	6	US-11-102-403-21	Sequence 21, Appl	812	33	63.5	234	4	US-10-684-109-91	Sequence 91, Appl
740	33	63.5	108	3	US-09-910-059-9	Sequence 9, Appli	813	33	63.5	234	4	US-10-684-109-91	Sequence 91, App
741	33	63.5	108	3	US-09-920-262A-8	Sequence 8, Appli	814	33	63.5	235	3	US-09-910-059-17	Sequence 17, Appl
742	33	63.5	108	4	US-10-412-703A-129	Sequence 129, App	815	33	63.5	235	3	US-09-910-059-52	Sequence 52, Appl
743	33	63.5	108	4	US-10-912-994-8	Sequence 8, Appli	816	33	63.5	235	3	US-09-910-059-97	Sequence 97, Appl
744	33	63.5	108	5	US-10-938-353-117	Sequence 117, App	817	33	63.5	235	3	US-09-910-059-99	Sequence 99, Appl
745	33	63.5	108	5	US-10-805-177-40	Sequence 40, Appl	818	33	63.5	235	4	US-10-608-710-2	Sequence 2, Appli
746	33	63.5	108	5	US-10-805-177-68	Sequence 68, Appl	819	33	63.5	236	4	US-10-038-591-47	Sequence 47, Appl
747	33	63.5	108	5	US-10-805-177-72	Sequence 72, Appl	820	33	63.5	236	4	US-10-775-444A-47	Sequence 47, Appl
748	33	63.5	108	5	US-10-975-883-8	Sequence 8, Appli	821	33	63.5	236	5	US-10-910-901-4	Sequence 4, Appli
749	33	63.5	108	5	US-10-975-740A-8	Sequence 8, Appli	822	33	63.5	236	5	US-10-938-353-20	Sequence 20, Appl
750	33	63.5	108	5	US-10-975-708-8	Sequence 8, Appli	823	33	63.5	238	5	US-10-937-046-10	Sequence 10, Appl
751	33	63.5	112	3	US-09-810-502-36	Sequence 36, Appl	824	33	63.5	241	3	US-09-791-578-6	Sequence 6, Appli
752	33	63.5	112	3	US-09-810-502-37	Sequence 37, Appl	825	33	63.5	241	3	US-09-791-578-6	Sequence 6, Appli
753	33	63.5	112	4	US-10-194-975-115	Sequence 115, App	826	33	63.5	241	5	US-10-915-059-6	Sequence 6, Appli
754	33	63.5	112	4	US-10-194-975-116	Sequence 116, App	827	33	63.5	241	5	US-10-909-948-6	Sequence 6, Appli
755	33	63.5	112	5	US-10-884-133-36	Sequence 36, Appl	828	33	63.5	242	4	US-10-336-210-5	Sequence 5, Appli
756	33	63.5	112	5	US-10-884-133-37	Sequence 37, Appl	829	33	63.5	244	4	US-09-880-748-1881	Sequence 1881, Ap
757	33	63.5	113	3	US-09-999-025-7	Sequence 7, Appli	830	33	63.5	244	4	US-10-293-418-1881	Sequence 1881, Ap

831	33	63.5	246	3	US-09-791-578-2	Sequence 2, Appl1	904	32	61.5	9	4	US-10-239-656-41	Sequence 41, Appl
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833	33	63.5	246	3	US-10-915-069-2	Sequence 2, Appl1	906	32	61.5	9	5	US-10-783-311-166	Sequence 186, Appl
834	33	63.5	246	5	US-10-909-948-2	Sequence 2, Appl1	907	32	61.5	9	5	US-10-808-538-6	Sequence 40, Appl1
835	33	63.5	249	3	US-09-956-086-2	Sequence 2, Appl1	908	32	61.5	9	5	US-10-986-089A-40	Sequence 28, Appl
836	33	63.5	249	3	US-09-956-087-2	Sequence 2, Appl1	909	32	61.5	13	4	US-10-300-215-22	Sequence 22, Appl
837	33	63.5	249	6	US-11-093-103-86	Sequence 86, Appl	910	32	61.5	21	3	US-09-747-802-88	Sequence 88, Appl
838	33	63.5	249	6	US-11-093-103-86	Sequence 86, Appl	911	32	61.5	21	4	US-10-789-619-88	Sequence 88, Appl
839	33	63.5	250	4	US-10-072-301-21	Sequence 21, Appl	912	32	61.5	29	4	US-10-424-599-279143	Sequence 279143, Ap
840	33	63.5	250	4	US-10-072-301-29	Sequence 29, Appl	913	32	61.5	30	5	US-10-808-187-1313	Sequence 1313, Ap
841	33	63.5	250	4	US-10-071-866-21	Sequence 21, Appl	914	32	61.5	30	5	US-10-807-808A-1313	Sequence 1313, Ap
842	33	63.5	250	4	US-10-071-866-29	Sequence 29, Appl	915	32	61.5	37	3	US-09-864-408A-3814	Sequence 3814, Ap
843	33	63.5	250	4	US-10-360-828-21	Sequence 21, Appl	916	32	61.5	58	4	US-10-424-599-235178	Sequence 235178, Sequence
844	33	63.5	250	4	US-10-360-828-21	Sequence 21, Appl	917	32	61.5	71	4	US-10-437-968-121856	Sequence 121856, Sequence
845	33	63.5	250	5	US-10-988-485-21	Sequence 21, Appl	918	32	61.5	72	4	US-10-424-599-180650	Sequence 180650, Sequence
846	33	63.5	250	5	US-10-988-485-29	Sequence 29, Appl	919	32	61.5	73	4	US-10-029-386-27653	Sequence 27653, A
847	33	63.5	255	3	US-09-866-050A-683	Sequence 683, App	920	32	61.5	79	4	US-10-424-599-167479	Sequence 167479, Sequence
848	33	63.5	257	3	US-09-791-578-4	Sequence 4, Appl1	921	32	61.5	94	4	US-10-425-115-327264	Sequence 327264, Sequence
849	33	63.5	257	3	US-09-791-540-4	Sequence 4, Appl1	922	32	61.5	95	4	US-10-194-975-61	Sequence 61, Appl
850	33	63.5	257	3	US-09-983-580-2	Sequence 2, Appl1	923	32	61.5	95	4	US-10-194-975-62	Sequence 62, Appl1
851	33	63.5	257	3	US-09-985-442-2	Sequence 2, Appl1	924	32	61.5	95	4	US-10-308-817-8	Sequence 8, Appl1
852	33	63.5	257	5	US-10-915-069-4	Sequence 4, Appl1	925	32	61.5	95	4	US-10-308-817-9	Sequence 9, Appl1
853	33	63.5	257	5	US-10-909-948-4	Sequence 4, Appl1	926	32	61.5	95	4	US-10-453-698-8	Sequence 8, Appl1
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855	33	63.5	260	4	US-10-936-210-4	Sequence 4, Appl1	928	32	61.5	95	4	US-10-379-392-68	Sequence 68, Appl
856	33	63.5	269	3	US-09-983-580-4	Sequence 4, Appl1	929	32	61.5	95	4	US-10-379-392-69	Sequence 69, Appl
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861	33	63.5	284	4	US-10-255-478-70	Sequence 70, Appl	934	32	61.5	97	4	US-10-425-115-263400	Sequence 263400, Sequence
862	33	63.5	291	4	US-10-258-662-12	Sequence 12, Appl	935	32	61.5	97	5	US-10-473-287-8	Sequence 8, Appl1
863	33	63.5	294	6	US-11-093-103-100	Sequence 100, App	936	32	61.5	97	5	US-10-473-287-9	Sequence 9, Appl1
864	33	63.5	296	6	US-10-437-963-127979	Sequence 127979, Sequence	937	32	61.5	102	5	US-10-502-307-10	Sequence 6, Appl1
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868	33	63.5	340	3	US-10-369-493-143	Sequence 143, App	941	32	61.5	107	3	US-09-749-873-130	Sequence 130, App
869	33	63.5	405	6	US-11-097-143-22647	Sequence 22647, A	942	32	61.5	107	3	US-09-749-873-131	Sequence 131, App
870	33	63.5	423	5	US-10-739-930-9269	Sequence 9269, Ap	943	32	61.5	107	3	US-09-848-798-29	Sequence 29, Appl
871	33	63.5	444	4	US-10-013-173-49	Sequence 49, Appl	944	32	61.5	107	3	US-09-848-798A-58	Sequence 58, Appl
872	33	63.5	444	4	US-10-150-762-49	Sequence 49, Appl	945	32	61.5	107	4	US-10-300-215-249	Sequence 249, App
873	33	63.5	444	4	US-10-244-821-49	Sequence 49, Appl	946	32	61.5	107	4	US-10-300-215-251	Sequence 251, App
874	33	63.5	444	4	US-10-296-115-1171	Sequence 1171, Ap	947	32	61.5	107	4	US-10-239-656-38	Sequence 38, Appl
875	33	63.5	473	4	US-10-417-700A-127	Sequence 127, App	948	32	61.5	107	4	US-10-239-656-38	Sequence 38, Appl
876	33	63.5	478	5	US-10-450-763-39243	Sequence 39243, A	949	32	61.5	107	4	US-10-251-088B-111	Sequence 111, App
877	33	63.5	478	5	US-10-450-763-43515	Sequence 43515, A	950	32	61.5	107	4	US-10-383-447-4	Sequence 4, Appl1
878	33	63.5	491	4	US-10-282-122A-67513	Sequence 67513, A	951	32	61.5	107	4	US-10-632-706-75	Sequence 75, Appl
879	33	63.5	504	4	US-10-114-893-67	Sequence 67, Appl	952	32	61.5	107	4	US-10-737-252-111	Sequence 111, App
880	33	63.5	529	4	US-10-282-122A-69623	Sequence 69623, A	953	32	61.5	107	5	US-10-727-155-16	Sequence 16, Appl
881	33	63.5	529	4	US-10-424-599-173634	Sequence 173634, Sequence	954	32	61.5	107	5	US-10-727-155-138	Sequence 138, App
882	33	63.5	568	4	US-10-238-075-1080	Sequence 1080, Ap	955	32	61.5	107	5	US-10-727-155-184	Sequence 184, App
883	33	63.5	568	3	US-09-908-193-34	Sequence 34, Appl	956	32	61.5	107	5	US-10-727-155-314	Sequence 314, App
884	33	63.5	594	4	US-10-425-115-316947	Sequence 316947, Sequence	957	32	61.5	107	5	US-10-938-353-107	Sequence 107, App
885	33	63.5	598	5	US-10-450-763-53954	Sequence 53954, A	958	32	61.5	107	5	US-10-895-133-44	Sequence 44, Appl
886	33	63.5	660	5	US-10-450-763-36054	Sequence 36054, A	959	32	61.5	107	6	US-11-071-30A-3	Sequence 3, Appl1
887	33	63.5	695	3	US-09-764-898-191	Sequence 191, App	960	32	61.5	107	6	US-11-021-715-72	Sequence 72, Appl
888	33	63.5	722	6	US-11-093-103-90	Sequence 90, Appl	961	32	61.5	108	3	US-09-155-106-22	Sequence 22, Appl
889	33	63.5	754	3	US-09-908-193-32	Sequence 32, Appl	962	32	61.5	108	3	US-09-155-106-23	Sequence 23, Appl
890	33	63.5	775	4	US-10-232-9728-2	Sequence 2, Appl1	963	32	61.5	108	3	US-09-155-106-24	Sequence 24, Appl
891	33	63.5	776	3	US-09-908-193-33	Sequence 33, Appl	964	32	61.5	108	3	US-09-155-106-28	Sequence 28, Appl
892	33	63.5	776	5	US-10-239-032-9	Sequence 9, Appl1	965	32	61.5	108	4	US-09-155-106-30	Sequence 30, Appl
893	33	63.5	776	5	US-09-908-193-8	Sequence 8, Appl1	966	32	61.5	108	4	US-10-383-447-30	Sequence 30, Appl
894	33	63.5	779	3	US-09-908-193-10	Sequence 10, Appl	967	32	61.5	108	4	US-10-383-447-32	Sequence 32, Appl
895	33	63.5	926	6	US-11-097-143-22197	Sequence 22197, A	968	32	61.5	108	4	US-10-383-447-34	Sequence 34, Appl
896	33	63.5	938	4	US-10-437-963-144017	Sequence 144017, A	969	32	61.5	108	5	US-10-808-538-22	Sequence 22, Appl
897	33	63.5	1665	6	US-11-097-143-18822	Sequence 18822, A	970	32	61.5	108	5	US-10-808-538-23	Sequence 23, Appl
898	33	63.5	1849	5	US-10-487-092-6	Sequence 6, Appl1	971	32	61.5	108	5	US-10-808-538-24	Sequence 24, Appl
899	32	61.5	8	4	US-10-275-046-42	Sequence 42, Appl	972	32	61.5	108	5	US-10-808-538-28	Sequence 28, Appl
900	32	61.5	9	3	US-09-749-873-120	Sequence 120, App	973	32	61.5	108	5	US-10-808-538-30	Sequence 30, Appl
901	32	61.5	9	3	US-09-155-106-6	Sequence 6, Appl1	974	32	61.5	109	3	US-09-144-886-79	Sequence 79, Appl
902	32	61.5	9	3	US-09-842-776A-39	Sequence 39, Appl	975	32	61.5	109	3	US-09-144-886-96	Sequence 96, Appl
903	32	61.5	9	4	US-10-239-656-31	Sequence 31, Appl	976	32	61.5	109	4	US-10-803-622-268	Sequence 268, App

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980	32	61.5	109	4
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997	32	61.5	109	4
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ALIGNMENTS

RESULT 1
US-09-795-798-15
Sequence 15, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-795-798-15
Query Match 100.0%; Score 52; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEVPLT 9
Db 1 OOHNEVPLT 9

RESULT 2

US-10-727-737-60

Sequence 60, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-727-737-60

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OOHNEVPLT 9
Db 1 OOHNEVPLT 9

RESULT 3

US-11-003-819-10

Sequence 10, Application US/11003819
Publication No. US20050158323A1
GENERAL INFORMATION:
APPLICANT: Evans, Elizabeth E.
APPLICANT: Paris, Mark J.
APPLICANT: Sahasrabudhe, Deepak M.
APPLICANT: Zauderer, Maurice
APPLICANT: Smith, Ernest S.
TITLE OF INVENTION: Methods of Killing Tumor Cells by Targeting Internal Antigens

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE OF INVENTION: Exposed on Apoptotic Tumor Cells
FILE REFERENCE: 1843.0190002
CURRENT APPLICATION NUMBER: US/11/003,819
CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: US 60/256,572
PRIOR FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US 60/531,688
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
LENGTH: 107
TYPE: PRT
ORGANISM: Mus sp.
US-11-003-819-10

Query Match 100.0%; Score 52; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYPILT 9
Db 89 QOHNEYPILT 97

RESULT 4

US-09-795-798-1
Sequence 1, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-795-798-1

Query Match 100.0%; Score 52; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYPILT 9

Db 89 QOHNEYPILT 97

RESULT 5

US-09-795-798-2
Sequence 2, Application US/09795798
Publication No. US20030207336A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,798
FILING DATE: 28-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,899
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-795-798-2

Query Match 100.0%; Score 52; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYPILT 9
Db 89 QOHNEYPILT 97

RESULT 6

US-10-727-737-1
Sequence 1, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-727-737-1

Query Match 100.0%; Score 52; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QOHNEYP.LT 9
| | | | | | | |
Db 89 QOHNEYP.LT 97

RESULT 7
US-10-727-737-2
Sequence 2, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-727-737-2

Query Match 100.0%; Score 52; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QOHNEYP.LT 9
| | | | | | | |
Db 89 QOHNEYP.LT 97

RESULT 8
US-10-877-532-5
Sequence 5, Application US/10877532
Publication No. US20050038231A1
GENERAL INFORMATION:
APPLICANT: FAHRNER, ROBERT L.
LAVEDIERE, AMY
APPLICANT: MCDONALD, PAUL J.
APPLICANT: O'LEARY, RHONA M.
TITLE OF INVENTION: REDUCING PROTEIN A LEACHING DURING PROTEIN A AFFINITY CHROMATOGRAPHY
FILE REFERENCE: P2015R1
CURRENT APPLICATION NUMBER: US/10/877,532
CURRENT FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: US 60/490,500
PRIOR FILING DATE: 2003-07-28
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 5
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-10-877-532-5

Query Match 100.0%; Score 52; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QOHNEYP.LT 9
| | | | | | | |
Db 89 QOHNEYP.LT 97

RESULT 9
US-09-726-258-47
Sequence 47, Application US/09726258
Publication No. US20030021790A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hseil, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPac (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,258
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/094003
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-09-726-258-47

Query Match 100.0%; Score 52; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYPYT 9
|||||
DB 90 QOHNEYPYT 98

RESULT 10
US-10-423-299-3
Sequence 3, Application US/10423299
Publication No. US20030229212A1
GENERAL INFORMATION:
APPLICANT: FAHRNER, ROBERT
APPLICANT: FOLLMAN, DEBORAH
APPLICANT: LEBRETON, BENEDICTE
APPLICANT: VAN REIS, ROBERT
TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF PROTEINS
FILE REFERENCE: 39766-0121A
CURRENT APPLICATION NUMBER: US/10/423,299
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/375,953
PRIOR FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
LENGTH: 214
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized
US-10-423-299-3

Query Match 100.0%; Score 52; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYPYT 9
|||||
DB 89 QOHNEYPYT 97

RESULT 11
US-10-010-729-23
Sequence 23, Application US/10010729

Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: System
FILE REFERENCE: 1199-1-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 101
TYPE: PRT
ORGANISM: Mus musculus
US-10-010-729-23

Query Match 90.4%; Score 47; DB 4; Length 101;
Best Local Similarity 88.9%; Pred. No. 0.61;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPYT 9
|||||
DB 89 QOHNEYPYT 97

RESULT 12
US-10-010-729-43
Sequence 43, Application US/10010729
Publication No. US20030185827A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Pease, Larry R.
TITLE OF INVENTION: Human IgM Antibodies and Diagnostic and
TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
TITLE OF INVENTION: System
FILE REFERENCE: 1199-1-005CIP2
CURRENT APPLICATION NUMBER: US/10/010,729
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/730,473
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 09/580,787
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/322,862
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 08/779,784
PRIOR FILING DATE: 1997-01-07
PRIOR APPLICATION NUMBER: 08/692,084
PRIOR FILING DATE: 1996-08-08
PRIOR APPLICATION NUMBER: 08/236,520
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 108
TYPE: PRT
ORGANISM: Mus musculus
US-10-010-729-43

```

Query Match          90.4%; Score 47; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 0.66;
Matches      8; Conservative    0; Mismatches     1; Indels       0; Gaps        0;

QY      1 QOHNEYPLT 9
      ||||| |
Db      89 QOHNEYPYT 97

RESULT 13
US-10-727-737-64
; Sequence 64, Application US/10727737
; Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-10-727-737-64

Query Match          88.5%; Score 46; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative    0; Mismatches     1; Indels       0; Gaps        0;

QY      1 QOHNEYPLT 9
      ||||| |
Db      1 QOHNAYPLT 9

RESULT 14
US-10-727-737-63
; Sequence 63, Application US/10727737
; Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79

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CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-727-737-63

Query Match      84.6%; Score 44; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 QQHNEYPLT 9
      ||| |||
Db      1 QQHAEYPLT 9

RESULT 15
US-10-727-737-65
; Sequence 65, Application US/10727737
; Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
      Jardieu, Paula M.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997

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APPLICATION NUMBER: 60/031945
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-727-737-65

Query Match 82.7%; Score 43; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEPPLT 9
Db 1 QOHNEPPLT 9

RESULT 16
US-10-727-737-62
Sequence 62, Application US/10727737
Publication No. US20040146507A1
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Mutants
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/727,737
FILING DATE: 03-Dec-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/975,329B
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 60/031945
FILING DATE: 27-Nov-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1064R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-10-727-737-62

Query Match 80.8%; Score 42; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEPPLT 9
Db 1 QOHNEPPLT 9

RESULT 17
US-10-726-332-151
Sequence 151, Application US/10726332
Publication No. US20050058649A1
GENERAL INFORMATION:
APPLICANT: Gregory M. Landes
APPLICANT: Mary Haak-Frendscho
APPLICANT: Ling Chen
APPLICANT: Yen-wah R. Lee
APPLICANT: Meina Liang
APPLICANT: Xiao Peng
APPLICANT: Xiao-Chi Jia
APPLICANT: Mark R. Nocerini
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
FILE REFERENCE: ARGENTX 072A
CURRENT APPLICATION NUMBER: US/10/726,332
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: n/a
NUMBER OF SEQ ID NOS: 222
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 151
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-726-332-151

Query Match 80.8%; Score 42; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNEPPLT 9
Db 2 QHNEPPLT 9

RESULT 18
US-10-893-576-88
Sequence 88, Application US/10893576
Publication No. US20050118643A1
GENERAL INFORMATION:
APPLICANT: BURGESS, TERESA L.
APPLICANT: COXON, ANGELA
APPLICANT: GREEN, LARRY L.
APPLICANT: ZHANG, KE
TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR
FILE REFERENCE: 06843.0051-00000
CURRENT APPLICATION NUMBER: US/10/893,576
CURRENT FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: US 60/488,681
PRIOR FILING DATE: 2003-07-18
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 88
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic light chain
US-10-893-576-88

Query Match 80.8%; Score 42; DB 5; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEVPLT 9
 Db 2 QHNSVPLT 9

RESULT 19

US-10-330-613-14
 ; Sequence 14, Application US/10330613
 ; Publication No. US20030147809A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guada, Jean
 ; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
 ; FILE REFERENCE: ABGENIX.022A
 ; CURRENT FILING DATE: 2002-12-26
 ; PRIOR APPLICATION NUMBER: 60/346299
 ; PRIOR FILING DATE: 2001-12-18
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-330-613-14

Query Match 80.8%; Score 42; DB 4; Length 107;
 Best Local Similarity 87.5%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEVPLT 9
 Db 90 QHNSVPLT 97

RESULT 20

US-10-330-530-14
 ; Sequence 14, Application US/10330530
 ; Publication No. US20030152514A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guada, Jean
 ; TITLE OF INVENTION: METHODS FOR USING ANTI-MUC18 ANTIBODIES
 ; FILE REFERENCE: ABGENIX.031A
 ; CURRENT APPLICATION NUMBER: US/10/330,530
 ; CURRENT FILING DATE: 2002-12-26
 ; PRIOR APPLICATION NUMBER: 60/346414
 ; PRIOR FILING DATE: 2001-12-18
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-330-530-14

Query Match 80.8%; Score 42; DB 4; Length 107;
 Best Local Similarity 87.5%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEVPLT 9
 Db 90 QHNSVPLT 97

RESULT 21

US-10-041-860-14
 ; Sequence 14, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong

; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-14

Query Match 80.8%; Score 42; DB 4; Length 107;
 Best Local Similarity 87.5%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEVPLT 9
 Db 90 QHNSVPLT 97

RESULT 22

US-10-041-860-18
 ; Sequence 18, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard
 ; APPLICANT: Bezabeh, Binyam
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
 ; FILE REFERENCE: ABGENIX.051A
 ; CURRENT APPLICATION NUMBER: US/10/041,860
 ; CURRENT FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 377
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-041-860-18

Query Match 80.8%; Score 42; DB 4; Length 107;
 Best Local Similarity 87.5%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEVPLT 9
 Db 90 QHNSVPLT 97

RESULT 23

US-10-041-860-229
 ; Sequence 229, Application US/10041860
 ; Publication No. US20030157109A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Corvalan, Jose R.F.
 ; APPLICANT: Jia, Xiao-Chi
 ; APPLICANT: Feng, Xiao
 ; APPLICANT: Yang, Xiao-Dong
 ; APPLICANT: Chen, Francine
 ; APPLICANT: Gazit, Gadi
 ; APPLICANT: Weber, Richard

```

; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 229
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-229

```

```

Query Match      80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 QHNEYPLT 9
      ||| |||
      90 QHNSYPLT 97

```

```

RESULT 24
US-10-041-860-233
; Sequence 233, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-233

```

```

Query Match      80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 QHNEYPLT 9
      ||| |||
      90 QHNSYPLT 97

```

```

RESULT 25
US-10-041-860-263
; Sequence 263, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07

```

```

; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-263

```

```

Query Match      80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 QHNEYPLT 9
      ||| |||
      90 QHNSYPLT 97

```

```

RESULT 26
US-10-041-860-267
; Sequence 267, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-267

```

```

Query Match      80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2 QHNEYPLT 9
      ||| |||
      90 QHNSYPLT 97

```

```

RESULT 27
US-10-041-860-285
; Sequence 285, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07

```

NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 285
LENGTH: 107
TYPE: PRT
ORGANISM: homo sapiens
US-10-041-860-285

Query Match 80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEYPILT 9
Db 90 QHNSYPLT 97

RESULT 28
US-10-309-762-51
Sequence 51, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-51

Query Match 80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEYPILT 9
Db 90 QHNSYPLT 97

RESULT 29
US-10-309-762-57
Sequence 57, Application US/10309762
Publication No. US20040018198A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Foltz, Ian
APPLICANT: Handa, Masahisa
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
FILE REFERENCE: ABGENIX.027A
CURRENT APPLICATION NUMBER: US/10/309,762
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/337275
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 57
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-762-57

Query Match 80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEYPILT 9
Db 90 QHNSYPLT 97

RESULT 30
US-10-038-591-14
Sequence 14, Application US/10038591
Publication No. US20040086503A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PP2
CURRENT APPLICATION NUMBER: US/10/038,591
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-038-591-14

Query Match 80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEYPILT 9
Db 90 QHNSYPLT 97

RESULT 31
US-10-660-357-14
Sequence 14, Application US/10660357
Publication No. US20040115205A1
GENERAL INFORMATION:
APPLICANT: Bar-Eli, Menashe
APPLICANT: Green, Larry L.
TITLE OF INVENTION: USE OF ANTIBODIES AGAINST THE MUC18
FILE REFERENCE: ABGENIX.030C1
CURRENT APPLICATION NUMBER: US/10/660,357
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 10/330,580
PRIOR FILING DATE: 2002-12-26
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 107
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-660-357-14

Query Match 80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEYPILT 9
Db 90 QHNSYPLT 97

```
RESULT 32
US-10-665-383-8
; Sequence 8, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadl
; APPLICANT: Keyt, Bruce
; APPLICANT: Larocheille, William
; APPLICANT: Lichenstein, Henry
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-8
```

```
Query Match      80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 QHNEYPLT 9
      ||| |||
      90 QHNSYPLT 97

RESULT 33
US-10-665-383-16
; Sequence 16, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadl
; APPLICANT: Keyt, Bruce
; APPLICANT: Larocheille, William
; APPLICANT: Lichenstein, Henry
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-665-383-16
```

```
Query Match      80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 QHNEYPLT 9
      ||| |||
      90 QHNSYPLT 97

RESULT 34
US-10-775-444A-14
; Sequence 14, Application US/10775444A
```

```
; Publication No. US20040202651A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Bedian, Vahne
; APPLICANT: Obrocea, Mihail
; APPLICANT: Gomez-Navarro, Jesus
; APPLICANT: Cuernano, John D.
; APPLICANT: Wang, Huijen F.
; APPLICANT: Page, Kelly L.
; APPLICANT: Guyot, Deborah J.
; TITLE OF INVENTION: USES OF ANTI-INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: PC25232A
; CURRENT APPLICATION NUMBER: US/10/775,444A
; CURRENT FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-444A-14
```

```
Query Match      80.8%; Score 42; DB 4; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 QHNEYPLT 9
      ||| |||
      90 QHNSYPLT 97

RESULT 35
US-10-727-155-4
; Sequence 4, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Poord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaawami
; APPLICANT: Craig Pigolt
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchu
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Yane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-4
```

```
Query Match      80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 QHNEYPLT 9
      ||| |||
```

Db 90 QHNNYPLT 97

RESULT 36

US-10-727-155-8
; Sequence 8, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchu
; APPLICANT: Raffaella Faggioni
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-8

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNNYPLT 9
||| |||
Db 90 QHNNYPLT 97

RESULT 37
US-10-727-155-12
; Sequence 12, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchu
; APPLICANT: Raffaella Faggioni
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729

; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-12

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNNYPLT 9
||| |||
Db 90 QHNNYPLT 97

RESULT 38
US-10-727-155-28
; Sequence 28, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendscho
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchu
; APPLICANT: Raffaella Faggioni
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-28

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNNYPLT 9
||| |||
Db 90 QHNNYPLT 97

RESULT 39
US-10-727-155-40
; Sequence 40, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp


```
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchu
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: AGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-40
```

```
Query Match      80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 QHNEYPILT 9
      ||| |||
Db      90 QHNSYPLT 97
```

```
RESULT 40
US-10-727-155-44
Sequence 44, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchu
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: AGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-44
```

```
Query Match      80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 QHNEYPILT 9
```

```
Db      90 QHNSYPLT 97
```

```
RESULT 41
US-10-727-155-78
Sequence 78, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchu
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: AGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 78
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-78
```

```
Query Match      80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      2 QHNEYPILT 9
      ||| |||
Db      90 QHNSYPLT 97
```

```
RESULT 42
US-10-727-155-176
Sequence 176, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchu
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: AGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
PRIOR FILING DATE: 2003-12-02
```

PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-176

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNEYPLT 9
DB 90 QHNSYPLT 97

RESULT 43
US-10-727-155-180

Sequence 180, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchu
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 180
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-180

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNEYPLT 9
DB 90 QHNSYPLT 97

RESULT 44
US-10-727-155-208

Sequence 208, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng

APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchu
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 208
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-208

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNEYPLT 9
DB 90 QHNSYPLT 97

RESULT 45
US-10-727-155-220

Sequence 220, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenchu
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 220
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-220

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNSYPLT 9
 ||| |||
 Db 90 QHNSYPLT 97

RESULT 46

US-10-727-155-224
 ; Sequence 224, Application US/10727155
 ; Publication No. US20050049402A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John S. Babcock
 ; APPLICANT: Jaspal S. Kang
 ; APPLICANT: Orit Foord
 ; APPLICANT: Larry Green
 ; APPLICANT: Xiao Feng
 ; APPLICANT: Scott Klakamp
 ; APPLICANT: Mary Haak-Frendescho
 ; APPLICANT: Palaniswami Rathanaswami
 ; APPLICANT: Craig Pigott
 ; APPLICANT: Meina Liang
 ; APPLICANT: Rozanne Lee
 ; APPLICANT: Kathy Manchulenchio
 ; APPLICANT: Raffaella Faggioni
 ; APPLICANT: Giorgio Senaldi
 ; APPLICANT: Qiaojuan Jane Su
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
 ; FILE REFERENCE: ABGENIX.073A
 ; CURRENT APPLICATION NUMBER: US/10/727,155
 ; CURRENT FILING DATE: 2003-12-02
 ; PRIOR APPLICATION NUMBER: 60/430729
 ; PRIOR FILING DATE: 2002-12-02
 ; NUMBER OF SEQ ID NOS: 320
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 224
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-727-155-224

Query Match 80.8%; Score 42; DB 5; Length 107;
 Best Local Similarity 87.5%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNSYPLT 9
 ||| |||
 Db 90 QHNSYPLT 97

RESULT 47
 US-10-727-155-252
 ; Sequence 252, Application US/10727155
 ; Publication No. US20050049402A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John S. Babcock
 ; APPLICANT: Jaspal S. Kang
 ; APPLICANT: Orit Foord
 ; APPLICANT: Larry Green
 ; APPLICANT: Xiao Feng
 ; APPLICANT: Scott Klakamp
 ; APPLICANT: Mary Haak-Frendescho
 ; APPLICANT: Palaniswami Rathanaswami
 ; APPLICANT: Craig Pigott
 ; APPLICANT: Meina Liang
 ; APPLICANT: Rozanne Lee
 ; APPLICANT: Kathy Manchulenchio
 ; APPLICANT: Raffaella Faggioni
 ; APPLICANT: Giorgio Senaldi
 ; APPLICANT: Qiaojuan Jane Su
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
 ; FILE REFERENCE: ABGENIX.073A
 ; CURRENT APPLICATION NUMBER: US/10/727,155

; CURRENT FILING DATE: 2003-12-02
 ; PRIOR APPLICATION NUMBER: 60/430729
 ; PRIOR FILING DATE: 2002-12-02
 ; NUMBER OF SEQ ID NOS: 320
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 252
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-727-155-252

Query Match 80.8%; Score 42; DB 5; Length 107;
 Best Local Similarity 87.5%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNSYPLT 9
 ||| |||
 Db 90 QHNSYPLT 97

RESULT 48
 US-10-727-155-256
 ; Sequence 256, Application US/10727155
 ; Publication No. US20050049402A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John S. Babcock
 ; APPLICANT: Jaspal S. Kang
 ; APPLICANT: Orit Foord
 ; APPLICANT: Larry Green
 ; APPLICANT: Xiao Feng
 ; APPLICANT: Scott Klakamp
 ; APPLICANT: Mary Haak-Frendescho
 ; APPLICANT: Palaniswami Rathanaswami
 ; APPLICANT: Craig Pigott
 ; APPLICANT: Meina Liang
 ; APPLICANT: Rozanne Lee
 ; APPLICANT: Kathy Manchulenchio
 ; APPLICANT: Raffaella Faggioni
 ; APPLICANT: Giorgio Senaldi
 ; APPLICANT: Qiaojuan Jane Su
 ; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
 ; FILE REFERENCE: ABGENIX.073A
 ; CURRENT APPLICATION NUMBER: US/10/727,155
 ; CURRENT FILING DATE: 2003-12-02
 ; PRIOR APPLICATION NUMBER: 60/430729
 ; PRIOR FILING DATE: 2002-12-02
 ; NUMBER OF SEQ ID NOS: 320
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 256
 ; LENGTH: 107
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-727-155-256

Query Match 80.8%; Score 42; DB 5; Length 107;
 Best Local Similarity 87.5%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNSYPLT 9
 ||| |||
 Db 90 QHNSYPLT 97

RESULT 49
 US-10-727-155-273
 ; Sequence 273, Application US/10727155
 ; Publication No. US20050049402A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John S. Babcock
 ; APPLICANT: Jaspal S. Kang
 ; APPLICANT: Orit Foord
 ; APPLICANT: Larry Green

APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenko
APPLICANT: Raffaella Faggioni
APPLICANT: Giorgio Senaldi
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 273
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-273

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEXPILT 9
Db 90 QHNSYPLT 97

RESULT 50
US-10-727-155-305
Sequence 305, Application US/10727155
Publication No. US20050049402A1
GENERAL INFORMATION:
APPLICANT: John S. Babcock
APPLICANT: Jaspal S. Kang
APPLICANT: Orit Foord
APPLICANT: Larry Green
APPLICANT: Xiao Feng
APPLICANT: Scott Klakamp
APPLICANT: Mary Haak-Frendscho
APPLICANT: Palaniswami Rathanaswami
APPLICANT: Craig Pigott
APPLICANT: Meina Liang
APPLICANT: Rozanne Lee
APPLICANT: Kathy Manchulenko
APPLICANT: Raffaella Faggioni
APPLICANT: Qiaojuan Jane Su
TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
FILE REFERENCE: ABGENIX.073A
CURRENT APPLICATION NUMBER: US/10/727,155
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/430729
NUMBER OF SEQ ID NOS: 320
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 305
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-10-727-155-305

Query Match 80.8%; Score 42; DB 5; Length 107;
Best Local Similarity 87.5%; Pred. No. 5.5; 1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QHNEXPILT 9
Db 90 QHNSYPLT 97

Search completed: January 17, 2006, 12:13:15
Job time : 45.7727 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 17, 2006, 11:59:34 ; Search time 3 Seconds
(without alignments)
28.363 Million cell updates/sec

Title: US-10-665-658-15
Perfect score: 52
Sequence: 1 OOHNEYPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 67062 seqs, 9454214 residues

Total number of hits satisfying chosen parameters: 67062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database :

Published Applications AA.New:*
1: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep:*
7: /cgn2_6/prodata/2/pubppa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	52	100.0	9	US-10-665-658-15	Sequence 15, App1
2	52	100.0	9	US-10-665-658-66	Sequence 66, App1
3	52	100.0	107	US-11-107-028-49	Sequence 49, App1
4	52	100.0	107	US-11-107-028-51	Sequence 51, App1
5	52	100.0	108	US-10-665-658-1	Sequence 1, App11
6	52	100.0	108	US-10-665-658-2	Sequence 2, App11
7	46	88.5	9	US-10-665-658-70	Sequence 70, App1
8	44	84.6	9	US-10-665-658-69	Sequence 69, App1
9	44	82.7	9	US-10-665-658-71	Sequence 71, App1
10	42	80.8	9	US-10-665-658-68	Sequence 68, App1
11	42	80.8	107	US-11-144-248-14	Sequence 14, App1
12	42	78.8	107	US-11-144-222-10	Sequence 10, App1
13	41	78.8	9	US-11-173-071-10	Sequence 16, App1
14	41	78.8	108	US-11-173-071-16	Sequence 18, App1
15	41	78.8	108	US-11-173-071-18	Sequence 20, App1
16	41	78.8	108	US-11-173-071-20	Sequence 22, App1
17	41	78.8	112	US-11-173-071-22	Sequence 42, App1
18	41	78.8	108	US-11-173-071-4	Sequence 4, App11
19	38	73.1	243	US-11-054-515-1943	Sequence 1943, Ap
20	38	73.1	243	US-11-054-515-2064	Sequence 2064, Ap
21	37	71.2	236	US-11-144-248-48	Sequence 48, App1
22	37	71.2	236	US-11-144-222-48	Sequence 48, App1
23	36	69.2	9	US-11-096-046-9	Sequence 9, App11
24	36	69.2	9	US-11-097-812-59	Sequence 59, App1
25	36	69.2	100	US-11-144-248-10	Sequence 10, App1

26	36	69.2	100	7	US-11-144-222-10	Sequence 10, App1
27	36	69.2	107	7	US-11-084-554-6	Sequence 6, App1
28	36	69.2	107	7	US-11-112-240-12	Sequence 12, App1
29	36	69.2	107	7	US-11-112-304A-12	Sequence 12, App1
30	36	69.2	108	6	US-10-771-257-78	Sequence 78, App1
31	36	69.2	108	7	US-11-127-677-76	Sequence 76, App1
32	36	69.2	108	7	US-11-097-812-45	Sequence 45, App1
33	36	69.2	108	7	US-11-097-812-46	Sequence 46, App1
34	36	69.2	108	7	US-11-097-812-50	Sequence 50, App1
35	36	69.2	108	7	US-11-097-812-51	Sequence 51, App1
36	36	69.2	108	7	US-11-097-812-52	Sequence 52, App1
37	36	69.2	109	7	US-11-097-812-37	Sequence 37, App1
38	36	69.2	109	7	US-11-097-812-42	Sequence 42, App1
39	36	69.2	109	7	US-11-097-812-43	Sequence 43, App1
40	36	69.2	109	7	US-11-097-812-48	Sequence 48, App1
41	36	69.2	115	7	US-11-097-812-54	Sequence 54, App1
42	36	69.2	115	7	US-11-097-812-38	Sequence 38, App1
43	36	69.2	136	7	US-11-144-248-2	Sequence 2, App11
44	36	69.2	136	7	US-11-144-222-2	Sequence 2, App11
45	36	69.2	236	7	US-11-144-248-51	Sequence 51, App1
46	36	69.2	236	7	US-11-144-248-52	Sequence 52, App1
47	36	69.2	236	7	US-11-144-222-51	Sequence 51, App1
48	36	69.2	236	7	US-11-144-222-52	Sequence 52, App1
49	36	69.2	239	7	US-11-054-515-1882	Sequence 1882, Ap
50	36	69.2	239	7	US-11-054-515-1822	Sequence 1922, Ap
51	36	69.2	241	7	US-11-054-515-1889	Sequence 1889, Ap
52	36	69.2	241	7	US-11-054-515-1901	Sequence 1901, Ap
53	36	69.2	241	7	US-11-054-515-1948	Sequence 1948, Ap
54	36	69.2	243	7	US-11-054-515-1883	Sequence 1883, Ap
55	36	69.2	243	7	US-11-054-515-1935	Sequence 1935, Ap
56	36	69.2	243	7	US-11-054-515-1945	Sequence 1945, Ap
57	36	69.2	243	7	US-11-054-515-2063	Sequence 2063, Ap
58	36	69.2	245	7	US-11-054-515-1900	Sequence 1900, Ap
59	36	69.2	245	7	US-11-054-515-1902	Sequence 1902, Ap
60	36	69.2	246	7	US-11-054-515-1920	Sequence 1920, Ap
61	36	69.2	246	7	US-11-054-515-2062	Sequence 2062, Ap
62	36	69.2	247	7	US-11-054-515-969	Sequence 969, App
63	36	69.2	247	7	US-11-054-515-1177	Sequence 1177, Ap
64	36	69.2	247	7	US-11-054-515-1923	Sequence 1923, Ap
65	36	69.2	247	7	US-11-054-515-3342	Sequence 3242, Ap
66	36	69.2	248	7	US-11-054-515-1008	Sequence 1008, Ap
67	36	69.2	248	7	US-11-054-515-1421	Sequence 1421, Ap
68	36	69.2	248	7	US-11-054-515-1170	Sequence 1700, Ap
69	36	69.2	248	7	US-11-054-515-1771	Sequence 1771, Ap
70	36	69.2	248	7	US-11-054-515-1778	Sequence 1778, Ap
71	36	69.2	249	7	US-11-054-515-918	Sequence 918, App
72	36	69.2	249	7	US-11-054-515-919	Sequence 919, App
73	36	69.2	249	7	US-11-054-515-926	Sequence 926, App
74	36	69.2	249	7	US-11-054-515-1188	Sequence 1188, App
75	36	69.2	250	7	US-11-054-515-932	Sequence 932, App
76	36	69.2	251	7	US-11-054-515-922	Sequence 922, App
77	36	69.2	251	7	US-11-054-515-1320	Sequence 1320, Ap
78	36	69.2	255	7	US-11-054-515-1603	Sequence 1603, Ap
79	36	69.2	809	7	US-11-091-018-2	Sequence 2, App11
80	35	67.3	9	6	US-10-850-635-68	Sequence 68, App1
81	35	67.3	9	6	US-11-105-268-20	Sequence 20, App1
82	35	67.3	105	7	US-11-105-268-30	Sequence 30, App1
83	35	67.3	107	6	US-10-850-635-18	Sequence 18, App1
84	35	67.3	107	7	US-11-105-268-25	Sequence 25, App1
85	35	67.3	107	7	US-11-105-268-28	Sequence 28, App1
86	35	67.3	107	7	US-11-105-268-32	Sequence 32, App1
87	35	67.3	107	7	US-11-051-453-30	Sequence 30, App1
88	35	67.3	107	7	US-11-051-453-31	Sequence 31, App1
89	35	67.3	107	7	US-11-051-453-32	Sequence 32, App1
90	35	67.3	107	7	US-11-051-453-33	Sequence 33, App1
91	35	67.3	107	7	US-11-051-453-44	Sequence 44, App1
92	35	67.3	129	7	US-11-051-453-45	Sequence 45, App1
93	35	67.3	129	7	US-11-051-453-46	Sequence 46, App1
94	35	67.3	129	7	US-11-051-453-47	Sequence 47, App1
95	35	67.3	543	6	US-10-495-664-3	Sequence 3, App11
96	34	65.4	9	6	US-10-850-635-56	Sequence 56, App1
97	34	65.4	9	7	US-11-125-837-9	Sequence 9, App11
98	34	65.4	9	7	US-11-097-812-118	Sequence 118, App1

99	34	65.4	107	6	US-10-850-635-14	Sequence 14, Appl	172	32	61.5	126	6	US-10-839-799-59	Sequence 59, Appl
100	34	65.4	110	7	US-11-097-812-99	Sequence 99, Appl	173	32	61.5	126	6	US-10-839-799-63	Sequence 63, Appl
101	34	65.4	110	7	US-11-097-812-100	Sequence 100, App	174	32	61.5	126	6	US-10-839-799-65	Sequence 65, Appl
102	34	65.4	110	7	US-11-097-812-171	Sequence 171, App	175	32	61.5	126	6	US-10-839-799-69	Sequence 69, Appl
103	34	65.4	110	7	US-11-097-812-174	Sequence 174, App	176	32	61.5	126	6	US-10-839-799-73	Sequence 73, Appl
104	34	65.4	111	7	US-11-097-812-178	Sequence 178, App	177	32	61.5	126	6	US-10-839-799-75	Sequence 75, Appl
105	34	65.4	111	7	US-11-097-812-180	Sequence 180, App	178	32	61.5	126	6	US-10-839-799-77	Sequence 77, Appl
106	34	65.4	130	7	US-11-125-837-21	Sequence 21, Appl	179	32	61.5	126	6	US-10-839-799-81	Sequence 81, Appl
107	34	65.4	652	7	US-11-192-801-22	Sequence 2, Appl	180	32	61.5	126	6	US-10-839-799-85	Sequence 85, Appl
108	34	65.4	652	7	US-11-192-801-4	Sequence 4, Appl	181	32	61.5	126	6	US-10-839-799-87	Sequence 87, Appl
109	34	65.4	652	7	US-11-192-801-6	Sequence 6, Appl	182	32	61.5	126	6	US-10-839-799-91	Sequence 91, Appl
110	34	65.4	653	7	US-11-192-801-8	Sequence 8, Appl	183	32	61.5	127	6	US-10-839-799-97	Sequence 97, Appl
111	34	65.4	653	7	US-11-192-801-10	Sequence 10, Appl	184	32	61.5	129	6	US-11-051-453-52	Sequence 52, Appl
112	34	65.4	653	7	US-11-192-801-12	Sequence 12, Appl	185	32	61.5	129	6	US-10-512-184-32	Sequence 32, Appl
113	34	65.4	653	7	US-11-192-801-14	Sequence 14, Appl	186	32	61.5	253	6	US-10-524-647-84	Sequence 84, Appl
114	34	65.4	653	7	US-11-192-801-16	Sequence 16, Appl	187	32	61.5	262	6	US-10-524-647-82	Sequence 82, Appl
115	34	65.4	653	7	US-11-192-801-18	Sequence 18, Appl	188	32	61.5	269	6	US-10-839-799-109	Sequence 109, App
116	34	65.4	653	7	US-11-192-801-20	Sequence 20, Appl	189	32	61.5	300	7	US-11-052-554A-4	Sequence 4, Appl
117	34	65.4	653	7	US-11-192-801-22	Sequence 22, Appl	190	32	61.5	300	7	US-11-052-554A-178	Sequence 178, Appl
118	34	65.4	653	7	US-11-192-801-24	Sequence 24, Appl	191	32	61.5	317	6	US-10-512-184-69	Sequence 69, Appl
119	34	65.4	653	7	US-11-192-801-37	Sequence 37, Appl	192	32	61.5	413	6	US-10-517-939-332	Sequence 332, Appl
120	34	65.4	653	7	US-11-192-801-39	Sequence 39, Appl	193	31	59.6	8	7	US-11-055-163-24	Sequence 24, Appl
121	33	63.5	9	7	US-11-097-812-126	Sequence 126, App	194	31	59.6	9	7	US-11-097-812-193	Sequence 193, App
122	33	63.5	95	7	US-11-054-669-59	Sequence 59, Appl	195	31	59.6	105	7	US-11-097-812-53	Sequence 53, Appl
123	33	63.5	95	7	US-11-054-669-60	Sequence 60, Appl	196	31	59.6	107	7	US-11-064-174-40	Sequence 40, Appl
124	33	63.5	95	7	US-11-084-554-115	Sequence 115, App	197	31	59.6	113	7	US-11-097-812-175	Sequence 175, App
125	33	63.5	95	7	US-11-061-848-34	Sequence 34, Appl	198	31	59.6	113	7	US-11-097-812-186	Sequence 186, App
126	33	63.5	95	7	US-11-061-848-38	Sequence 38, Appl	199	31	59.6	113	7	US-11-097-812-187	Sequence 187, App
127	33	63.5	95	7	US-11-061-848-61	Sequence 61, Appl	200	31	59.6	129	6	US-10-721-753-23	Sequence 23, Appl
128	33	63.5	95	7	US-11-061-848-72	Sequence 72, Appl	201	31	59.6	241	7	US-11-054-515-1887	Sequence 1887, Ap
129	33	63.5	96	7	US-11-144-248-40	Sequence 40, Appl	202	31	59.6	258	6	US-10-524-647-16	Sequence 16, Appl
130	33	63.5	96	7	US-11-144-248-6	Sequence 6, Appl	203	31	59.6	1189	6	US-10-821-234-1209	Sequence 1209, Ap
131	33	63.5	96	7	US-11-144-222-40	Sequence 40, Appl	204	30	57.7	9	7	US-11-097-812-61	Sequence 61, Appl
132	33	63.5	102	6	US-10-771-257-104	Sequence 104, App	205	30	57.7	9	7	US-11-097-812-121	Sequence 121, App
133	33	63.5	102	6	US-11-097-812-109	Sequence 109, App	206	30	57.7	9	7	US-11-097-812-127	Sequence 127, App
134	33	63.5	103	6	US-10-771-257-98	Sequence 98, Appl	207	30	57.7	56	6	US-11-097-812-130	Sequence 130, App
135	33	63.5	103	6	US-10-771-257-109	Sequence 109, App	208	30	57.7	6	7	US-10-997-201A-16	Sequence 16, App
136	33	63.5	107	7	US-11-144-222-6	Sequence 6, Appl	209	30	57.7	7	7	US-11-105-268-18	Sequence 18, Appl
137	33	63.5	112	7	US-11-054-669-117	Sequence 117, App	210	30	57.7	107	7	US-11-097-812-101	Sequence 101, App
138	33	63.5	112	7	US-11-054-669-118	Sequence 118, App	211	30	57.7	108	6	US-10-771-257-69	Sequence 69, App
139	33	63.5	112	7	US-11-054-669-119	Sequence 119, App	212	30	57.7	108	7	US-11-127-677-67	Sequence 67, Appl
140	33	63.5	112	7	US-11-144-248-47	Sequence 47, Appl	213	30	57.7	109	7	US-11-097-812-41	Sequence 41, Appl
141	33	63.5	236	7	US-11-144-222-47	Sequence 47, Appl	214	30	57.7	109	7	US-11-097-812-49	Sequence 49, Appl
142	33	63.5	244	7	US-11-054-515-1881	Sequence 1881, Ap	215	30	57.7	109	7	US-11-097-812-55	Sequence 55, Appl
143	33	63.5	293	7	US-11-116-939-10	Sequence 10, Appl	216	30	57.7	111	7	US-11-097-812-105	Sequence 105, App
144	33	63.5	412	7	US-11-116-939-12	Sequence 12, Appl	217	30	57.7	112	7	US-11-097-812-169	Sequence 169, App
145	33	63.5	824	7	US-11-116-939-11	Sequence 11, Appl	218	30	57.7	112	7	US-11-097-812-176	Sequence 176, App
146	32	61.5	9	6	US-10-839-799-120	Sequence 120, App	219	30	57.7	112	7	US-11-097-812-182	Sequence 182, App
147	32	61.5	9	7	US-11-097-812-122	Sequence 122, App	220	30	57.7	112	7	US-11-097-812-183	Sequence 183, App
148	32	61.5	9	7	US-11-051-453-24	Sequence 24, Appl	221	30	57.7	113	7	US-11-097-812-170	Sequence 170, App
149	32	61.5	95	7	US-11-054-669-61	Sequence 61, Appl	222	30	57.7	113	7	US-11-097-812-173	Sequence 173, App
150	32	61.5	95	7	US-11-054-669-62	Sequence 62, Appl	223	30	57.7	113	7	US-11-097-812-177	Sequence 177, App
151	32	61.5	95	7	US-11-084-554-121	Sequence 121, App	224	30	57.7	113	7	US-11-097-812-181	Sequence 181, App
152	32	61.5	95	7	US-11-061-848-35	Sequence 35, Appl	225	30	57.7	113	7	US-11-097-812-204	Sequence 204, App
153	32	61.5	95	7	US-11-061-848-59	Sequence 59, Appl	226	30	57.7	241	7	US-11-054-515-1577	Sequence 1577, App
154	32	61.5	95	7	US-11-061-848-60	Sequence 60, Appl	227	30	57.7	242	7	US-11-054-515-1915	Sequence 1915, Ap
155	32	61.5	95	7	US-11-061-848-60	Sequence 60, Appl	228	30	57.7	246	7	US-11-054-515-1268	Sequence 1268, App
156	32	61.5	95	7	US-11-061-848-70	Sequence 70, Appl	229	30	57.7	247	7	US-11-054-515-3240	Sequence 3240, Ap
157	32	61.5	107	6	US-10-839-799-130	Sequence 130, App	230	30	57.7	248	7	US-11-054-515-1446	Sequence 1446, Ap
158	32	61.5	107	6	US-10-839-799-131	Sequence 131, App	231	30	57.7	250	7	US-11-054-515-1952	Sequence 1952, App
159	32	61.5	107	6	US-10-839-799-131	Sequence 131, App	232	30	57.7	251	7	US-11-054-515-1921	Sequence 1921, Ap
160	32	61.5	107	7	US-11-064-174-29	Sequence 29, Appl	233	30	57.7	257	7	US-11-054-515-10	Sequence 10, Appl
161	32	61.5	107	7	US-11-051-453-6	Sequence 6, Appl	234	30	57.7	311	6	US-10-055-877-182	Sequence 182, App
162	32	61.5	108	6	US-10-771-257-25	Sequence 25, Appl	235	30	57.7	363	7	US-11-000-463-335	Sequence 335, App
163	32	61.5	108	6	US-11-127-677-25	Sequence 25, Appl	236	30	57.7	397	6	US-10-467-657-3944	Sequence 3944, Ap
164	32	61.5	109	6	US-10-771-257-71	Sequence 71, Appl	237	30	57.7	430	7	US-11-055-882-960	Sequence 960, App
165	32	61.5	109	7	US-11-127-677-69	Sequence 69, Appl	238	30	57.7	478	6	US-10-131-826A-138	Sequence 138, App
166	32	61.5	109	7	US-11-097-812-113	Sequence 113, App	239	30	57.7	478	7	US-11-174-150-27	Sequence 27, Appl
167	32	61.5	126	6	US-10-839-799-43	Sequence 43, Appl	240	30	57.7	562	7	US-11-033-039-1345	Sequence 1345, Ap
168	32	61.5	126	6	US-10-839-799-47	Sequence 47, Appl	241	30	57.7	562	7	US-10-665-658-67	Sequence 67, Appl
169	32	61.5	126	6	US-10-839-799-51	Sequence 51, Appl	242	29	55.8	11	7	US-11-097-812-115	Sequence 115, App
170	32	61.5	126	6	US-10-839-799-53	Sequence 53, Appl	243	29	55.8	11	7	US-11-033-039-1175	Sequence 1175, Ap
171	32	61.5	126	6	US-10-839-799-57	Sequence 57, Appl	244	29	55.8	18	7		

245	29	55.8	18	7	US-11-033-039-1201	Sequence 1201, Ap	318	28	53.8	306	7	US-11-017-550-53	Sequence 53, Appl
246	29	55.8	95	7	US-11-054-669-63	Sequence 63, Appl	319	28	53.8	306	7	US-11-017-550-54	Sequence 54, Appl
247	29	55.8	95	7	US-11-054-669-64	Sequence 64, Appl	320	28	53.8	306	7	US-11-017-550-55	Sequence 55, Appl
248	29	55.8	95	7	US-11-084-554-128	Sequence 128, App	321	28	53.8	306	7	US-11-017-550-56	Sequence 56, Appl
249	29	55.8	95	7	US-11-084-554-136	Sequence 136, App	322	28	53.8	306	7	US-11-017-550-57	Sequence 57, Appl
250	29	55.8	95	7	US-11-061-848-10	Sequence 40, Appl	323	28	53.8	306	7	US-11-017-550-58	Sequence 58, Appl
251	29	55.8	95	7	US-11-061-848-41	Sequence 41, Appl	324	28	53.8	306	7	US-11-017-550-59	Sequence 59, Appl
252	29	55.8	109	6	US-10-771-257-64	Sequence 64, Appl	325	28	53.8	306	7	US-11-017-550-60	Sequence 60, Appl
253	29	55.8	109	6	US-11-127-677-62	Sequence 62, Appl	326	28	53.8	306	7	US-11-017-550-61	Sequence 61, Appl
254	29	55.8	113	7	US-11-097-812-108	Sequence 108, App	327	28	53.8	306	7	US-11-017-550-62	Sequence 62, Appl
255	29	55.8	128	6	US-10-721-763-31	Sequence 31, Appl	328	28	53.8	306	7	US-11-017-550-63	Sequence 63, Appl
256	29	55.8	129	6	US-10-721-763-19	Sequence 19, Appl	329	28	53.8	306	7	US-11-014-402-1	Sequence 1, Appl
257	29	55.8	123	6	US-10-793-626-1034	Sequence 1034, Ap	330	28	53.8	306	7	US-11-014-402-2	Sequence 2, Appl
258	29	55.8	251	6	US-10-467-657-9088	Sequence 9088, Ap	331	28	53.8	306	7	US-11-014-402-3	Sequence 3, Appl
259	29	55.8	259	6	US-10-512-184-31	Sequence 31, Appl	332	28	53.8	306	7	US-11-014-402-4	Sequence 4, Appl
260	29	55.8	259	6	US-10-512-184-33	Sequence 33, Appl	333	28	53.8	306	7	US-11-014-402-5	Sequence 5, Appl
261	29	55.8	289	7	US-11-060-008-12	Sequence 12, Appl	334	28	53.8	306	7	US-11-014-402-6	Sequence 6, Appl
262	29	55.8	329	6	US-10-512-184-68	Sequence 68, Appl	335	28	53.8	306	7	US-11-137-850-3	Sequence 3, Appl
263	29	55.8	329	6	US-10-512-184-70	Sequence 70, Appl	336	28	53.8	306	7	US-11-137-850-4	Sequence 4, Appl
264	29	55.8	388	6	US-10-858-730-98	Sequence 98, Appl	337	28	53.8	306	7	US-11-137-850-6	Sequence 6, Appl
265	29	55.8	470	6	US-10-979-821-14	Sequence 14, Appl	338	28	53.8	306	7	US-10-821-234-926	Sequence 926, App
266	29	55.8	470	6	US-11-114-922-14	Sequence 14, Appl	339	28	53.8	488	6	US-10-467-657-630	Sequence 630, Appl
267	29	55.8	503	6	US-10-467-657-6606	Sequence 6606, Ap	340	28	53.8	507	6	US-10-467-657-630	Sequence 19, Appl
268	29	55.8	564	7	US-11-133-360-11	Sequence 11, Appl	341	28	53.8	558	7	US-11-133-360-19	Sequence 1072, Ap
269	29	55.8	564	7	US-11-133-360-13	Sequence 13, Appl	342	28	53.8	633	6	US-10-453-372-1072	Sequence 1078, Ap
270	29	55.8	564	7	US-11-133-360-15	Sequence 15, Appl	343	28	53.8	633	6	US-10-453-372-1078	Sequence 2, Appl
271	29	55.8	564	7	US-11-133-360-17	Sequence 17, Appl	344	28	53.8	644	6	US-10-509-121-2	Sequence 4, Appl
272	29	55.8	568	7	US-11-033-039-1154	Sequence 1154, Ap	345	28	53.8	644	6	US-10-509-121-6	Sequence 6, Appl
273	29	55.8	766	6	US-10-793-626-420	Sequence 420, App	346	28	53.8	644	6	US-10-509-121-8	Sequence 8, Appl
274	29	55.8	888	6	US-10-131-826A-544	Sequence 544, App	347	28	53.8	644	6	US-10-509-111-39	Sequence 39, Appl
275	29	55.8	2323	6	US-10-793-626-760	Sequence 760, App	348	28	53.8	886	6	US-10-873-528-126	Sequence 126, App
276	29	55.8	642	6	US-10-467-657-5900	Sequence 5900, Ap	349	28	53.8	959	6	US-10-453-372-1074	Sequence 1076, Ap
277	28	53.8	9	7	US-11-108-135-12	Sequence 12, Appl	350	28	53.8	1021	6	US-10-453-372-1076	Sequence 1076, Ap
278	28	53.8	9	7	US-11-097-812-123	Sequence 123, App	351	28	53.8	1025	6	US-10-453-372-1078	Sequence 1068, App
279	28	53.8	20	7	US-11-054-515-2131	Sequence 2131, Ap	352	28	53.8	1025	6	US-10-453-372-1078	Sequence 1070, App
280	28	53.8	76	6	US-10-925-366A-322	Sequence 322, Appl	353	28	53.8	1063	6	US-10-453-372-1076	Sequence 1066, Ap
281	28	53.8	107	7	US-11-108-135-18	Sequence 18, Appl	354	28	53.8	1063	6	US-10-453-372-1066	Sequence 1080, Ap
282	28	53.8	107	7	US-11-108-135-20	Sequence 20, Appl	355	28	53.8	3003	6	US-10-453-372-1082	Sequence 1082, Ap
283	28	53.8	107	7	US-11-108-135-22	Sequence 22, Appl	356	28	53.8	3061	6	US-10-453-372-1082	Sequence 14, Appl
284	28	53.8	107	7	US-11-108-135-26	Sequence 26, Appl	357	28	53.8	6893	7	US-11-205-109-14	Sequence 15, Appl
285	28	53.8	109	6	US-10-771-257-101	Sequence 101, App	358	28	53.8	8695	7	US-11-205-109-15	Sequence 15, Appl
286	28	53.8	109	6	US-10-771-257-105	Sequence 105, App	359	27	51.9	9	6	US-10-925-366A-54	Sequence 54, Appl
287	28	53.8	109	6	US-10-771-257-107	Sequence 107, App	360	27	51.9	9	7	US-11-097-812-60	Sequence 18, Appl
288	28	53.8	109	6	US-10-771-257-112	Sequence 112, App	361	27	51.9	9	7	US-11-051-453-18	Sequence 18, Appl
289	28	53.8	110	7	US-11-097-812-179	Sequence 179, App	362	27	51.9	10	6	US-11-152-846-16	Sequence 16, Appl
290	28	53.8	113	7	US-11-097-812-102	Sequence 102, App	363	27	51.9	39	6	US-10-880-238-190	Sequence 190, App
291	28	53.8	175	6	US-10-467-657-7264	Sequence 7264, Ap	364	27	51.9	39	6	US-10-841-956A-3	Sequence 3, Appl
292	28	53.8	213	7	US-11-102-621-118	Sequence 118, App	365	27	51.9	40	7	US-11-023-003-3	Sequence 34, Appl
293	28	53.8	236	7	US-11-086-289-20	Sequence 20, Appl	366	27	51.9	49	7	US-11-112-277-34	Sequence 67, Appl
294	28	53.8	242	7	US-11-054-515-1844	Sequence 1844, Ap	367	27	51.9	95	7	US-11-054-659-84	Sequence 84, Appl
295	28	53.8	255	7	US-11-017-550-36	Sequence 36, Appl	368	27	51.9	95	7	US-11-054-659-84	Sequence 85, Appl
296	28	53.8	256	7	US-11-054-515-8	Sequence 8, Appl	369	27	51.9	95	7	US-11-054-659-85	Sequence 127, App
297	28	53.8	256	7	US-11-054-515-1253	Sequence 1253, Ap	370	27	51.9	95	7	US-11-084-554-127	Sequence 130, App
298	28	53.8	256	7	US-11-054-515-1279	Sequence 1279, Ap	371	27	51.9	95	7	US-11-084-554-130	Sequence 135, App
299	28	53.8	260	7	US-11-054-515-1039	Sequence 1039, Ap	372	27	51.9	95	7	US-11-061-848-44	Sequence 44, Appl
300	28	53.8	269	6	US-10-793-626-1158	Sequence 1158, Ap	373	27	51.9	95	7	US-11-061-848-50	Sequence 50, Appl
301	28	53.8	306	7	US-11-017-550-35	Sequence 35, Appl	374	27	51.9	95	7	US-11-061-848-51	Sequence 51, Appl
302	28	53.8	306	7	US-11-017-550-37	Sequence 37, Appl	375	27	51.9	95	7	US-11-061-848-57	Sequence 57, Appl
303	28	53.8	306	7	US-11-017-550-38	Sequence 38, Appl	376	27	51.9	95	7	US-11-061-848-67	Sequence 67, Appl
304	28	53.8	306	7	US-11-017-550-39	Sequence 39, Appl	377	27	51.9	95	7	US-11-061-848-73	Sequence 73, Appl
305	28	53.8	306	7	US-11-017-550-40	Sequence 40, Appl	378	27	51.9	95	7	US-11-061-848-81	Sequence 81, Appl
306	28	53.8	306	7	US-11-017-550-45	Sequence 45, Appl	379	27	51.9	103	6	US-10-771-257-100	Sequence 103, App
307	28	53.8	306	7	US-11-017-550-47	Sequence 47, Appl	380	27	51.9	105	6	US-10-771-257-103	Sequence 103, App
308	28	53.8	306	7	US-11-017-550-43	Sequence 43, Appl	381	27	51.9	107	7	US-11-105-268-16	Sequence 16, Appl
309	28	53.8	306	7	US-11-017-550-44	Sequence 44, Appl	382	27	51.9	107	7	US-11-051-453-4	Sequence 4, Appl
310	28	53.8	306	7	US-11-017-550-46	Sequence 46, Appl	383	27	51.9	107	7	US-11-051-453-34	Sequence 34, Appl
311	28	53.8	306	7	US-11-017-550-47	Sequence 47, Appl	384	27	51.9	107	7	US-11-149-943-56	Sequence 56, Appl
312	28	53.8	306	7	US-11-017-550-47	Sequence 47, Appl	385	27	51.9	108	6	US-10-665-658-3	Sequence 3, Appl
313	28	53.8	306	7	US-11-017-550-48	Sequence 48, Appl	386	27	51.9	108	7	US-11-120-338-3	Sequence 31, Appl
314	28	53.8	306	7	US-11-017-550-49	Sequence 49, Appl	387	27	51.9	108	7	US-11-064-174-31	Sequence 161, App
315	28	53.8	306	7	US-11-017-550-50	Sequence 50, Appl	388	27	51.9	108	7	US-11-064-174-161	Sequence 177, App
316	28	53.8	306	7	US-11-017-550-51	Sequence 51, Appl	389	27	51.9	108	7	US-11-064-174-177	Sequence 177, App
317	28	53.8	306	7	US-11-017-550-52	Sequence 52, Appl	390	27	51.9	108	7	US-11-106-820-3	Sequence 3, Appl

391	27	51.9	109	6	US-10-467-657-8000	Sequence 8000, App	464	26	50.0	296	6	US-10-878-556A-190	Sequence 190, App
392	27	51.9	109	7	US-11-096-046-5	Sequence 5, Appl1	465	26	50.0	296	7	US-11-204-187-1	Sequence 1, Appl1
393	27	51.9	109	7	US-11-097-812-40	Sequence 40, Appl1	466	26	50.0	296	7	US-11-204-187-1	Sequence 3, Appl1
394	27	51.9	111	7	US-11-077-978-1	Sequence 1, Appl1	467	26	50.0	296	7	US-11-205-562-1	Sequence 1, Appl1
395	27	51.9	111	7	US-11-077-978-4	Sequence 4, Appl1	468	26	50.0	296	7	US-11-205-562-3	Sequence 3, Appl1
396	27	51.9	111	7	US-11-125-837-33	Sequence 33, Appl1	469	26	50.0	300	7	US-11-186-284-145	Sequence 145, App
397	27	51.9	111	7	US-11-125-837-37	Sequence 37, Appl1	470	26	50.0	314	6	US-10-988-545-11	Sequence 11, Appl1
398	27	51.9	111	7	US-11-149-943-60	Sequence 60, Appl1	471	26	50.0	314	6	US-11-166-284-143	Sequence 143, App
399	27	51.9	129	7	US-11-051-453-43	Sequence 43, Appl1	472	26	50.0	344	6	US-10-523-477-9	Sequence 9, Appl1
400	27	51.9	129	7	US-11-051-453-48	Sequence 48, Appl1	473	26	50.0	344	6	US-10-770-726-84	Sequence 84, Appl1
401	27	51.9	187	6	US-10-467-657-5122	Sequence 5122, App	474	26	50.0	344	7	US-11-109-156-13	Sequence 13, Appl1
402	27	51.9	251	7	US-11-054-515-1238	Sequence 1238, App	475	26	50.0	344	7	US-11-092-188-2	Sequence 2, Appl1
403	27	51.9	251	7	US-11-054-515-1310	Sequence 1310, App	476	26	50.0	352	6	US-10-793-626-216	Sequence 216, App
404	27	51.9	252	6	US-10-485-517-156	Sequence 156, App	477	26	50.0	372	6	US-10-467-657-1354	Sequence 1354, App
405	27	51.9	253	7	US-11-054-515-936	Sequence 936, App	478	26	50.0	427	6	US-10-508-263-96	Sequence 96, Appl1
406	27	51.9	286	7	US-11-089-551A-37	Sequence 27, Appl1	479	26	50.0	433	6	US-10-131-826A-334	Sequence 334, App
407	27	51.9	295	6	US-10-485-517-277	Sequence 277, App	480	26	50.0	438	6	US-10-525-710-2	Sequence 2, Appl1
408	27	51.9	330	6	US-10-453-372-572	Sequence 572, App	481	26	50.0	468	6	US-10-793-626-2242	Sequence 2242, App
409	27	51.9	367	6	US-10-525-674-2	Sequence 2, Appl1	482	26	50.0	490	6	US-10-793-626-872	Sequence 872, App
410	27	51.9	385	7	US-11-074-176-192	Sequence 192, App	483	26	50.0	552	6	US-10-793-626-1182	Sequence 1182, App
411	27	51.9	405	7	US-11-089-551A-29	Sequence 29, Appl1	484	26	50.0	588	6	US-10-763-712A-95	Sequence 95, Appl1
412	27	51.9	405	7	US-11-089-551A-50	Sequence 50, Appl1	485	26	50.0	646	6	US-10-793-626-676	Sequence 676, App
413	27	51.9	470	6	US-10-793-626-1814	Sequence 1814, App	486	26	50.0	709	7	US-11-074-176-158	Sequence 158, App
414	27	51.9	524	6	US-10-689-742-13	Sequence 13, Appl1	487	26	50.0	724	7	US-11-109-156-19	Sequence 19, Appl1
415	27	51.9	530	6	US-10-453-372-566	Sequence 566, App	488	26	50.0	805	6	US-10-518-559-4	Sequence 4, Appl1
416	27	51.9	629	6	US-10-453-372-576	Sequence 576, App	489	26	50.0	806	6	US-10-518-559-24	Sequence 24, Appl1
417	27	51.9	629	6	US-10-453-372-578	Sequence 578, App	490	26	50.0	826	6	US-10-821-234-1048	Sequence 1048, App
418	27	51.9	630	6	US-10-517-939-42	Sequence 42, Appl1	491	26	50.0	831	6	US-10-467-657-4486	Sequence 4486, App
419	27	51.9	632	6	US-10-453-372-568	Sequence 568, App	492	26	50.0	858	6	US-10-645-441-18	Sequence 18, Appl1
420	27	51.9	655	7	US-11-184-860-1	Sequence 1, Appl1	493	26	50.0	858	6	US-10-644-441-20	Sequence 20, Appl1
421	27	51.9	655	7	US-11-124-368A-296	Sequence 296, App	494	26	50.0	871	6	US-10-467-657-4588	Sequence 4588, App
422	27	51.9	655	7	US-11-124-368A-297	Sequence 297, App	495	26	50.0	871	6	US-10-467-657-7182	Sequence 7182, App
423	27	51.9	677	6	US-10-131-826A-230	Sequence 230, App	496	26	50.0	1050	6	US-10-467-657-5656	Sequence 5656, App
424	27	51.9	756	7	US-11-074-176-202	Sequence 202, App	497	26	50.0	1050	6	US-10-523-477-12	Sequence 12, Appl1
425	27	51.9	760	6	US-10-821-234-1141	Sequence 1141, App	498	26	50.0	1050	6	US-10-770-726-47	Sequence 47, Appl1
426	27	51.9	798	6	US-10-453-372-570	Sequence 570, App	499	26	50.0	1162	6	US-10-451-375-3	Sequence 3, Appl1
427	27	51.9	811	6	US-10-453-372-580	Sequence 580, App	500	26	50.0	1198	6	US-10-451-375-4	Sequence 4, Appl1
428	27	51.9	821	6	US-10-453-372-600	Sequence 600, App	501	26	50.0	1386	7	US-11-091-643-6	Sequence 6, Appl1
429	27	51.9	837	6	US-10-453-372-594	Sequence 594, App	502	26	50.0	1627	6	US-10-821-234-1283	Sequence 1283, App
430	27	51.9	841	6	US-10-453-372-586	Sequence 586, App	503	26	50.0	1694	7	US-11-052-554A-83	Sequence 83, Appl1
431	27	51.9	841	6	US-10-453-372-592	Sequence 592, App	504	26	50.0	2674	6	US-10-995-561-759	Sequence 759, App
432	27	51.9	841	6	US-10-453-372-602	Sequence 602, App	505	26	50.0	3674	6	US-11-000-463-454	Sequence 454, App
433	27	51.9	1070	7	US/11/062	Sequence 7, Appl1	506	26	50.0	447	6	US-10-884-730-319	Sequence 319, App
434	27	51.9	1095	7	US/11/062	Sequence 20, Appl1	507	25	48.1	9	7	US-11-105-268-6	Sequence 62, Appl1
435	27	51.9	1169	7	US-11-077-550-20	Sequence 1109, App	508	25	48.1	9	7	US-11-097-812-62	Sequence 128, App
436	27	51.9	1207	6	US-10-821-234-1109	Sequence 8, Appl1	509	25	48.1	9	7	US-11-097-812-62	Sequence 25, Appl1
437	27	51.9	2504	9	US-10-647-956A-8	Sequence 40, Appl1	510	25	48.1	9	7	US-11-105-708-25	Sequence 17, Appl1
438	26	50.0	9	7	US-11-009-939-40	Sequence 119, App	511	25	48.1	10	7	US-11-093-274-117	Sequence 19, App
439	26	50.0	9	7	US-11-097-812-119	Sequence 124, App	512	25	48.1	10	7	US-11-097-812-197	Sequence 4276, App
440	26	50.0	9	7	US-11-097-812-124	Sequence 32, Appl1	513	25	48.1	31	6	US-10-467-657-4276	Sequence 8042, App
441	26	50.0	10	7	US-11-057-708-32	Sequence 609, App	514	25	48.1	31	6	US-10-467-657-8042	Sequence 1, Appl1
442	26	50.0	21	6	US-10-939-890-609	Sequence 1173, App	515	25	48.1	35	6	US-10-647-732A-1	Sequence 4, Appl1
443	26	50.0	75	6	US-10-821-234-1173	Sequence 37, Appl1	516	25	48.1	47	6	US-10-647-732A-2	Sequence 2, Appl1
444	26	50.0	108	7	US-11-009-939-37	Sequence 104, App	517	25	48.1	62	6	US-10-647-732A-3	Sequence 3, Appl1
445	26	50.0	110	7	US-11-097-812-104	Sequence 110, App	518	25	48.1	74	6	US-10-999-866-30	Sequence 30, Appl1
446	26	50.0	110	7	US-11-097-812-110	Sequence 107, App	519	25	48.1	87	6	US-10-999-866-30	Sequence 30, Appl1
447	26	50.0	111	6	US-11-097-812-107	Sequence 184, App	520	25	48.1	87	6	US-11-061-821-30	Sequence 30, Appl1
448	26	50.0	115	6	US-10-467-657-184	Sequence 4012, App	521	25	48.1	95	7	US-11-054-666-72	Sequence 72, App
449	26	50.0	115	6	US-10-467-657-4012	Sequence 2, Appl1	522	25	48.1	95	7	US-11-084-554-124	Sequence 124, App
450	26	50.0	193	6	US-10-981-873-2	Sequence 104, App	523	25	48.1	95	7	US-10-485-788A-647	Sequence 647, App
451	26	50.0	194	6	US-10-980-388-104	Sequence 3020, App	524	25	48.1	98	7	US-11-053-076-119	Sequence 119, App
452	26	50.0	205	6	US-10-793-626-3020	Sequence 42, Appl1	525	25	48.1	103	6	US-10-485-517-243	Sequence 243, App
453	26	50.0	228	7	US-11-100-183-42	Sequence 81, Appl1	526	25	48.1	106	6	US-11-105-268-8	Sequence 8, Appl1
454	26	50.0	234	7	US-11-100-183-41	Sequence 4, Appl1	527	25	48.1	107	6	US-10-925-368A-195	Sequence 195, App
455	26	50.0	240	7	US-11-007-282-8	Sequence 13, Appl1	528	25	48.1	108	6	US-10-771-257-77	Sequence 77, Appl1
456	26	50.0	240	7	US-11-007-282-13	Sequence 15, Appl1	529	25	48.1	108	6	US-11-093-274-23	Sequence 23, Appl1
457	26	50.0	240	7	US-11-007-282-14	Sequence 34, Appl1	530	25	48.1	108	7	US-11-127-677-75	Sequence 75, Appl1
458	26	50.0	240	7	US-11-007-282-15	Sequence 1972, App	531	25	48.1	108	7	US-11-097-812-39	Sequence 39, Appl1
459	26	50.0	245	7	US-11-054-515-1972	Sequence 34, Appl1	532	25	48.1	108	7	US-11-097-812-44	Sequence 44, Appl1
460	26	50.0	256	7	US-11-137-465-34	Sequence 6, Appl1	533	25	48.1	108	7	US-11-097-812-47	Sequence 47, Appl1
461	26	50.0	258	7	US-11-007-282-6	Sequence 4, Appl1	534	25	48.1	108	7	US-11-097-812-47	Sequence 207, App
462	26	50.0	295	7	US-11-804-187-4	Sequence 4, Appl1	535	25	48.1	110	7	US-11-097-812-207	
463	26	50.0	295	7	US-11-805-562-4	Sequence 4, Appl1	536	25	48.1	110	7	US-11-097-812-207	

537	25	48.1	111	7	US-11-097-812-112	Sequence 112, App	610	25	48.1	633	6	US-10-954-468-1	Sequence 1, Appl		
538	25	48.1	112	7	US-11-097-812-184	Sequence 184, App	611	25	48.1	752	6	US-10-793-626-348	Sequence 348, App		
539	25	48.1	112	7	US-11-097-812-185	Sequence 185, App	612	25	48.1	758	6	US-11-089-551A-31	Sequence 31, Appl		
540	25	48.1	161	6	US-10-793-626-2930	Sequence 2930, Ap	613	25	48.1	802	6	US-10-510-386-2	Sequence 2, Appl		
541	25	48.1	164	6	US-10-793-626-3040	Sequence 3040, Ap	614	25	48.1	816	6	US-11-057-058-10	Sequence 10, Appl		
542	25	48.1	176	7	US-11-052-554A-39	Sequence 39, Appl	615	25	48.1	883	6	US-10-793-626-754	Sequence 754, App		
543	25	48.1	176	7	US-11-052-554A-197	Sequence 197, App	616	25	48.1	915	6	US-10-647-966A-6	Sequence 6, Appl		
544	25	48.1	177	6	US-10-467-657-1282	Sequence 1282, Ap	617	25	48.1	937	6	US-11-057-058-55	Sequence 55, Appl		
545	25	48.1	177	6	US-10-873-528-108	Sequence 108, App	618	25	48.1	950	6	US-10-981-267-72	Sequence 24, App		
546	25	48.1	203	6	US-10-510-386-122	Sequence 122, App	619	25	48.1	952	6	US-10-981-234-1557	Sequence 1557, Ap		
547	25	48.1	204	6	US-10-131-826A-288	Sequence 288, App	620	25	48.1	952	7	US-11-057-058-54	Sequence 54, Appl		
548	25	48.1	208	6	US-10-821-234-1118	Sequence 1118, Ap	621	25	48.1	953	7	US-11-057-058-53	Sequence 53, Appl		
549	25	48.1	209	6	US-11-134-241-37	Sequence 37, Appl	622	25	48.1	953	7	US-11-057-058-56	Sequence 56, Appl		
550	25	48.1	230	6	US-10-454-437-294	Sequence 294, App	623	25	48.1	953	7	US-11-113-424-60	Sequence 33, Appl		
551	25	48.1	231	6	US-10-467-657-4662	Sequence 4662, Ap	624	25	48.1	984	7	US-11-134-241-37	Sequence 33, Appl		
552	25	48.1	240	7	US-11-134-241-33	Sequence 33, Appl	625	25	48.1	997	7	US-11-057-058-33	Sequence 33, Appl		
553	25	48.1	247	6	US-10-510-386-242	Sequence 242, App	626	25	48.1	1011	7	US-11-057-058-41	Sequence 41, Appl		
554	25	48.1	250	6	US-10-793-626-78	Sequence 78, Appl	627	25	48.1	1107	7	US-11-134-435-1	Sequence 1, Appl		
555	25	48.1	251	6	US-10-467-657-3134	Sequence 3134, Ap	628	25	48.1	1150	6	US-10-858-730-71	Sequence 71, Appl		
556	25	48.1	252	7	US-11-054-515-1376	Sequence 1376, Ap	629	25	48.1	1170	6	US-10-858-730-523	Sequence 223, App		
557	25	48.1	259	6	US-10-995-561-883	Sequence 883, App	630	25	48.1	1227	6	US-10-995-561-711	Sequence 711, App		
558	25	48.1	266	6	US-10-873-528-165	Sequence 165, App	631	25	48.1	1307	6	US-11-152-569-20	Sequence 20, Appl		
559	25	48.1	267	6	US-10-524-647-86	Sequence 86, Appl	632	25	48.1	1359	7	US-11-087-100-6	Sequence 6, Appl		
560	25	48.1	273	6	US-10-793-626-728	Sequence 728, App	633	25	48.1	1503	7	US-11-087-100-6	Sequence 6, Appl		
561	25	48.1	294	7	US-11-052-554A-227	Sequence 227, App	634	25	48.1	1503	7	US-11-087-100-6	Sequence 6, Appl		
562	25	48.1	309	6	US-10-467-657-160	Sequence 160, App	635	25	48.1	1503	6	US-10-055-877-145	Sequence 145, App		
563	25	48.1	309	6	US-10-467-657-7900	Sequence 7900, Ap	636	25	48.1	1637	6	US-10-055-877-144	Sequence 144, App		
564	25	48.1	311	6	US-10-055-877-181	Sequence 181, App	637	25	48.1	1892	7	US-11-075-185-6	Sequence 6, Appl		
565	25	48.1	313	7	US-11-000-463-427	Sequence 427, App	638	25	48.1	2059	7	US-11-087-100-4	Sequence 4, Appl		
566	25	48.1	321	7	US-11-134-241-35	Sequence 35, Appl	639	25	48.1	2059	7	US-11-087-100-4	Sequence 4, Appl		
567	25	48.1	322	7	US-11-109-156-33	Sequence 33, Appl	640	25	48.1	2059	7	US-11-087-100-4	Sequence 4, Appl		
568	25	48.1	334	6	US-10-793-626-282	Sequence 282, App	641	25	48.1	2515	7	US-11-113-424-53	Sequence 53, Appl		
569	25	48.1	340	6	US-10-873-528-188	Sequence 188, App	642	25	48.1	2612	6	US-10-453-372-38	Sequence 38, Appl		
570	25	48.1	341	6	US-10-467-657-5408	Sequence 5408, Ap	643	25	48.1	2669	6	US-10-453-372-36	Sequence 36, Appl		
571	25	48.1	347	7	US-11-066-648A-2	Sequence 2, Appl	644	25	48.1	3104	6	US-10-453-372-34	Sequence 34, Appl		
572	25	48.1	350	6	US-10-485-517-209	Sequence 209, App	645	25	48.1	3104	6	US-10-453-372-62	Sequence 62, Appl		
573	25	48.1	361	6	US-10-793-626-1914	Sequence 1914, Ap	646	25	48.1	3104	6	US-10-453-372-64	Sequence 64, Appl		
574	25	48.1	366	7	US-11-134-241-39	Sequence 39, Appl	647	25	48.1	3507	7	US-11-075-185-7	Sequence 7, Appl		
575	25	48.1	368	7	US-11-000-463-916	Sequence 916, App	648	25	48.1	3655	7	US-11-075-185-5	Sequence 5, Appl		
576	25	48.1	379	6	US-10-510-386-76	Sequence 76, Appl	649	25	48.1	3689	7	US-11-075-185-4	Sequence 4, Appl		
577	25	48.1	388	7	US-11-000-463-444	Sequence 444, App	650	25	48.1	5935	6	US-10-995-561-776	Sequence 776, App		
578	25	48.1	389	7	US-11-018-018-2	Sequence 2, Appl	651	25	48.1	9935	6	US-10-995-561-776	Sequence 776, App		
579	25	48.1	389	7	US-11-047-757-2	Sequence 2, Appl	652	25	48.1	111	6	US-10-507-662-15	Sequence 15, Appl		
580	25	48.1	396	6	US-10-793-626-3222	Sequence 3222, Ap	653	25	48.1	111	6	US-10-507-662-38	Sequence 38, Appl		
581	25	48.1	422	6	US-10-821-234-1313	Sequence 1313, Ap	654	25	48.1	136	6	US-10-467-657-8623	Sequence 8623, Ap		
582	25	48.1	422	7	US-11-055-822-626	Sequence 626, App	655	24	46.2	24.5	47.1	392	6	US-10-793-626-194	Sequence 194, App
583	25	48.1	422	7	US-11-186-284-75	Sequence 75, Appl	656	24	46.2	24	46.2	8	US-10-989-226-59	Sequence 59, Appl	
584	25	48.1	448	6	US-10-858-730-64	Sequence 64, Appl	657	24	46.2	9	6	US-10-925-366A-51	Sequence 51, Appl		
585	25	48.1	449	6	US-10-485-517-272	Sequence 272, App	658	24	46.2	9	6	US-10-925-366A-78	Sequence 78, Appl		
586	25	48.1	451	6	US-10-508-263-68	Sequence 68, App	659	24	46.2	9	6	US-11-097-812-194	Sequence 194, App		
587	25	48.1	451	6	US-10-508-263-70	Sequence 70, Appl	660	24	46.2	27	7	US-11-196-400-14	Sequence 14, Appl		
588	25	48.1	473	6	US-10-467-657-68	Sequence 68, Appl	661	24	46.2	47	7	US-11-196-400-12	Sequence 12, Appl		
589	25	48.1	473	6	US-10-467-657-3670	Sequence 3670, Ap	662	24	46.2	48	7	US-11-123-896-184	Sequence 384, App		
590	25	48.1	476	7	US-11-165-226-8	Sequence 8, Appl	663	24	46.2	50	7	US-11-136-400-11	Sequence 10, Appl		
591	25	48.1	476	7	US-11-165-226-8	Sequence 8, Appl	664	24	46.2	81	7	US-11-123-896-383	Sequence 383, App		
592	25	48.1	504	7	US-11-087-100-32	Sequence 32, Appl	665	24	46.2	82	6	US-10-485-517-372	Sequence 372, App		
593	25	48.1	504	7	US-11-087-085-32	Sequence 32, Appl	666	24	46.2	82	7	US-11-123-896-464	Sequence 464, App		
594	25	48.1	504	7	US-11-087-085-32	Sequence 32, Appl	667	24	46.2	82	7	US-11-084-554-119	Sequence 119, App		
595	25	48.1	510	7	US-11-087-100-26	Sequence 26, Appl	668	24	46.2	82	7	US-11-084-554-129	Sequence 129, App		
596	25	48.1	510	7	US-11-087-085-26	Sequence 26, Appl	669	24	46.2	82	7	US-11-084-554-137	Sequence 137, App		
597	25	48.1	510	7	US-11-087-085-26	Sequence 26, Appl	670	24	46.2	82	7	US-11-084-554-140	Sequence 140, App		
598	25	48.1	567	7	US-11-052-554A-324	Sequence 324, App	671	24	46.2	82	7	US-11-061-848-42	Sequence 42, Appl		
599	25	48.1	567	7	US-10-954-468-8	Sequence 8, Appl	672	24	46.2	82	7	US-11-061-848-43	Sequence 43, Appl		
600	25	48.1	568	7	US-11-049-348-5	Sequence 5, Appl	673	24	46.2	82	7	US-11-061-848-46	Sequence 46, Appl		
601	25	48.1	574	6	US-10-954-468-4	Sequence 4, Appl	674	24	46.2	82	7	US-11-061-848-49	Sequence 49, Appl		
602	25	48.1	587	6	US-10-954-468-6	Sequence 6, Appl	675	24	46.2	82	7	US-11-061-848-49	Sequence 49, Appl		
603	25	48.1	603	7	US-10-954-468-2	Sequence 2, Appl	676	24	46.2	82	7	US-11-061-848-49	Sequence 49, Appl		
604	25	48.1	603	7	US-11-134-241-43	Sequence 43, Appl	677	24	46.2	82	7	US-11-061-848-49	Sequence 49, Appl		
605	25	48.1	615	6	US-10-954-468-7	Sequence 7, Appl	678	24	46.2	82	7	US-11-061-848-49	Sequence 49, Appl		
606	25	48.1	619	6	US-11-205-109-30	Sequence 30, Appl	679	24	46.2	82	7	US-11-061-848-49	Sequence 49, Appl		
607	25	48.1	628	6	US-10-954-468-3	Sequence 3, Appl	680	24	46.2	82	7	US-11-061-848-49	Sequence 49, Appl		
608	25	48.1	628	6	US-10-954-468-5	Sequence 5, Appl	681	24	46.2	82	7	US-11-061-848-49	Sequence 49, Appl		
609	25	48.1	631	7	US-11-134-241-41	Sequence 41, Appl	682	24	46.2	82	7	US-11-061-848-49	Sequence 49, Appl		

683	24	46.2	95	7	US-11-061-848-69	Sequence 69, Appl	756	24	46.2	314	7	US-11-217-562-3	Sequence 3, Appl1
684	24	46.2	98	6	US-10-485-788A-792	Sequence 792, App	757	24	46.2	316	6	US-10-821-234-1526	Sequence 1526, App
685	24	46.2	98	7	US-11-053-076-174	Sequence 174, App	758	24	46.2	318	7	US-11-000-463-432	Sequence 432, App
686	24	46.2	101	6	US-10-771-251-2	Sequence 2, Appl1	759	24	46.2	318	7	US-11-000-463-904	Sequence 904, App
687	24	46.2	104	7	US-11-127-677-2	Sequence 2, Appl1	760	24	46.2	319	6	US-10-873-528-64	Sequence 64, Appl
688	24	46.2	104	7	US-11-217-566-9	Sequence 9, Appl1	761	24	46.2	336	6	US-10-793-626-1858	Sequence 1858, App
689	24	46.2	105	7	US-11-155-775-56	Sequence 56, Appl1	762	24	46.2	346	6	US-10-467-657-4620	Sequence 4620, App
690	24	46.2	106	7	US-11-000-463-305	Sequence 305, App	763	24	46.2	347	7	US-11-066-648A-12	Sequence 12, Appl
691	24	46.2	107	7	US-11-000-463-777	Sequence 777, Appl	764	24	46.2	347	7	US-11-066-648A-14	Sequence 14, Appl1
692	24	46.2	107	7	US-11-010-954-3	Sequence 3, Appl1	765	24	46.2	357	6	US-10-878-556A-83	Sequence 83, Appl
693	24	46.2	107	7	US-11-053-750-3	Sequence 3, Appl1	766	24	46.2	358	6	US-10-467-657-6970	Sequence 6970, App
694	24	46.2	107	7	US-11-053-749-3	Sequence 3, Appl1	767	24	46.2	359	7	US-10-467-657-582	Sequence 582, App
695	24	46.2	107	7	US-11-064-174-173	Sequence 173, App	768	24	46.2	366	6	US-10-467-657-582	Sequence 11, Appl
696	24	46.2	108	6	US-10-834-397-14	Sequence 2, Appl1	769	24	46.2	368	7	US-11-055-822-180	Sequence 180, App
697	24	46.2	108	7	US-11-061-848-2	Sequence 10, Appl1	770	24	46.2	370	7	US-11-055-822-190	Sequence 190, App
698	24	46.2	108	7	US-11-061-848-10	Sequence 10, Appl1	771	24	46.2	371	6	US-10-793-626-1294	Sequence 3294, App
699	24	46.2	108	7	US-11-061-848-11	Sequence 11, Appl1	772	24	46.2	374	7	US-11-060-008-14	Sequence 14, Appl
700	24	46.2	108	7	US-11-061-848-12	Sequence 12, Appl1	773	24	46.2	376	7	US-11-060-008-32	Sequence 32, Appl
701	24	46.2	108	7	US-11-061-848-13	Sequence 13, Appl1	774	24	46.2	377	6	US-10-858-730-286	Sequence 286, App
702	24	46.2	108	7	US-11-061-848-14	Sequence 14, Appl1	775	24	46.2	377	6	US-10-517-939-274	Sequence 274, App
703	24	46.2	108	7	US-11-061-848-15	Sequence 15, Appl1	776	24	46.2	377	7	US-11-055-822-178	Sequence 178, App
704	24	46.2	112	7	US-11-127-933-15	Sequence 15, Appl1	777	24	46.2	377	7	US-11-055-822-188	Sequence 188, App
705	24	46.2	112	7	US-11-127-903-15	Sequence 15, Appl1	778	24	46.2	377	7	US-10-858-730-212	Sequence 212, App
706	24	46.2	113	7	US-11-096-074-53	Sequence 53, Appl1	779	24	46.2	379	6	US-10-858-284-169	Sequence 169, App
707	24	46.2	113	7	US-11-095-822-53	Sequence 53, Appl1	780	24	46.2	388	6	US-10-793-626-618	Sequence 618, App
708	24	46.2	120	6	US-10-467-657-2330	Sequence 2330, App	781	24	46.2	389	6	US-10-485-517-335	Sequence 235, App
709	24	46.2	125	6	US-10-821-234-1451	Sequence 1451, App	782	24	46.2	395	6	US-10-467-657-1516	Sequence 8, Appl1
710	24	46.2	133	6	US-10-467-657-3442	Sequence 3442, App	783	24	46.2	397	7	US-11-060-008-8	Sequence 86, Appl1
711	24	46.2	145	7	US-11-074-176-140	Sequence 140, App	784	24	46.2	397	6	US-10-453-372-86	Sequence 86, Appl1
712	24	46.2	147	6	US-10-467-657-7446	Sequence 7446, App	785	24	46.2	407	6	US-10-698-618-1	Sequence 1, Appl1
713	24	46.2	152	6	US-10-485-517-418	Sequence 418, App	786	24	46.2	409	6	US-10-467-657-742	Sequence 742, App
714	24	46.2	179	7	US-11-055-822-684	Sequence 684, App	787	24	46.2	410	6	US-10-467-657-1864	Sequence 4864, App
715	24	46.2	192	6	US-10-793-626-582	Sequence 582, App	788	24	46.2	412	6	US-10-858-730-82	Sequence 82, Appl1
716	24	46.2	195	6	US-10-353-793-44	Sequence 44, Appl1	789	24	46.2	413	7	US-11-060-008-9	Sequence 9, Appl1
717	24	46.2	198	7	US-11-214-199-6	Sequence 6, Appl1	790	24	46.2	418	6	US-10-485-517-174	Sequence 174, App
718	24	46.2	202	6	US-10-980-388-109	Sequence 109, App	791	24	46.2	419	7	US-11-112-882-36	Sequence 36, Appl1
719	24	46.2	207	6	US-10-520-820-10	Sequence 10, Appl1	792	24	46.2	422	7	US-11-166-993-6	Sequence 6, Appl1
720	24	46.2	209	7	US-11-214-613-28	Sequence 28, App	793	24	46.2	421	7	US-11-166-993-2	Sequence 2, Appl1
721	24	46.2	224	6	US-10-793-626-496	Sequence 496, App	794	24	46.2	421	7	US-11-166-993-4	Sequence 4, Appl1
722	24	46.2	224	6	US-10-793-626-1366	Sequence 1366, App	795	24	46.2	422	7	US-11-082-389-444	Sequence 444, App
723	24	46.2	226	7	US-11-082-389-406	Sequence 406, App	796	24	46.2	422	7	US-11-166-993-7	Sequence 7, Appl1
724	24	46.2	230	6	US-10-793-626-3314	Sequence 3314, App	797	24	46.2	422	7	US-11-166-993-113	Sequence 113, App
725	24	46.2	234	7	US-11-100-183-36	Sequence 36, Appl1	798	24	46.2	425	7	US-11-112-882-60	Sequence 60, Appl1
726	24	46.2	239	7	US-11-100-183-25	Sequence 25, Appl1	799	24	46.2	426	6	US-10-131-826A-218	Sequence 218, App
727	24	46.2	249	6	US-10-527-500-25	Sequence 25, Appl1	800	24	46.2	426	6	US-10-454-437-70	Sequence 70, Appl1
728	24	46.2	254	6	US-10-995-561-841	Sequence 841, App	801	24	46.2	426	6	US-10-454-437-72	Sequence 72, Appl1
729	24	46.2	254	7	US-11-054-515-1958	Sequence 1958, App	802	24	46.2	426	6	US-10-525-710-8	Sequence 8, Appl1
730	24	46.2	257	6	US-10-467-657-176	Sequence 176, App	803	24	46.2	430	6	US-10-821-234-1463	Sequence 1463, App
731	24	46.2	257	6	US-10-467-657-3698	Sequence 3698, App	804	24	46.2	432	6	US-10-467-657-1434	Sequence 1434, App
732	24	46.2	260	6	US-10-055-877-166	Sequence 166, App	805	24	46.2	433	6	US-10-467-657-1990	Sequence 2, Appl1
733	24	46.2	261	6	US-10-055-877-164	Sequence 165, App	806	24	46.2	433	7	US-11-093-814-2	Sequence 72, Appl1
734	24	46.2	261	6	US-10-055-877-165	Sequence 29, Appl1	807	24	46.2	433	7	US-11-074-176-72	Sequence 804, App
735	24	46.2	263	6	US-10-512-184-29	Sequence 486, App	808	24	46.2	433	6	US-10-793-626-804	Sequence 82, Appl1
736	24	46.2	267	6	US-10-793-626-486	Sequence 51, Appl1	809	24	46.2	433	6	US-10-453-372-104	Sequence 104, App
737	24	46.2	272	6	US-10-495-597-5	Sequence 71, Appl1	810	24	46.2	433	6	US-10-453-372-106	Sequence 106, App
738	24	46.2	273	6	US-10-873-528-71	Sequence 3407, App	811	24	46.2	433	6	US-10-453-372-108	Sequence 108, App
739	24	46.2	273	6	US-11-113-424-16	Sequence 16, Appl1	812	24	46.2	433	6	US-10-453-372-110	Sequence 110, App
740	24	46.2	273	7	US-11-113-424-18	Sequence 18, Appl1	813	24	46.2	433	6	US-10-453-372-112	Sequence 112, App
741	24	46.2	281	7	US-11-214-613-2	Sequence 2, Appl1	814	24	46.2	433	6	US-10-453-372-110	Sequence 5134, App
742	24	46.2	281	7	US-11-214-613-18	Sequence 18, Appl1	815	24	46.2	437	6	US-10-467-657-5134	Sequence 164, App
743	24	46.2	287	7	US-11-214-613-18	Sequence 1434, App	816	24	46.2	437	6	US-10-878-556A-162	Sequence 84, Appl1
744	24	46.2	292	6	US-10-793-626-1434	Sequence 26, Appl1	817	24	46.2	437	6	US-10-821-234-1151	Sequence 1151, App
745	24	46.2	293	7	US-11-214-613-26	Sequence 39, Appl1	818	24	46.2	437	6	US-10-793-626-946	Sequence 946, App
746	24	46.2	299	7	US-11-214-613-39	Sequence 42, Appl1	819	24	46.2	475	6	US-10-453-372-96	Sequence 96, App
747	24	46.2	301	7	US-11-214-613-42	Sequence 22, Appl1	820	24	46.2	476	7	US-11-055-822-942	Sequence 942, App
748	24	46.2	306	7	US-11-214-613-24	Sequence 24, Appl1	821	24	46.2	476	7	US-10-453-372-90	Sequence 90, Appl1
749	24	46.2	307	6	US-10-793-626-1282	Sequence 1282, App	822	24	46.2	478	6	US-10-793-626-768	Sequence 768, App
750	24	46.2	307	7	US-11-055-822-682	Sequence 682, App	823	24	46.2	497	6	US-10-453-372-92	Sequence 92, Appl1
751	24	46.2	311	7	US-11-214-613-16	Sequence 16, Appl1	824	24	46.2	497	6	US-10-453-372-100	Sequence 100, App
752	24	46.2	311	7	US-11-214-613-30	Sequence 40, Appl1	825	24	46.2	497	6	US-10-453-372-102	Sequence 102, App
753	24	46.2	312	7	US-11-217-562-4	Sequence 20, Appl1	826	24	46.2				
754	24	46.2	313	7	US-11-214-613-20		827	24	46.2				
755	24	46.2	313	7	US-11-214-613-20		828	24	46.2				

829	24	46.2	498	6	US-10-453-372-94	Sequence 94, Appl	902	23	44.2	8	7	US-11-045-024-4242	Sequence 4242, Ap
830	24	46.2	501	6	US-10-453-372-96	Sequence 96, Appl	903	23	44.2	8	7	US-11-045-024-4243	Sequence 4245, Ap
831	24	46.2	510	6	US-11-093-814-1	Sequence 1, Appl1	904	23	44.2	8	7	US-11-045-024-4247	Sequence 7437, Ap
832	24	46.2	538	6	US-10-763-712A-58	Sequence 58, Appl	905	23	44.2	8	7	US-11-045-024-9400	Sequence 9400, Ap
833	24	46.2	559	6	US-10-821-234-947	Sequence 947, App	906	23	44.2	8	7	US-11-045-024-12674	Sequence 12674, A
834	24	46.2	567	6	US-10-503-051-5	Sequence 5, Appl1	907	23	44.2	9	6	US-10-507-662-89	Sequence 59, Appl1
835	24	46.2	582	6	US-10-793-626-2482	Sequence 2482, Ap	908	23	44.2	9	7	US-11-009-939-30	Sequence 939, Ap
836	24	46.2	587	6	US-11-090-439-58	Sequence 58, Appl	909	23	44.2	9	7	US-11-045-024-5272	Sequence 5272, Ap
837	24	46.2	585	6	US-11-205-109-36	Sequence 36, Appl	910	23	44.2	9	7	US-11-045-024-5726	Sequence 5726, Ap
838	24	46.2	582	6	US-10-467-657-3160	Sequence 3160, Ap	911	23	44.2	9	7	US-11-045-024-5462	Sequence 5462, Ap
839	24	46.2	594	6	US-10-467-657-3952	Sequence 3952, Ap	912	23	44.2	9	7	US-11-045-024-3396	Sequence 9396, Ap
840	24	46.2	605	6	US-10-131-826A-160	Sequence 160, App	913	23	44.2	9	7	US-11-045-024-73764	Sequence 13764, A
841	24	46.2	606	6	US-11-126-313-23	Sequence 23, Appl	914	23	44.2	9	7	US-11-097-812-191	Sequence 191, App
842	24	46.2	618	6	US-10-467-657-2332	Sequence 2332, Ap	915	23	44.2	9	7	US-11-041-893-88	Sequence 88, Appl
843	24	46.2	618	6	US-10-523-912-4	Sequence 4, Appl1	916	23	44.2	9	7	US-11-045-024-1306	Sequence 1306, App
844	24	46.2	624	6	US-10-467-657-1740	Sequence 1740, Ap	917	23	44.2	10	7	US-11-045-024-4360	Sequence 4360, App
845	24	46.2	626	6	US-11-082-389-392	Sequence 392, App	918	23	44.2	10	7	US-11-045-024-4282	Sequence 4282, Ap
846	24	46.2	628	7	US-11-082-389-402	Sequence 402, App	919	23	44.2	10	7	US-11-045-024-4282	Sequence 4282, Ap
847	24	46.2	630	7	US-11-196-400-5	Sequence 5, Appl1	920	23	44.2	10	7	US-11-045-024-4285	Sequence 4285, Ap
848	24	46.2	634	7	US-11-082-389-390	Sequence 390, App	921	23	44.2	10	7	US-11-045-024-5278	Sequence 5278, Ap
849	24	46.2	646	6	US-10-995-561-695	Sequence 695, App	922	23	44.2	10	7	US-11-045-024-5684	Sequence 5684, Ap
850	24	46.2	648	6	US-10-793-626-1060	Sequence 1060, Ap	923	23	44.2	10	7	US-11-045-024-7440	Sequence 7440, Ap
851	24	46.2	684	6	US-10-793-626-2098	Sequence 2098, Ap	924	23	44.2	10	7	US-11-045-024-7442	Sequence 7442, Ap
852	24	46.2	686	6	US-10-821-234-1027	Sequence 1027, Ap	925	23	44.2	10	7	US-11-045-024-12668	Sequence 12668, A
853	24	46.2	708	6	US-10-636-320-2	Sequence 2, Appl	926	23	44.2	10	7	US-11-097-812-120	Sequence 120, App
854	24	46.2	715	7	US-11-089-551A-47	Sequence 47, Appl	927	23	44.2	11	7	US-11-045-024-5287	Sequence 5287, Ap
855	24	46.2	721	7	US-11-052-554A-253	Sequence 253, App	928	23	44.2	11	7	US-11-045-024-9411	Sequence 9411, App
856	24	46.2	725	7	US-11-078-189-15	Sequence 15, Appl	929	23	44.2	15	7	US-11-022-562-119	Sequence 119, App
857	24	46.2	726	7	US-11-052-554A-127	Sequence 127, App	930	23	44.2	15	7	US-11-022-562-120	Sequence 120, App
858	24	46.2	731	6	US-10-613-744-10	Sequence 10, Appl	931	23	44.2	15	7	US-11-022-562-121	Sequence 121, App
859	24	46.2	733	7	US-11-145-035-43	Sequence 43, Appl	932	23	44.2	15	7	US-11-045-024-13078	Sequence 13078, A
860	24	46.2	755	7	US-11-037-243-68	Sequence 68, Appl	933	23	44.2	15	7	US-11-045-024-13082	Sequence 13082, A
861	24	46.2	765	7	US-11-037-243-80	Sequence 80, Appl	934	23	44.2	15	7	US-11-045-024-13100	Sequence 13100, A
862	24	46.2	768	7	US-11-147-109-10	Sequence 10, Appl	935	23	44.2	15	7	US-11-045-024-13108	Sequence 13108, A
863	24	46.2	799	7	US-11-074-176-348	Sequence 348, App	936	23	44.2	18	7	US-11-033-039-985	Sequence 985, App
864	24	46.2	805	7	US-11-074-176-172	Sequence 172, App	937	23	44.2	18	7	US-11-033-039-1006	Sequence 1006, App
865	24	46.2	845	7	US-11-147-047-46	Sequence 46, Appl	938	23	44.2	19	6	US-10-503-575-332	Sequence 332, App
866	24	46.2	847	6	US-10-995-561-634	Sequence 634, App	939	23	44.2	19	6	US-10-503-575-333	Sequence 333, App
867	24	46.2	866	6	US-10-467-657-7004	Sequence 7004, Ap	940	23	44.2	20	7	US-11-022-562-332	Sequence 332, App
868	24	46.2	918	6	US-10-995-561-696	Sequence 696, App	941	23	44.2	20	7	US-11-022-562-333	Sequence 333, App
869	24	46.2	963	6	US-10-467-962B-2	Sequence 2, Appl1	942	23	44.2	21	7	US-11-022-562-334	Sequence 334, App
870	24	46.2	1020	6	US-10-513-786-4	Sequence 4, Appl1	943	23	44.2	21	7	US-11-022-562-335	Sequence 335, App
871	24	46.2	1027	6	US-10-793-626-3106	Sequence 3106, Ap	944	23	44.2	22	7	US-11-127-877-513	Sequence 577, App
872	24	46.2	1095	6	US-10-793-626-3154	Sequence 3154, Ap	945	23	44.2	22	7	US-10-467-657-4086	Sequence 4086, App
873	24	46.2	1145	6	US-10-793-626-1432	Sequence 1432, Ap	946	23	44.2	32	6	US-10-467-657-1186	Sequence 1186, Ap
874	24	46.2	1259	6	US-10-995-561-625	Sequence 625, App	947	23	44.2	38	6	US-10-467-657-9212	Sequence 9212, Ap
875	24	46.2	1267	6	US-11-109-156-35	Sequence 35, App	948	23	44.2	42	6	US-10-967-537A-18	Sequence 18, App
876	24	46.2	1286	6	US-10-995-561-628	Sequence 628, App	949	23	44.2	46	6	US-10-986-501-209	Sequence 209, App
877	24	46.2	1315	6	US-10-995-561-630	Sequence 630, App	950	23	44.2	80	7	US-11-030-313-1	Sequence 1, Appl1
878	24	46.2	1341	6	US-10-995-561-621	Sequence 621, App	951	23	44.2	82	6	US-10-467-657-1738	Sequence 1738, Ap
879	24	46.2	1348	6	US-10-995-561-624	Sequence 624, App	952	23	44.2	85	6	US-10-467-657-788	Sequence 788, App
880	24	46.2	1377	6	US-10-821-234-1070	Sequence 1070, Ap	953	23	44.2	86	6	US-10-467-657-3378	Sequence 3378, Ap
881	24	46.2	1365	6	US-10-467-657-2704	Sequence 2704, Ap	954	23	44.2	102	6	US-10-816-768-46	Sequence 46, Appl
882	24	46.2	1543	7	US-11-052-554A-172	Sequence 172, App	955	23	44.2	102	6	US-10-771-257-108	Sequence 108, App
883	24	46.2	1786	6	US-11-196-400-3	Sequence 3, Appl1	956	23	44.2	103	6	US-10-771-257-102	Sequence 102, Appl
884	24	46.2	1900	6	US-10-513-786-3	Sequence 3, Appl1	957	23	44.2	105	7	US-11-084-554-12	Sequence 12, Appl
885	24	46.2	1933	6	US-10-523-912-2	Sequence 2, Appl1	958	23	44.2	106	6	US-10-821-234-1191	Sequence 1191, Ap
886	24	46.2	2236	6	US-10-995-561-633	Sequence 633, App	959	23	44.2	107	6	US-10-507-662-40	Sequence 40, Appl
887	24	46.2	2355	6	US-10-995-561-623	Sequence 623, App	960	23	44.2	107	6	US-10-507-662-63	Sequence 63, Appl
888	24	46.2	2355	6	US-10-995-561-627	Sequence 627, App	961	23	44.2	107	6	US-10-999-866-43	Sequence 43, Appl
889	24	46.2	2384	6	US-10-821-234-1545	Sequence 1545, Ap	962	23	44.2	107	6	US-11-084-554-1	Sequence 1, Appl1
890	24	46.2	2386	6	US-10-995-561-626	Sequence 626, App	963	23	44.2	108	6	US-10-925-366A-330	Sequence 330, App
891	24	46.2	2417	6	US-10-453-372-228	Sequence 228, App	964	23	44.2	108	6	US-11-009-939-27	Sequence 27, Appl
892	24	46.2	3704	6	US-10-513-786-1	Sequence 1, Appl1	965	23	44.2	110	7	US-11-097-812-98	Sequence 98, Appl
893	24	46.2	4128	6	US-10-770-726-77	Sequence 77, Appl	966	23	44.2	110	7	US-11-097-812-98	Sequence 98, Appl
894	24	46.2	4655	6	US-10-995-561-556	Sequence 556, App	967	23	44.2	111	7	US-11-184-005-5	Sequence 5, Appl1
895	24	46.2	4913	6	US-10-453-372-1142	Sequence 1142, Ap	968	23	44.2	112	7	US-11-000-463-470	Sequence 470, App
896	24	46.2	4961	6	US-10-453-372-1132	Sequence 1132, Ap	969	23	44.2	112	7	US-11-000-463-942	Sequence 942, App
897	24	46.2	7968	7	US-11-186-731-5	Sequence 5, Appl1	970	23	44.2	113	6	US-10-952-535A-20	Sequence 20, Appl
898	23	44.2	7	7	US-11-064-785-5	Sequence 191, App	971	23	44.2	113	7	US-11-097-812-188	Sequence 188, App
899	23	44.2	8	7	US-11-045-024-191	Sequence 1128, Ap	972	23	44.2	114	6	US-10-923-337-1	Sequence 1, Appl1
900	23	44.2	8	7	US-11-045-024-1128	Sequence 4048, Ap	973	23	44.2	114	6	US-10-923-337-2	Sequence 2, Appl1
901	23	44.2	8	7	US-11-045-024-4048		974	23	44.2	114	6	US-10-923-337-3	Sequence 3, Appl1

975	23	44.2	117	6	US-10-467-657-8828	Sequence 8828, Ap
976	23	44.2	119	6	US-10-925-366A-210	Sequence 210, App
977	23	44.2	128	7	US-11-105-864-4	Sequence 4, Appli
978	23	44.2	132	7	US-11-073-605-15	Sequence 15, Appli
979	23	44.2	134	7	US-11-064-774A-151	Sequence 151, App
980	23	44.2	132	6	US-10-467-657-8024	Sequence 8024, Ap
981	23	44.2	136	7	US-11-051-267-29	Sequence 159, Appl
982	23	44.2	137	6	US-10-485-517-159	Sequence 159, App
983	23	44.2	144	6	US-10-793-626-1640	Sequence 1640, Ap
984	23	44.2	144	6	US-10-793-626-1958	Sequence 1958, App
985	23	44.2	149	6	US-10-467-657-712	Sequence 712, App
986	23	44.2	150	6	US-10-793-626-2324	Sequence 27, Appl
987	23	44.2	157	7	US-11-051-267-27	Sequence 27, Appl
988	23	44.2	168	7	US-11-052-554A-320	Sequence 320, App
989	23	44.2	171	6	US-10-467-657-1838	Sequence 1838, Ap
990	23	44.2	175	6	US-10-821-234-1074	Sequence 1074, Ap
991	23	44.2	182	6	US-10-467-657-2626	Sequence 2626, Ap
992	23	44.2	183	7	US-11-051-568-23	Sequence 23, Appl
993	23	44.2	184	6	US-10-467-657-3356	Sequence 3356, Ap
994	23	44.2	190	6	US-10-793-626-3140	Sequence 3140, Ap
995	23	44.2	191	6	US-10-793-626-1340	Sequence 1340, Ap
996	23	44.2	193	6	US-10-981-873-1	Sequence 1, Appli
997	23	44.2	207	7	US-11-022-562-222	Sequence 222, App
998	23	44.2	215	7	US-11-119-212-9	Sequence 9, Appli
999	23	44.2	218	6	US-10-793-626-562	Sequence 562, App
1000	23	44.2	218	6	US-10-923-327-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-665-658-15
Sequence 15, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-Nov-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-Oct-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-Feb-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-665-658-15

Query Match 100.0%; Score 52; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COHNEHYPLT 9
|||||
DB 1 COHNEHYPLT 9

RESULT 2
US-10-665-658-66
Sequence 66, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-Nov-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-Nov-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-Oct-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-Feb-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1CID1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-665-658-66

Query Match 100.0%; Score 52; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.1e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 COHNEHYPLT 9
|||||
DB 1 COHNEHYPLT 9

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RESULT 3
US-11-107-028-49
; Sequence 49, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 49
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-49

Query Match
Best Local Similarity 100.0%; Score 52; DB 7; Length 107;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OOHNEYPPLT 9
| | | | |
Db 89 OOHNEYPPLT 97

RESULT 4
US-11-107-028-51
; Sequence 51, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 51
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-107-028-51

Query Match
Best Local Similarity 100.0%; Score 52; DB 7; Length 107;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OOHNEYPPLT 9
| | | | |
Db 89 OOHNEYPPLT 97

RESULT 5
US-10-665-658-1
; Sequence 1, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014RIC1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-665-658-1

Query Match
Best Local Similarity 100.0%; Score 52; DB 6; Length 108;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OOHNEYPPLT 9
| | | | |
Db 89 OOHNEYPPLT 97

RESULT 6
US-10-665-658-2
; Sequence 2, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-665-658-2

Query Match 100.0%; Score 52; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
|||||
Db 89 QOHNEYP1T 97

RESULT 7
US-10-665-658-70
Sequence 70, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-665-658-70

Query Match 88.5%; Score 46; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.1e+04;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
|||||
Db 1 QOHNEYP1T 9

RESULT 8
US-10-665-658-69
Sequence 69, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001
ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-10-665-658-69

Query Match 84.6%; Score 44; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.1e+04;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYP1T 9
|||||

Db 1 QOANEYPLT 9

RESULT 9
US-10-665-658-71
Sequence 71, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
PRESTA, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-10-665-658-71

Query Match 82.7%; Score 43; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.1e+04;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOANEYPLT 9
Db 1 QOANEYPLT 9

RESULT 10
US-10-665-658-68
Sequence 68, Application US/10665658
Publication No. US20050276801A1
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
PRESTA, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/665,658
FILING DATE: 19-Sep-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 27-NOV-1996
APPLICATION NUMBER: 08/974899
FILING DATE: 20-NOV-1997
APPLICATION NUMBER: 09/420745
FILING DATE: 20-OCT-1999
APPLICATION NUMBER: 09/975798
FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:
NAME: Tan, Lee K.
REGISTRATION NUMBER: 39,447
REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-4462
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-10-665-658-68

Query Match 80.8%; Score 42; DB 6; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.1e+04;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOANEYPLT 9
Db 1 QOANEYPLT 9

RESULT 11
US-11-144-248-14
Sequence 14, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-14

Query Match 80.8%; Score 42; DB 7; Length 107;
Best Local Similarity 87.5%; Pred. No. 0.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNEYPPLT 9
||| |||
Db 90 QHNSYPLT 97

RESULT 12
US-11-144-222-14
; Sequence 14, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-222-14

Query Match 80.8%; Score 42; DB 7; Length 107;
Best Local Similarity 87.5%; Pred. No. 0.1;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QHNEYPPLT 9
||| |||
Db 90 QHNSYPLT 97

RESULT 13
US-11-173-071-10
; Sequence 10, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
; APPLICANT: ERICKSON-MILLER, CONNIE
; APPLICANT: HOLMES, STEPHEN D.
; APPLICANT: TAYLOR, ALEXANDER H.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
; FILE REFERENCE: P50911
; CURRENT APPLICATION NUMBER: US/11/173,071
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/958,620
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: PCT/US00/10284
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,263
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-173-071-10

Query Match 78.8%; Score 41; DB 7; Length 9;

Best Local Similarity 77.8%; Pred. No. 5.1e+04;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPPLT 9
||:| |||
Db 1 QOYNSYPLT 9

RESULT 14
US-11-173-071-16
; Sequence 16, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
; APPLICANT: ERICKSON-MILLER, CONNIE
; APPLICANT: HOLMES, STEPHEN D.
; APPLICANT: TAYLOR, ALEXANDER H.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
; FILE REFERENCE: P50911
; CURRENT APPLICATION NUMBER: US/11/173,071
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/958,620
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: PCT/US00/10284
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,263
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region 3GSHZLC1-0
US-11-173-071-16

Query Match 78.8%; Score 41; DB 7; Length 108;
Best Local Similarity 77.8%; Pred. No. 0.17;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPPLT 9
||:| |||
Db 95 QOYNSYPLT 103

RESULT 15
US-11-173-071-18
; Sequence 18, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
; APPLICANT: ERICKSON-MILLER, CONNIE
; APPLICANT: HOLMES, STEPHEN D.
; APPLICANT: TAYLOR, ALEXANDER H.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
; FILE REFERENCE: P50911
; CURRENT APPLICATION NUMBER: US/11/173,071
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/958,620
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: PCT/US00/10284
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,263
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-173-071-18

Query Match 78.8%; Score 41; DB 7; Length 108;
Best Local Similarity 77.8%; Pred. No. 0.17;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OOHNEYPILT 9
||:||||
Db 95 OQYNSYPLT 103

RESULT 16
US-11-173-071-20

; Sequence 20, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
; APPLICANT: ERICKSON-MILLER, CONNIE
; APPLICANT: HOLMES, STEPHEN D.
; APPLICANT: TAYLOR, ALEXANDER H.
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
; FILE REFERENCE: P50911
; CURRENT APPLICATION NUMBER: US/11/173,071
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/958,620
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: PCT/US00/10284
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,263
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-173-071-20

Query Match 78.8%; Score 41; DB 7; Length 108;
Best Local Similarity 77.8%; Pred. No. 0.17;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OOHNEYPILT 9
||:||||
Db 95 OQYNSYPLT 103

RESULT 17
US-11-173-071-22

; Sequence 22, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
; APPLICANT: ERICKSON-MILLER, CONNIE
; APPLICANT: HOLMES, STEPHEN D.
; APPLICANT: TAYLOR, ALEXANDER H.
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
; FILE REFERENCE: P50911
; CURRENT APPLICATION NUMBER: US/11/173,071
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/958,620
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: PCT/US00/10284
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,263
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-173-071-22

Query Match 78.8%; Score 41; DB 7; Length 108;

Best Local Similarity 77.8%; Pred. No. 0.17;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OOHNEYPILT 9
||:||||
Db 95 OQYNSYPLT 103

RESULT 18
US-11-173-071-4

; Sequence 4, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
; APPLICANT: ERICKSON-MILLER, CONNIE
; APPLICANT: HOLMES, STEPHEN D.
; APPLICANT: TAYLOR, ALEXANDER H.
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
; FILE REFERENCE: P50911
; CURRENT APPLICATION NUMBER: US/11/173,071
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/958,620
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: PCT/US00/10284
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,263
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 369 light chain variable region
US-11-173-071-4

Query Match 78.8%; Score 41; DB 7; Length 112;
Best Local Similarity 77.8%; Pred. No. 0.17;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OOHNEYPILT 9
||:||||
Db 89 OQYNSYPLT 97

RESULT 19
US-11-054-515-1943

; Sequence 1943, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248

;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1943
;; LENGTH: 243
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-1943

Query Match 73.1%; Score 38; DB 7; Length 243;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYPYT 9
||:|||||
Db 224 QOYSDYPLT 232

RESULT 20
US-11-054-515-2064
; Sequence 2064, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:

;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly's
;; FILE REFERENCE: PFS23P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 2064
;; LENGTH: 243
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-2064

Query Match 73.1%; Score 38; DB 7; Length 243;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOHNEYPYT 9
||:|||||
Db 224 QOYSDYPLT 232

RESULT 21
US-11-144-248-48
; Sequence 48, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.

;; APPLICANT: Beebe, Jean
;; APPLICANT: Miller, Penelope E.
;; APPLICANT: Moyer, James D.
;; APPLICANT: Corvatan, Jose R.
;; APPLICANT: Gallo, Michael
;; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
;; FILE REFERENCE: ABX-PP2
;; CURRENT APPLICATION NUMBER: US/11/144,248
;; CURRENT FILING DATE: 2005-06-02
;; PRIOR APPLICATION NUMBER: US/10/038,591
;; PRIOR FILING DATE: 2002-01-04
;; PRIOR APPLICATION NUMBER: 60/259,927
;; PRIOR FILING DATE: 2001-01-05
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 48
;; LENGTH: 236
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-144-248-48

Query Match 71.2%; Score 37; DB 7; Length 236;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QHNSYPT 9
||| ||| |||
Db 112 QHNSYPT 119

RESULT 22
US-11-144-222-48
; Sequence 48, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:

;; APPLICANT: Cohen, Bruce D.
;; APPLICANT: Beebe, Jean
;; APPLICANT: Miller, Penelope E.
;; APPLICANT: Moyer, James D.
;; APPLICANT: Corvatan, Jose R.
;; APPLICANT: Gallo, Michael
;; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
;; FILE REFERENCE: ABX-PP2
;; CURRENT APPLICATION NUMBER: US/11/144,222
;; CURRENT FILING DATE: 2005-06-02
;; PRIOR APPLICATION NUMBER: US/10/038,591
;; PRIOR FILING DATE: 2002-01-04
;; PRIOR APPLICATION NUMBER: 60/259,927
;; PRIOR FILING DATE: 2001-01-05
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 48
;; LENGTH: 236
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-144-222-48

Query Match 71.2%; Score 37; DB 7; Length 236;
Best Local Similarity 75.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QHNSYPT 9
||| ||| |||
Db 112 QHNSYPT 119

RESULT 23
US-11-096-046-9
; Sequence 9, Application US/11096046
; Publication No. US20050276802A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, CAMELLIA W.
; APPLICANT: FERRARA, NAPOLEONE

```
; APPLICANT: FILVAROFF, ELLEN H.
; APPLICANT: MAO, WEIGUANG
; APPLICANT: PRESTA, LEONARD G.
; APPLICANT: TEJADA, MAX L.
; TITLE OF INVENTION: Humanized Anti-TGF-Beta Antibodies
; FILE REFERENCE: P1954RIUS
; CURRENT APPLICATION NUMBER: US/11/096,046
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US 60/558,290
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-096-046-9
```

```
Query Match          69.2%; Score 36; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.1e+04;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 QOHNEYPRT 9
||:|||||
Db 1 QOYSSYPRT 9
```

```
RESULT 24
US-11-097-812-59
; Sequence 59, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakapagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 9
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-59
```

```
Query Match          69.2%; Score 36; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.1e+04;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 QOHNEYPRT 9
||:|||||
Db 1 QOYSSYPRT 9
```

```
RESULT 25
US-11-144-248-10
; Sequence 10, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-10
```

```
Query Match          69.2%; Score 36; DB 7; Length 100;
Best Local Similarity 75.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 QHNNYPT 9
|||:|||
Db 82 QHNNYPT 89
```

```
RESULT 26
US-11-144-222-10
; Sequence 10, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-222-10
```

```
Query Match          69.2%; Score 36; DB 7; Length 100;
Best Local Similarity 75.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 QHNNYPT 9
|||:|||
Db 82 QHNNYPT 89
```

```
RESULT 27
US-11-084-554-6
; Sequence 6, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Stiid-Ai
```

APPLICANT: Green, Larry L.
APPLICANT: Kover, Wouter
TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
FILE REFERENCE: ABGENTX.100A
CURRENT APPLICATION NUMBER: US/11/084,554
CURRENT FILING DATE: 2005-03-17
PRIOR APPLICATION NUMBER: 60/554,372
PRIOR FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: 60/574,661
PRIOR FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-11-084-554-6

Query Match 69.2%; Score 36; DB 7; Length 107;
Best Local Similarity 75.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QOHNEYPPLT 9
|||
Db 90 QHKSYPPLT 97

RESULT 28
US-11-112-240-12
Sequence 12, Application US/11112240
Publication No. US20050287140A1
GENERAL INFORMATION:
APPLICANT: Smothers, James F.
APPLICANT: Farnlow, IIT, William C.
APPLICANT: Kariy, Revital
TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITTING DOMAINS OF CD148
FILE REFERENCE: A-953A(US)
CURRENT APPLICATION NUMBER: US/11/112,240
CURRENT FILING DATE: 2005-04-21
PRIOR APPLICATION NUMBER: US 60/564,885
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/585,885
PRIOR FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-11-112-240-12

Query Match 69.2%; Score 36; DB 7; Length 107;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPPLT 9
|||
Db 89 QOYSNPPLT 97

RESULT 29
US-11-112-304A-12
Sequence 12, Application US/11112304A
Publication No. US20060002931A1
GENERAL INFORMATION:
APPLICANT: AMGEN, INC.
APPLICANT: Smothers, James
APPLICANT: Farnlow, IIT, William C.
APPLICANT: Kariy, Revital
TITLE OF INVENTION: ANTIBODIES OF ANGIOGENESIS INHIBITTING DOMAINS OF CD148
FILE REFERENCE: 3447

CURRENT APPLICATION NUMBER: US/11/112,304A
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/565,158
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/564,885
PRIOR FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/571,566
PRIOR FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: US 60/585,686
PRIOR FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.3
SEQ ID NO 12
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-11-112-304A-12

Query Match 69.2%; Score 36; DB 7; Length 107;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPPLT 9
|||
Db 89 QOYSNPPLT 97

RESULT 30
US-10-771-257-78
Sequence 78, Application US/10771257
Publication No. US20050288864A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Sissa - Scuola Superiore Internazionale di Studi Avanzati
APPLICANT: Cattaneo, Antonio
APPLICANT: Maritan, Amos
APPLICANT: Visintin, Michela
APPLICANT: Rabbitts, Terrence H
APPLICANT: Settlani, Giovanni
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2272
CURRENT APPLICATION NUMBER: US/10/771,257
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: PCT/GB02/03512
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: GB 0119004.0
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: GB 0121577.1
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: GB 0200928.0
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: GB 0203569.9
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: IT RM2001A000633
PRIOR FILING DATE: 2001-10-25
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.1
SEQ ID NO 78
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-10-771-257-78

Query Match 69.2%; Score 36; DB 6; Length 108;
Best Local Similarity 77.8%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOHNEYPPLT 9
|||
Db 89 QOLNSYPLT 97

RESULT 31

US-11-127-677-76
; Sequence 76, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbits, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-76

Query Match 69.2%; Score 36; DB 7; Length 108;
Best Local Similarity 77.8%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOHNRYPLT 9
||:||||
DB 89 QOLNSYPLT 97

RESULT 32
US-11-097-812-45
; Sequence 45, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 108
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-45

Query Match 69.2%; Score 36; DB 7; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNRYPLT 9
||:||||
DB 88 QOYSSYPLT 96

RESULT 33
US-11-097-812-46
; Sequence 46, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 108
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-50

Query Match 69.2%; Score 36; DB 7; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNRYPLT 9
||:||||
DB 88 QOYSSYPLT 96

RESULT 34
US-11-097-812-50
; Sequence 50, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 108
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-50

Query Match 69.2%; Score 36; DB 7; Length 108;

Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNEYPPLT 9
|::|||
Db 88 QOYSSYPPLT 96

RESULT 35

US-11-097-812-51
; Sequence 51, Application US/11097812
; Publication No. US20050281828A1

; GENERAL INFORMATION:

; APPLICANT: Kretz-Rommel, Anke

; APPLICANT: Dakappagari, Naveen

; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN

; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)

; CURRENT APPLICATION NUMBER: US/11/097,812

; CURRENT FILING DATE: 2005-04-01

; PRIOR APPLICATION NUMBER: US 11/016,647

; PRIOR FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: PCT/US04/06570

; PRIOR FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: US 60/548,385

; PRIOR FILING DATE: 2004-02-28

; PRIOR APPLICATION NUMBER: US 60/529,500

; PRIOR FILING DATE: 2003-12-15

; PRIOR APPLICATION NUMBER: US 60/451,816

; PRIOR FILING DATE: 2003-03-04

; NUMBER OF SEQ ID NOS: 207

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 51

; LENGTH: 108

; TYPE: PRT

; ORGANISM: mouse

US-11-097-812-51

Query Match 69.2%; Score 36; DB 7; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNEYPPLT 9
|::|||
Db 89 QOYSSYPPLT 97

RESULT 36

US-11-097-812-52
; Sequence 52, Application US/11097812

; Publication No. US20050281828A1

; GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Kretz-Rommel, Anke

; APPLICANT: Dakappagari, Naveen

; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN

; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)

; CURRENT APPLICATION NUMBER: US/11/097,812

; CURRENT FILING DATE: 2005-04-01

; PRIOR APPLICATION NUMBER: US 11/016,647

; PRIOR FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: PCT/US04/06570

; PRIOR FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: US 60/548,385

; PRIOR FILING DATE: 2004-02-28

; PRIOR APPLICATION NUMBER: US 60/529,500

; PRIOR FILING DATE: 2003-12-15

; PRIOR APPLICATION NUMBER: US 60/451,816

; PRIOR FILING DATE: 2003-03-04

; NUMBER OF SEQ ID NOS: 207

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 52
; LENGTH: 108
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-52

Query Match 69.2%; Score 36; DB 7; Length 108;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNEYPPLT 9
|::|||
Db 88 QOYSSYPPLT 96

RESULT 37

US-11-097-812-37
; Sequence 37, Application US/11097812

; Publication No. US20050281828A1

; GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Kretz-Rommel, Anke

; APPLICANT: Dakappagari, Naveen

; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN

; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)

; CURRENT APPLICATION NUMBER: US/11/097,812

; CURRENT FILING DATE: 2005-04-01

; PRIOR APPLICATION NUMBER: US 11/016,647

; PRIOR FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: PCT/US04/06570

; PRIOR FILING DATE: 2004-03-04

; PRIOR APPLICATION NUMBER: US 60/548,385

; PRIOR FILING DATE: 2004-02-28

; PRIOR APPLICATION NUMBER: US 60/529,500

; PRIOR FILING DATE: 2003-12-15

; PRIOR APPLICATION NUMBER: US 60/451,816

; PRIOR FILING DATE: 2003-03-04

; NUMBER OF SEQ ID NOS: 207

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 37

; LENGTH: 109

; TYPE: PRT

; ORGANISM: artificial sequence

; OTHER INFORMATION: majority antibody sequence

US-11-097-812-37

Query Match 69.2%; Score 36; DB 7; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOHNEYPPLT 9
|::|||
Db 89 QOYSSYPPLT 97

RESULT 38

US-11-097-812-42
; Sequence 42, Application US/11097812

; Publication No. US20050281828A1

; GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Kretz-Rommel, Anke

; APPLICANT: Dakappagari, Naveen

; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN

; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)

; CURRENT APPLICATION NUMBER: US/11/097,812

; CURRENT FILING DATE: 2005-04-01

; PRIOR APPLICATION NUMBER: US 11/016,647

; PRIOR FILING DATE: 2004-12-17

; PRIOR APPLICATION NUMBER: PCT/US04/06570

```

; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-42
```

```

Query Match          69.2%; Score 36; DB 7; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 0QHNEYPLT 9
        ||::|||
Db      89 QOYSSYPLT 97
```

```

RESULT 39
US-11-097-812-43
; Sequence 43, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakapagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-43
```

```

Query Match          69.2%; Score 36; DB 7; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 0QHNEYPLT 9
        ||::|||
Db      89 QOYSSYPLT 97
```

```

RESULT 40
US-11-097-812-48
; Sequence 48, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakapagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
```

```

; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-48
```

```

Query Match          69.2%; Score 36; DB 7; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 0QHNEYPLT 9
        ||::|||
Db      89 QOYSSYPLT 97
```

```

RESULT 41
US-11-097-812-54
; Sequence 54, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakapagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-54
```

```

Query Match          69.2%; Score 36; DB 7; Length 109;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 0QHNEYPLT 9
        ||::|||
Db      89 QOYSSYPLT 97
```

```

RESULT 42
US-11-097-812-38
```

```
; Sequence 38, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 38
; LENGTH: 115
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-38
```

```
Query Match          69.2%; Score 36; DB 7; Length 115;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 QHNEYPLT 9
||: |||
Db 88 QOYSSYPLT 96
```

```
RESULT 43
US-11-144-248-2
; Sequence 2, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-2
```

```
Query Match          69.2%; Score 36; DB 7; Length 136;
Best Local Similarity 75.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 QHNEYPLT 9
||| |||
Db 78 QHNNYPT 85
```

```
RESULT 44
US-11-144-222-2
; Sequence 2, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Beebe, Jean
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-222-2
```

```
Query Match          69.2%; Score 36; DB 7; Length 136;
Best Local Similarity 75.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 QHNEYPLT 9
||| |||
Db 78 QHNNYPT 85
```

```
RESULT 45
US-11-144-248-51
; Sequence 51, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 51
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-51
```

```
Query Match          69.2%; Score 36; DB 7; Length 236;
Best Local Similarity 75.0%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 QHNEYPLT 9
||| |||
Db 112 QHNNYPT 119
```


RESULT 46
US-11-144-248-52
; Sequence 52, Application US/11144222
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-52

Query Match 69.2%; Score 36; DB 7; Length 236;
Best Local Similarity 75.0%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QHNEYPLT 9
Db 112 QHNSYFMT 119

RESULT 47
US-11-144-222-51
; Sequence 51, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-222-51

Query Match 69.2%; Score 36; DB 7; Length 236;
Best Local Similarity 75.0%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QHNEYPLT 9
Db 112 QHNSYFMT 119

RESULT 48

US-11-144-222-52
; Sequence 52, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-222-52

Query Match 69.2%; Score 36; DB 7; Length 236;
Best Local Similarity 75.0%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 QHNEYPLT 9
Db 112 QHNSYFMT 119

RESULT 49
US-11-054-515-1882
; Sequence 1882, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1882
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1882

Query Match 69.2%; Score 36; DB 7; Length 239;
Best Local Similarity 66.7%; Pred. No. 3.6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 220 QOYSNYPLT 228

RESULT 50

US-11-054-515-1922
; Sequence 1922, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1922
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1922

Query Match 69.2%; Score 36; DB 7; Length 239;
Best Local Similarity 66.7%; Pred. No. 3.6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOHNEYPLT 9
||: ||||
Db 220 QOYSNYPLT 228

Search completed: January 17, 2006, 12:13:36
Job time : 4 secs